

Db 89 KENLKGKTG 97

RESULT 7
US-10-668-767-2

Sequence 2, Application US/10668767
GENERAL INFORMATION:
APPLICANT: Caspar, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Guttridge, Steven
APPLICANT: Rauh, James
APPLICANT: Smith, Rejane
APPLICANT: Tao, Yong
APPLICANT: Wu, Lihong
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
FILE REFERENCE: B1513 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/427,324
PRIOR FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 5142
TYPE: PRT
ORGANISM: Heliothis virescens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1755)..(1755)
OTHER INFORMATION: Xaa = Ser
FEATURE:
NAME/KEY: misc feature
LOCATION: (4250)..(4250)
OTHER INFORMATION: Xaa = Thr
US-10-668-767-2

Query Match 70.2%; Score 33; DB 6; Length 5142;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDNVKGVTG 9
Db 89 KENLKGKTG 97

RESULT 8
US-10-668-767-144

Sequence 144, Application US/10668767
GENERAL INFORMATION:
APPLICANT: Caspar, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Guttridge, Steven
APPLICANT: Rauh, James
APPLICANT: Smith, Rejane
APPLICANT: Tao, Yong
APPLICANT: Wu, Lihong
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
FILE REFERENCE: B1513 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/427,324
PRIOR FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 144
LENGTH: 5142
TYPE: PRT
ORGANISM: Heliothis virescens

FEATURE:
OTHER INFORMATION: PXL-HV3
US-10-668-767-144

Query Match 70.2%; Score 33; DB 6; Length 5142;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDNVKGVTG 9
Db 89 KENLKGKTG 97

RESULT 9
PCT-US03-21379-80

Sequence 80, Application PC/TUS0321379
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MCHKS AS MODIFIERS OF THE CHK1 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX03-047C-PC
CURRENT APPLICATION NUMBER: PCT/US03/21379
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 60/394,845
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/410,986
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.2
SEQ ID NO 80
LENGTH: 6669
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-21379-80

Query Match 70.2%; Score 33; DB 1; Length 6669;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDNVKGVT 8
Db 6310 KENVGRAT 6317

RESULT 10
US-09-897-516A-4963

Sequence 4963, Application US/09897516A
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hueising, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 4963
LENGTH: 295
TYPE: PRT
ORGANISM: Xenorhabdus sp.
US-09-897-516A-4963

Query Match 68.1%; Score 32; DB 5; Length 295;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KDNVKGVTG 9

Db 159 KINIGKXVG 167

RESULT 11

US-10-425-114A-42903

Sequence 42903, Application US/10425114A

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 42903

LENGTH: 399

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700475408_Flti.pep

US-10-425-114A-42903

Query Match 68.1%; Score 32; DB 6; Length 399;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVGVYTG 9

Db 324 KDNIGKGG 332

RESULT 12

US-10-374-903A-13

Sequence 13, Application US/10374903A

GENERAL INFORMATION:

APPLICANT: University of Oviedo

APPLICANT: Astur Pharma, S.A.

TITLE OF INVENTION: The gene cluster for thienamycin biosynthesis,

FILE REFERENCE: Thienamycin-NO-AP

CURRENT APPLICATION NUMBER: US/10/374,903A

CURRENT FILING DATE: 2003-02-26

NUMBER OF SEQ ID NOS: 33

SEQ ID NO 13

LENGTH: 483

TYPE: PRT

ORGANISM: Streptomyces cattleya

US-10-374-903A-13

Query Match 68.1%; Score 32; DB 6; Length 483;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVGVYTG 9

Db 226 RDGIGSVTG 234

RESULT 13

US-60-478-196-3183

Sequence 3183, Application US/60478196

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Lemieux, Sebastien

APPLICANT: Hu, Wengqi

APPLICANT: Roemer, Terry

TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND ME

TITLE OF INVENTION: USE

FILE REFERENCE: 10182-026-888

CURRENT APPLICATION NUMBER: US/60/478,196

CURRENT FILING DATE: 2003-06-13

NUMBER OF SEQ ID NOS: 4000

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3183

LENGTH: 490

TYPE: PRT

ORGANISM: Aspergillus fumigatus

US-60-478-196-3183

Query Match 68.1%; Score 32; DB 7; Length 490;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVGVYTG 9

Db 451 DNMGVKNTG 458

RESULT 14

US-09-897-516A-7143

Sequence 7143, Application US/09897516A

GENERAL INFORMATION:

APPLICANT: Corbin, David R.

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Huesing, Joseph E.

APPLICANT: Malvar, Thomas M.

APPLICANT: Krasomil-Osterfeld, Karina C.

APPLICANT: Slater, Steven C.

APPLICANT: Spiridonov, Sergei

TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof

FILE REFERENCE: 38-21(51847)B

CURRENT APPLICATION NUMBER: US/09/897,516A

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/215,161

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 8415

SEQ ID NO 7143

LENGTH: 570

TYPE: PRT

ORGANISM: Xenorhabdus sp.

US-09-897-516A-7143

Query Match 68.1%; Score 32; DB 5; Length 570;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDNVGVYTG 9

Db 480 KDSDGKLTG 488

RESULT 15

US-10-425-114A-71443

Sequence 71443, Application US/10425114A

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 71443

LENGTH: 594

TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73247B01_FLI.pep
US-10-425-114A-71443

Query Match 68.1%; Score 32; DB 6; Length 594;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 KDNVGVKVTG 9
Db 519 KDNIGKGGG 527

Search completed: October 15, 2003, 17:42:36
Job time : 5.04192 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:57:11 ; Search time 128.97 Seconds
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77.608 Million cell updates/sec

Title: US-09-555-115A-9
Perfect score: 66
Sequence: 1 CAGGTPTNTAC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	19	US-09-555-115A-9

2	66	100.0	82	12	US-08-882-431B-17	Sequence 17, Appl
3	66 <th>100.0</th> <td>82</td> <td>12</td> <td>US-08-882-431B-19</td> <td>Sequence 19, Appl</td>	100.0	82	12	US-08-882-431B-19	Sequence 19, Appl
4	66 <th>100.0</th> <td>82</td> <td>26</td> <td>US-10-002-784A-32</td> <td>Sequence 32, Appl</td>	100.0	82	26	US-10-002-784A-32	Sequence 32, Appl
5	66 <th>100.0</th> <td>82</td> <td>26</td> <td>US-10-002-784A-34</td> <td>Sequence 34, Appl</td>	100.0	82	26	US-10-002-784A-34	Sequence 34, Appl
6	66 <th>100.0</th> <td>226</td> <td>8</td> <td>US-08-491-746-23</td> <td>Sequence 23, Appl</td>	100.0	226	8	US-08-491-746-23	Sequence 23, Appl
7	66 <th>100.0</th> <td>226</td> <td>21</td> <td>US-09-708-008B-24</td> <td>Sequence 24, Appl</td>	100.0	226	21	US-09-708-008B-24	Sequence 24, Appl
8	66 <th>100.0</th> <td>227</td> <td>23</td> <td>US-08-869-136-11</td> <td>Sequence 11, Appl</td>	100.0	227	23	US-08-869-136-11	Sequence 11, Appl
9	66 <th>100.0</th> <td>230</td> <td>9</td> <td>US-08-551-277-5</td> <td>Sequence 5, Appl</td>	100.0	230	9	US-08-551-277-5	Sequence 5, Appl
10	66 <th>100.0</th> <td>232</td> <td>8</td> <td>US-08-491-746-22</td> <td>Sequence 22, Appl</td>	100.0	232	8	US-08-491-746-22	Sequence 22, Appl
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12	66 <th>100.0</th> <td>233</td> <td>1</td> <td>PCT-US96-07432A-4</td> <td>Sequence 4, Appl</td>	100.0	233	1	PCT-US96-07432A-4	Sequence 4, Appl
13	66 <th>100.0</th> <td>233</td> <td>1</td> <td>PCT-US98-16766-4</td> <td>Sequence 4, Appl</td>	100.0	233	1	PCT-US98-16766-4	Sequence 4, Appl
14	66 <th>100.0</th> <td>233</td> <td>9</td> <td>US-08-551-277-4</td> <td>Sequence 4, Appl</td>	100.0	233	9	US-08-551-277-4	Sequence 4, Appl
15	66 <th>100.0</th> <td>233</td> <td>12</td> <td>US-08-882-431A-4</td> <td>Sequence 4, Appl</td>	100.0	233	12	US-08-882-431A-4	Sequence 4, Appl
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18	66 <th>100.0</th> <td>233</td> <td>17</td> <td>US-09-339-552-4</td> <td>Sequence 4, Appl</td>	100.0	233	17	US-09-339-552-4	Sequence 4, Appl
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20	66 <th>100.0</th> <td>233</td> <td>22</td> <td>US-09-791-537-17287</td> <td>Sequence 17287, A</td>	100.0	233	22	US-09-791-537-17287	Sequence 17287, A
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22	66 <th>100.0</th> <td>233</td> <td>24</td> <td>US-09-900-766-3</td> <td>Sequence 2, Appl</td>	100.0	233	24	US-09-900-766-3	Sequence 2, Appl
23	66 <th>100.0</th> <td>233</td> <td>24</td> <td>US-09-900-766-4</td> <td>Sequence 3, Appl</td>	100.0	233	24	US-09-900-766-4	Sequence 3, Appl
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26	66 <th>100.0</th> <td>233</td> <td>26</td> <td>US-10-283-838-7</td> <td>Sequence 4, Appl</td>	100.0	233	26	US-10-283-838-7	Sequence 4, Appl
27	66 <th>100.0</th> <td>233</td> <td>28</td> <td>US-10-283-838-8</td> <td>Sequence 8, Appl</td>	100.0	233	28	US-10-283-838-8	Sequence 8, Appl
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30	66 <th>100.0</th> <td>248</td> <td>23</td> <td>US-09-870-759-16</td> <td>Sequence 16, Appl</td>	100.0	248	23	US-09-870-759-16	Sequence 16, Appl
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32	66 <th>100.0</th> <td>257</td> <td>7</td> <td>US-08-360-107-123</td> <td>Sequence 123, Appl</td>	100.0	257	7	US-08-360-107-123	Sequence 123, Appl
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34	66 <th>100.0</th> <td>257</td> <td>8</td> <td>US-08-471-913-113</td> <td>Sequence 113, Appl</td>	100.0	257	8	US-08-471-913-113	Sequence 113, Appl
35	66 <th>100.0</th> <td>257</td> <td>8</td> <td>US-08-475-668-112</td> <td>Sequence 112, Appl</td>	100.0	257	8	US-08-475-668-112	Sequence 112, Appl
36	66 <th>100.0</th> <td>257</td> <td>8</td> <td>US-08-475-668-113</td> <td>Sequence 113, Appl</td>	100.0	257	8	US-08-475-668-113	Sequence 113, Appl
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43	66 <th>100.0</th> <td>257</td> <td>8</td> <td>US-08-485-551-112</td> <td>Sequence 112, Appl</td>	100.0	257	8	US-08-485-551-112	Sequence 112, Appl
44	66 <th>100.0</th> <td>257</td> <td>8</td> <td>US-08-485-551-113</td> <td>Sequence 113, Appl</td>	100.0	257	8	US-08-485-551-113	Sequence 113, Appl
45	66 <th>100.0</th> <td>257</td> <td>8</td> <td>US-08-487-266-112</td> <td>Sequence 112, Appl</td>	100.0	257	8	US-08-487-266-112	Sequence 112, Appl

ALIGNMENTS

RESULT 1
US-09-555-115A-9
; Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136 USWO
; CURRENT APPLICATION NUMBER: US/09/555, 115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067, 357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-9

Query Match 100.0%; Score 66; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
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Db 1 CAGGTPNKTAC 11

RESULT 2

US-08-882-431B-17
; Sequence 17, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-2065
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-17

Query Match 100.0%; Score 66; DB 12; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||
Db 54 CAGGTPNKTAC 64

RESULT 3
US-08-882-431B-19
; Sequence 19, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-19

Query Match 100.0%; Score 66; DB 12; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||
Db 54 CAGGTPNKTAC 64

RESULT 4
US-10-002-784A-32
; Sequence 32, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin A
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match 100.0%; Score 66; DB 26; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||
Db 54 CAGGTPNKTAC 64

RESULT 5

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US-10-002-784A-34
; Sequence 34, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 34
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin E
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-34

Query Match      100.0%; Score 66; DB 26; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTPNKTAC 11
      |||||
Db      54 CAGGTPNKTAC 64

RESULT 6
US-08-491-746-23
; Sequence 23, Application US/08491746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
; FILE REFERENCE: 09629/006002
; CURRENT APPLICATION NUMBER: US/08/491,746
; PRIOR FILING DATE: 1995-06-19
; EARLIER APPLICATION NUMBER: 08/189,424
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/025,144
; EARLIER FILING DATE: 1993-03-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: PCT/US91/00342
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-491-746-23

Query Match      100.0%; Score 66; DB 8; Length 226;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTPNKTAC 11
      |||||
Db      93 CAGGTPNKTAC 103

RESULT 7
US-09-708-008B-24
; Sequence 24, Application US/09708008B
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS

```

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; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-24

Query Match      100.0%; Score 66; DB 21; Length 226;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTPNKTAC 11
      |||||
Db      93 CAGGTPNKTAC 103

RESULT 8
US-09-869-136-11
; Sequence 11, Application US/09869136
; GENERAL INFORMATION:
; APPLICANT: FRASER, JOHN DAVID
; APPLICANT: PROFT, THOMAS
; TITLE OF INVENTION: SUPERANTIGENS
; FILE REFERENCE: 3911-8
; CURRENT APPLICATION NUMBER: US/09/869,136
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/NZ99/00228
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: NZ 333589
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Superantigen
; OTHER INFORMATION: peptide sequence
US-09-869-136-11

Query Match      100.0%; Score 66; DB 23; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTPNKTAC 11
      |||||
Db      95 CAGGTPNKTAC 105

RESULT 9
US-08-551-277-5
; Sequence 5, Application US/08551277
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Zadriskie, John B.
; TITLE OF INVENTION: STAPHYLOCOCCAL EXOTOXIN ASSOCIATED WITH
; TITLE OF INVENTION: TOXIC SHOCK SYNDROME AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey

```

```
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,277
FILING DATE: 31-OCT-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
IMMEDIATE SOURCE:
CLONE: SEE
US-08-551-277-5

Query Match          100.0%; Score 66; DB 9; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CAGGTPNKTAC 11
Db      93 CAGGTPNKTAC 103
```

```
RESULT 10
US-08-491-746-22
Sequence 22, Application US/08491746
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: METHOD OF CANCER TREATMENT
FILE REFERENCE: 09629/006002
CURRENT APPLICATION NUMBER: US/08/491,746
CURRENT FILING DATE: 1995-06-19
EARLIER APPLICATION NUMBER: 08/189,424
EARLIER FILING DATE: 1994-01-31
EARLIER APPLICATION NUMBER: 08/025,144
EARLIER FILING DATE: 1993-03-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: PCT/US91/00342
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 232
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-491-746-22
```

```
Query Match          100.0%; Score 66; DB 8; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CAGGTPNKTAC 11
Db      95 CAGGTPNKTAC 105
```

```
RESULT 11
US-09-708-008B-23
Sequence 23, Application US/09708008B
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US/08/896,933
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 08/252,978
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 232
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-708-008B-23
```

```
Query Match          100.0%; Score 66; DB 21; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CAGGTPNKTAC 11
Db      95 CAGGTPNKTAC 105
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RESULT 12
PCT-US96-07432A-4
Sequence 4, Application PC/TUS9607432A
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmelle, Robyn E.
APPLICANT: Pottery, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07432A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-0223
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07432A-4

Query Match 100.0%; Score 66; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTPNKATC 11
Db 96 CAGGTPNKATC 106

RESULT 13
PCT-US98-16766-4
Sequence 4, Application PC/TUS9816766
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/16766
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ. ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
PCT-US98-16766-4

MCMR-JA (John)

Query Match 100.0%; Score 66; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTPNKATC 11
Db 96 CAGGTPNKATC 106

RESULT 14
US-08-551-277-4
Sequence 4, Application US/08551277
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.

APPLICANT: Zabrickie, John B.
TITLE OF INVENTION: STAPHYLOCOCCAL EXOTOXIN ASSOCIATED WITH
TITLE OF INVENTION: TOXIC SHOCK SYNDROME AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,277
FILING DATE: 31-OCT-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ. ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
IMMEDIATE SOURCE:
CLONE: SEA
US-08-551-277-4

Query Match 100.0%; Score 66; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTPNKATC 11
Db 96 CAGGTPNKATC 106

RESULT 15
US-08-882-431-4
Sequence 4, Application US/08882431
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 100.0%; Score 66; DB 12; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGTPNKTAC 11
Db 96 CAGGTPNKTAC 106

Search completed: October 15, 2003, 17:41:14
Job time : 129.97 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 4.94012 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-9
Perfect score: 66
Sequence: 1 CAGGTPNKTKAC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues
Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New:*
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3: /cgn2_6/ptodaca/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodaca/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodaca/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodaca/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodaca/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	233	1 PCT-US03-20322-226	Sequence 226, App
2	66	100.0	252	5 US-09-350-841A-1599	Sequence 1599, Ap
3	57	86.4	254	5 US-09-350-841A-1598	Sequence 1598, Ap
4	54	81.8	300	6 US-10-425-114A-70954	Sequence 70954, A
5	45	68.2	184	5 US-09-936-271B-57	Sequence 57, Appl
6	45	68.2	247	7 US-60-495-114-1210	Sequence 1210, Ap
7	45	68.2	248	5 US-09-936-271B-60	Sequence 60, Appl
8	45	68.2	248	5 US-60-495-114-1213	Sequence 1213, Ap
9	45	68.2	254	5 US-09-936-271B-59	Sequence 59, Appl
10	45	68.2	254	7 US-60-495-114-1211	Sequence 1211, Ap
11	44	66.7	804	1 PCT-US03-26780-3289	Sequence 3289, Ap
12	44	66.7	5820	1 PCT-US03-26780-3116	Sequence 3116, Ap
13	44	66.7	8973	1 PCT-US03-26780-3117	Sequence 3117, Ap
14	43	65.2	643	1 PCT-US03-26780-2512	Sequence 2512, Ap
15	43	65.2	976	1 PCT-US03-26780-2686	Sequence 2686, Ap
16	42	63.6	444	1 PCT-US03-26780-3476	Sequence 3476, Ap
17	42	63.6	1010	1 PCT-US03-26780-3294	Sequence 3294, Ap
18	42	63.6	2454	1 PCT-US03-26780-2467	Sequence 2467, Ap
19	41	62.1	294	1 PCT-US03-26780-3074	Sequence 3074, Ap
20	41	62.1	399	1 PCT-US03-26780-3315	Sequence 3315, Ap
21	41	62.1	414	1 PCT-US03-26780-3475	Sequence 3475, Ap
22	41	62.1	933	1 PCT-US03-26780-3484	Sequence 3484, Ap
23	41	62.1	939	1 PCT-US03-26780-2724	Sequence 2724, Ap
24	41	62.1	1305	1 PCT-US03-26780-3387	Sequence 3387, Ap
25	41	62.1	1314	1 PCT-US03-26780-3195	Sequence 3195, Ap
26	41	62.1	1456	1 PCT-US03-26780-2921	Sequence 2921, Ap

27	41	62.1	1683	7 US-60-470-920-38	Sequence 38, Appl
28	41	62.1	5357	1 PCT-US03-26780-3066	Sequence 3066, Ap
29	41	62.1	5546	6 US-10-296-734-1210	Sequence 1210, Ap
30	41	62.1	6729	1 PCT-US03-26780-3358	Sequence 3358, Ap
31	41	62.1	11328	1 PCT-US03-26780-3308	Sequence 3308, Ap
32	40	60.6	204	1 PCT-US03-26780-3418	Sequence 3418, Ap
33	40	60.6	204	1 PCT-US03-26780-3419	Sequence 3419, Ap
34	40	60.6	204	1 PCT-US03-26780-3420	Sequence 3420, Ap
35	40	60.6	204	1 PCT-US03-26780-3422	Sequence 3422, Ap
36	40	60.6	231	1 PCT-US03-26780-2627	Sequence 2627, Ap
37	40	60.6	231	1 PCT-US03-26780-2630	Sequence 2630, Ap
38	40	60.6	480	1 PCT-US03-26780-3482	Sequence 3482, Ap
39	40	60.6	610	1 PCT-US03-26780-3262	Sequence 3262, Ap
40	40	60.6	638	1 PCT-US03-26780-2511	Sequence 2511, Ap
41	40	60.6	903	1 PCT-US03-26780-3292	Sequence 3292, Ap
42	40	60.6	1128	1 PCT-US03-26780-2481	Sequence 2481, Ap
43	40	60.6	1380	1 PCT-US03-26780-3564	Sequence 3564, Ap
44	40	60.6	1518	1 PCT-US03-26780-3530	Sequence 3530, Ap
45	40	60.6	1551	5 US-09-674-546A-1832	Sequence 1832, Ap

ALIGNMENTS

RESULT 1
PCT-US03-20322-226
Sequence 226, Application PC/TUS0320322
GENERAL INFORMATION:
APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
FILE REFERENCE: DFN-043PC
CURRENT APPLICATION NUMBER: PCT/US03/20322
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 226
LENGTH: 233
TYPE: PRT
ORGANISM: Staphylococcus aureus
PCT-US03-20322-226

Query Match 100.0%; Score 66; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

Cy 1 CAGGTPNKTKAC 11
Db 96 CAGGTPNKTKAC 106

RESULT 2
US-09-350-841A-1599
Sequence 1599, Application US/09350841A
GENERAL INFORMATION:
APPLICANT: Jeffers, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
FILE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1599
LENGTH: 252
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1599
Query Match 100.0%; Score 66; DB 5; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTTPNKTAC 11
|||||
Db 116 CAGTTPNKTAC 126

RESULT 3
US-09-350-841A-1598
; Sequence 1598, Application US/09350841A
; GENERAL INFORMATION:
; APPLICANT: Jettis, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match 86.4%; Score 57; DB 5; Length 254;
Best Local Similarity 81.8%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGTTPNKTAC 11
|||||
Db 117 CAGTTPNKTAC 127

RESULT 4
US-10-425-114A-70954
; Sequence 70954, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70954
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17005E04_FLI pep
US-10-425-114A-70954

Query Match 81.8%; Score 54; DB 6; Length 300;
Best Local Similarity 81.8%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGTTPNKTAC 11
|||||
Db 103 CAGGAPNVTAC 113

RESULT 5
US-09-936-271B-57
; Sequence 57, Application US/09936271B
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios

; TITLE OF INVENTION: Novel Human Kallikrein-Like Genes
; FILE REFERENCE: MTS3USA
; CURRENT APPLICATION NUMBER: US/09/936,271B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/CA00/00258
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/124,260
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/127,386
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: US 60/144,919
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-936-271B-57

Query Match 68.2%; Score 45; DB 5; Length 184;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGTTPNKTAC 11
|||||
Db 173 CAGGVPQDQAC 183

RESULT 6
US-60-495-114-1210
; Sequence 1210, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1210
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1210

Query Match 68.2%; Score 45; DB 7; Length 247;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGTTPNKTAC 11
|||||
Db 185 CAGGVPQDQAC 195

RESULT 7
US-09-936-271B-60
; Sequence 60, Application US/09936271B
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios
; TITLE OF INVENTION: Novel Human Kallikrein-Like Genes
; FILE REFERENCE: MTS3USA
; CURRENT APPLICATION NUMBER: US/09/936,271B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/CA00/00258
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/124,260
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/127,386
; PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: US 60/144,919
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 60
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-09-936-271B-60

Query Match 68.2%; Score 45; DB 5; Length 248;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGTPTKAC 11
||| | : ||
Db 186 CAGVPGQDAC 196

RESULT 8
US-60-495-114-1213
Sequence 1213, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
FILE REFERENCE: CLO01480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1213
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1213

Query Match 68.2%; Score 45; DB 7; Length 248;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGTPTKAC 11
||| | : ||
Db 186 CAGVPGQDAC 196

RESULT 9
US-09-936-271B-59
Sequence 59, Application US/09936271B
GENERAL INFORMATION:
APPLICANT: Yousef, George M.
TITLE OF INVENTION: Novel Human Kallikrein-Like Genes
FILE REFERENCE: MTS3USA
CURRENT APPLICATION NUMBER: US/09/936,271B
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/CA00/00258
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,260
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/127,386
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US 60/144,919
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-09-936-271B-59

Query Match 68.2%; Score 45; DB 5; Length 254;
Best Local Similarity 63.6%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGTPTKAC 11
||| | : ||
Db 186 CAGVPGQDAC 196

RESULT 10
US-60-495-114-1211
Sequence 1211, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
FILE REFERENCE: CLO01480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1211
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1211

Query Match 68.2%; Score 45; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGTPTKAC 11
||| | : ||
Db 186 CAGVPGQDAC 196

RESULT 11
PCT-US03-26780-3289
Sequence 3289, Application PC/TUS0326780
GENERAL INFORMATION:
APPLICANT: FIVEPRIME THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
FILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PCT/US03/26780
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: 60/406,616
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,579
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,655
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,642
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,640
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,588
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,576
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,646
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3700
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3289
LENGTH: 804
TYPE: PRT

```

; ORGANISM: Homo sapiens
PCT-US03-26780-3289

Query Match      66.7%; Score 44; DB 1; Length 804;
Best Local Similarity 72.7%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAGGTPNKAC 11
      |||||
Db      92 CAGGTACTAC 102

RESULT 12
PCT-US03-26780-3116
; Sequence 3116, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3116
; LENGTH: 5820
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-3116

Query Match      66.7%; Score 44; DB 1; Length 5820;
Best Local Similarity 72.7%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAGGTPNKAC 11
      |||||
Db      4055 CAGGTACTAC 4065

RESULT 13
PCT-US03-26780-3117
; Sequence 3117, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2512
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-2512

Query Match      66.7%; Score 44; DB 1; Length 8973;
Best Local Similarity 72.7%; Pred. No. 1.5e+03;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAGGTPNKAC 11
      |||||
Db      4076 CAGGTACTAC 4086

RESULT 14
PCT-US03-26780-2512
; Sequence 2512, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
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; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2512
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-2512
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Query Match 65.2%; Score 43; DB 1; Length 643;
Best Local Similarity 72.7%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTPNKTTAC 11
|||||
Db 546 CAGGTGTCTAC 556

RESULT 15

PCT-US03-26780-2686
; Sequence 2686, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2686
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-2686

Query Match 65.2%; Score 43; DB 1; Length 976;
Best Local Similarity 72.7%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTPNKTTAC 11
|||||
Db 921 CAGGTGTCTAC 931

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OM protein - protein search, using SW model

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Title: US-09-555-115A-10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	121	100.0	21	US-09-555-115A-10	Sequence 10, Appl

2	113	93.4	89	12	US-08-882-431B-20	Sequence 20, Appl
3	113	93.4	89	26	US-10-002-784A-35	Sequence 35, Appl
4	113	93.4	165	25	US-09-611-529-5670	Sequence 5670, Ap
5	113	93.4	165	25	US-09-950-084-5670	Sequence 5670, Ap
6	113	93.4	238	22	US-09-791-537-119781	Sequence 119781,
7	113	93.4	239	8	US-08-491-746-25	Sequence 25, Appl
8	113	93.4	239	21	US-09-708-008B-26	Sequence 26, Appl
9	113	93.4	239	22	US-09-791-537-68519	Sequence 88519, A
10	113	93.4	255	17	PCT-US96-07432A-2	Sequence 2, Appl
11	113	93.4	255	17	US-09-339-552-2	Sequence 2, Appl
12	113	93.4	255	29	US-10-354-948-2	Sequence 2, Appl
13	113	93.4	265	1	PCT-US98-16766-6	Sequence 6, Appl
14	113	93.4	265	12	US-08-882-431-6	Sequence 6, Appl
15	113	93.4	266	12	US-08-882-431A-6	Sequence 6, Appl
16	113	93.4	266	12	US-08-882-431B-6	Sequence 6, Appl
17	113	93.4	266	22	US-09-751-708A-10	Sequence 10, Appl
18	113	93.4	266	22	US-09-791-537-94052	Sequence 94052, A
19	113	93.4	266	23	US-09-870-759-10	Sequence 10, Appl
20	113	93.4	266	26	US-10-002-784A-6	Sequence 6, Appl
21	113	93.4	266	27	US-10-151-336-8	Sequence 8, Appl
22	110	90.9	239	15	US-09-150-947B-12	Sequence 12, Appl
23	110	90.9	239	15	US-09-150-947F-12	Sequence 12, Appl
24	110	90.9	239	15	US-09-150-947F-12	Sequence 12, Appl
25	110	90.9	239	27	US-10-172-425B-12	Sequence 12, Appl
26	104	86.0	239	1	PCT-US98-16766-10	Sequence 10, Appl
27	104	86.0	239	12	US-08-882-431A-10	Sequence 10, Appl
28	104	86.0	239	12	US-08-882-431A-10	Sequence 10, Appl
29	104	86.0	239	12	US-08-882-431B-10	Sequence 10, Appl
30	104	86.0	239	26	US-10-002-784A-10	Sequence 10, Appl
31	104	86.0	265	1	PCT-US98-16766-8	Sequence 8, Appl
32	104	86.0	265	12	US-08-882-431-8	Sequence 8, Appl
33	104	86.0	266	12	US-08-882-431A-8	Sequence 8, Appl
34	104	86.0	266	12	US-08-882-431B-8	Sequence 8, Appl
35	104	86.0	266	26	US-10-002-784A-8	Sequence 8, Appl
36	95	78.5	239	8	US-08-491-746-21	Sequence 21, Appl
37	95	78.5	239	21	US-09-708-008B-21	Sequence 21, Appl
38	50	41.3	91	30	US-10-421-684-453	Sequence 453, App
39	50	41.3	91	32	US-60-169-340-453	Sequence 453, App
40	49.5	40.9	262	16	US-09-270-767-39925	Sequence 39925, A
41	49.5	40.9	262	16	US-09-270-767-55142	Sequence 55142, A
42	49.5	40.9	262	16	US-09-270-849B-192251	Sequence 192251, A
43	49.5	40.9	321	22	US-09-791-537-46059	Sequence 46059, A
44	49.5	40.9	366	28	US-10-282-122A-71662	Sequence 71662, A
45	49.5	40.9	477	20	US-09-614-150-42126	Sequence 42126, A

ALIGNMENTS

RESULT 1
US-09-555-115A-10
; Sequence 10, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS.
; FILE REFERENCE: 12136_USMO
; CURRENT APPLICATION NUMBER: US/09/555, 115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067, 357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-10

Query Match 100.0%; Score 121, DB 19, Length 21;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; PRIOR FILING DATE: 1996-05-02
 ; PRIOR APPLICATION NUMBER: US 60/020,016
 ; PRIOR FILING DATE: 1996-06-14
 ; NUMBER OF SEQ ID NOS: 7451
 ; SEQ ID NO 5670
 ; LENGTH: 165
 ; TYPE: PRF
 ; ORGANISM: Staphylococcus aureus
 US-09-611-529-5670

Query Match 93.4%; Score 113; DB 20; Length 165;
 Best Local Similarity 95.2%; Pred. No. 2.1e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFSKKTNDINSHQTPKRTK 21
 DB 121 CFSKKTNDINSHQTPKRTK 141

RESULT 5
 US-09-950-084-5670
 ; Sequence 5670, Application US/09950084
 ; GENERAL INFORMATION:
 ; APPLICANT: George H. Shimer, Jr.
 ; APPLICANT: George H. Miller
 ; APPLICANT: Roberta S. Hare
 ; APPLICANT: Karen J. Shaw
 ; TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
 ; FILE REFERENCE: 1034/1C963US2
 ; CURRENT APPLICATION NUMBER: US/09/950,084
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: US 09/417,811
 ; PRIOR FILING DATE: 1999-10-14
 ; PRIOR APPLICATION NUMBER: US 09/353,718
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: US 09/266,557
 ; PRIOR FILING DATE: 1999-03-11
 ; PRIOR APPLICATION NUMBER: US 09/266,556
 ; PRIOR FILING DATE: 1999-03-11
 ; PRIOR APPLICATION NUMBER: US 09/266,555
 ; PRIOR FILING DATE: 1999-03-11
 ; PRIOR APPLICATION NUMBER: US 09/266,542
 ; PRIOR FILING DATE: 1999-03-11
 ; PRIOR APPLICATION NUMBER: US 09/266,541
 ; PRIOR FILING DATE: 1999-03-11
 ; PRIOR APPLICATION NUMBER: US 09/037,934
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: US 09/036,720
 ; PRIOR FILING DATE: 1998-03-06
 ; PRIOR APPLICATION NUMBER: US 09/036,338
 ; PRIOR FILING DATE: 1998-03-06
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 7451
 ; SEQ ID NO 5670
 ; LENGTH: 165
 ; TYPE: PRF
 ; ORGANISM: Staphylococcus aureus
 US-09-950-084-5670

Query Match 93.4%; Score 113; DB 25; Length 165;
 Best Local Similarity 95.2%; Pred. No. 2.1e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFSKKTNDINSHQTPKRTK 21
 DB 121 CFSKKTNDINSHQTPKRTK 141

RESULT 6
 US-09-791-537-119781
 ; Sequence 119781, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 119781
 ; LENGTH: 238
 ; TYPE: PRF
 ; ORGANISM: pdb 3SEB
 US-09-791-537-119781

Query Match 93.4%; Score 113; DB 22; Length 238;
 Best Local Similarity 95.2%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFSKKTNDINSHQTPKRTK 21
 DB 93 CFSKKTNDINSHQTPKRTK 113

RESULT 7
 US-08-491-746-25
 ; Sequence 25, Application US/08491746
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
 ; FILE REFERENCE: 09629/006002
 ; CURRENT APPLICATION NUMBER: US/08/491,746
 ; CURRENT FILING DATE: 1995-06-19
 ; EARLIER APPLICATION NUMBER: 08/189,424
 ; EARLIER FILING DATE: 1994-01-31
 ; EARLIER APPLICATION NUMBER: 08/025,144
 ; EARLIER FILING DATE: 1993-03-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: PCT/US91/00342
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 239
 ; TYPE: PRF
 ; ORGANISM: Staphylococcus aureus
 US-08-491-746-25

Query Match 93.4%; Score 113; DB 8; Length 239;
 Best Local Similarity 95.2%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFSKKTNDINSHQTPKRTK 21
 DB 93 CFSKKTNDINSHQTPKRTK 113

RESULT 8
 US-09-708-008B-26
 ; Sequence 26, Application US/09708008B
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/09/708,008B
 ; CURRENT FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: US/08/896,933
 ; PRIOR FILING DATE: 1997-07-18
 ; PRIOR APPLICATION NUMBER: 08/252,978

PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 239
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-708-008B-26

Query Match 93.4%; Score 113; DB 21; Length 239;
Best Local Similarity 95.2%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSKKTNDINSHQTPRKRTC 21
Db 93 CYFSKKTNDINSHQTPRKRTC 113

RESULT 9
US-09-791-537-88519
Sequence 88519, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomix, Inc.
APPLICANT: Dabe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 88519
LENGTH: 239
TYPE: PRT
ORGANISM: pdb 1SE3
US-09-791-537-88519

Query Match 93.4%; Score 113; DB 22; Length 239;
Best Local Similarity 95.2%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSKKTNDINSHQTPRKRTC 21
Db 93 CYFSKKTNDINSHQTPRKRTC 113

RESULT 10
PCT-US96-07432A-2
Sequence 2, Application PC/TUS9607432A
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL
TITLE OF INVENTION: REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07432A
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07432A-2

Query Match 93.4%; Score 113; DB 1; Length 255;
Best Local Similarity 95.2%; Pred. No. 3.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSKKTNDINSHQTPRKRTC 21
Db 109 CYFSKKTNDINSHQTPRKRTC 129

RESULT 11
US-09-339-552-2
Sequence 2, Application US/09339552
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,552
FILING DATE: 24-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-339-552-2

Query Match 93.4%; Score 113; DB 17; Length 255;
Best Local Similarity 95.2%; Pred. No. 3.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSKKTNDINSHQTPRKRTC 21

Db 109 CYFSKKTNDINSHQTDKRTKC 129

RESULT 12

US-10-354-948-2
Sequence 2, Application US/10354948
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
Elmalle, Robyn E.
Porter, Terence A.

TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match 93.4%; Score 113; DB 29; Length 255;
Best Local Similarity 95.2%; Pred. No. 3,4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTDKRTKC 21
Db 109 CYFSKKTNDINSHQTDKRTKC 129

RESULT 13

PCT-US98-16766-6
Sequence 6, Application PC/RUS9816766
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSER: John Moran
STREET: US Army MRC -504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA

MCMR-JA (John Moran-Patent Atty)

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/16766
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431

FILING DATE: June 25, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Moran, John

REGISTRATION NUMBER: 26,313

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
PCT-US98-16766-6

Query Match 93.4%; Score 113; DB 1; Length 265;
Best Local Similarity 95.2%; Pred. No. 3,6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTDKRTKC 21
Db 120 CYFSKKTNDINSHQTDKRTKC 140

RESULT 14

US-08-882-431-6
Sequence 6, Application US/0882431

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSER: John Moran
STREET: US Army MRC -504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Moran, John

REGISTRATION NUMBER: 26,313

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065

Search completed: October 15, 2003, 17:41:15
Job time : 247.216 secs

TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-6

Query Match 93.4%; Score 113; DB 12; Length 265;
Best Local Similarity 95.2%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSKTTNDINSHOTPKKTC 21
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Db 120 CYFSKTTNDINSHOTDKKTC 140

RESULT 15

US-08-882-431A-6
Sequence 6, Application US/08882431A
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431A
FILING DATE: June 25, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431A-6

Query Match 93.4%; Score 113; DB 12; Length 265;
Best Local Similarity 95.2%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSKTTNDINSHOTPKKTC 21
|||
Db 120 CYFSKTTNDINSHOTDKKTC 140

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 / Search time 9.4314 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-10

Sequence: 1 CYFSKKTNDINSHQTPKRTKC 21

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Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/pcodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/pcodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/pcodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/pcodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/pcodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	37.2	247	6	US-10-652-928-36
2	42.5	35.1	382	5	US-09-714-935A-139
3	41.5	34.3	520	6	US-10-425-114A-38941
4	41	33.9	163	5	US-09-697-516A-8056
5	41	33.9	575	6	US-10-425-114A-72419
6	40	33.1	991	1	PCT-US03-28227-4468
7	40	33.1	1046	1	PCT-US03-14382-78
8	40	33.1	1046	1	PCT-US03-14382A-78
9	40	33.1	1088	7	US-60-500-337-1679
10	40	33.1	1088	7	US-60-500-337-1680
11	40	33.1	1102	7	US-60-490-890-842
12	39.5	32.6	341	1	PCT-US03-24575-8
13	39.5	32.6	621	6	US-10-425-114A-56465
14	39	32.2	239	6	US-10-425-114A-44813
15	39	32.2	286	6	US-10-425-114A-58752
16	39	32.2	511	6	US-10-425-114A-38525
17	39	32.2	712	7	US-60-478-196-3281
18	39	32.2	1616	5	US-09-820-843B-16
19	38.5	31.8	94	6	US-10-425-114A-38107
20	38.5	31.8	1048	6	US-10-392-234A-14
21	38	31.4	39	6	US-10-652-928-66
22	38	31.4	186	6	US-10-425-114A-71673
23	38	31.4	228	6	US-10-425-114A-36973
24	38	31.4	235	7	US-10-425-114A-57432
25	38	31.4	238	7	US-60-500-115-1640
26	38	31.4	242	6	US-10-425-114A-60741

27	38	31.4	245	6	US-10-425-114A-63529	Sequence 63529, A
28	38	31.4	247	6	US-10-425-114A-59436	Sequence 59436, A
29	38	31.4	252	6	US-10-425-114A-66807	Sequence 66807, A
30	38	31.4	253	1	PCT-US03-26780-1753	Sequence 1753, Ap
31	38	31.4	261	6	US-10-425-114A-66215	Sequence 66215, A
32	38	31.4	264	6	US-10-425-114A-44505	Sequence 44505, A
33	38	31.4	266	6	US-10-425-114A-72134	Sequence 72134, A
34	38	31.4	268	6	US-10-425-114A-63145	Sequence 63145, A
35	38	31.4	269	6	US-10-425-114A-50585	Sequence 50585, A
36	38	31.4	269	6	US-10-425-114A-72162	Sequence 72162, A
37	38	31.4	269	6	US-10-425-114A-72180	Sequence 72180, A
38	38	31.4	270	6	US-10-425-114A-60079	Sequence 60079, A
39	38	31.4	274	6	US-10-425-114A-66637	Sequence 66637, A
40	38	31.4	275	6	US-10-425-114A-66540	Sequence 66540, A
41	38	31.4	275	6	US-10-425-114A-66844	Sequence 66844, A
42	38	31.4	275	6	US-10-425-114A-67072	Sequence 67072, A
43	38	31.4	280	6	US-10-425-114A-66111	Sequence 66111, A
44	38	31.4	321	1	PCT-US03-18440-72	Sequence 72, Ap1
45	38	31.4	322	1	PCT-US03-10213-18	Sequence 18, Ap1

ALIGNMENTS

```

RESULT 1
US-10-652-928-36
; Sequence 36, Application US/10652928
; GENERAL INFORMATION:
; APPLICANT: Chlaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/652,928
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-928-36

Query Match      37.2%; Score 45; DB 6; Length 247;
Best Local Similarity 33.3%; Pred. No. 14;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSKKTNDINSHQTPKRTKC 21
DB      33  CYFSKKTNDINSHQTPKRTKC 53

RESULT 2
US-09-714-935A-139
; Sequence 139, Application US/09714935A
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamicheva, Natasha
; TITLE OF INVENTION: FEN Endonucleases
; FILE REFERENCE: FORS-04580
; CURRENT APPLICATION NUMBER: US/09/714,935A
; CURRENT FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 410
; SOFTWARE: PatentIn Ver. 2.0

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SEQ ID NO 139
LENGTH: 382
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-714-935A-139

Query Match 35.1%; Score 42.5; DB 5; Length 382;
Best Local Similarity 42.9%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 1 CY-FSKXTNDINSHQTPKRTK 20
DB 83 CYVFDGKPPDKSHLTKRSS 103

RESULT 3
US-10-425-114A-38941
Sequence 38941, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38941
LENGTH: 520
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700995421_FLI.pep
US-10-425-114A-38941

Query Match 34.3%; Score 41.5; DB 6; Length 520;
Best Local Similarity 40.0%; Pred. No. 79;
Matches 8; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 2 YFSKXTNDINSHQTPKRTK 21
DB 421 YF-RKTDVVKRKSRDRTK 439

RESULT 4
US-09-897-516A-8056
Sequence 8056, Application US/09897516A
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huebner, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Spitidonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(5184)B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 8056
LENGTH: 163
TYPE: PRT
ORGANISM: Xenorhabdus sp.
US-09-897-516A-8056

Query Match 33.9%; Score 41; DB 5; Length 163;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TNDINSHQTP 16
DB 3 TNDISSAQTP 12

RESULT 5
US-10-425-114A-72419
Sequence 72419, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 72419
LENGTH: 575
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701124227_FLI.pep
US-10-425-114A-72419

Query Match 33.9%; Score 41; DB 6; Length 575;
Best Local Similarity 60.0%; Pred. No. 16+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 SKXTNDINSHQTPK 18
DB 80 STSSNDINSPSTWKR 94

RESULT 6
PCT-US03-28227-4468
Sequence 4468, Application PC/TUS0328227
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Pan;
APPLICANT: HARTSHORNE, Joannette A.; SUCHOWSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyana H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STIVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HUMWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIBTZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260

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PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 4468
LENGTH: 991
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 960507.PT71P
CCT-US03-28227-4468

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Query Match	33.1%	Score 40;	DB 1;	Length 991;
Best Local Similarity	50.0%;	Pred. No. 2.1e+02;		
Matches 7;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;

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QY      1 CYFSKKTNDINSHQ 14
        | : || |||
Db      400 CPVPSTRNSFNSHQ 413
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RESULT 7
PCT-US03-14382-78
Sequence 78, Application PC/TUS0314382
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: ANTIVIRAL AGENTS
FILE REFERENCE: 12804-011W01
CURRENT APPLICATION NUMBER: PCT/US03/14382
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/378,711
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 501
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 78
LENGTH: 1046
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-14382-78

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Query Match Similarity 33.1%; Score 40; DB 1; Length 1046;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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QY      1 CYFSKKTNDINSHQ 14
      : || |||
Db      359 CPVPSRTNSFNSHQ 372
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RESULT 8
PCT-US03-14382A-78
; Sequence 78, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 1046
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-78

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Query Match	33.1%;	Score 40;	DB 1;	Length 1046;
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Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY      1  CYFSKKTNDINSHQ  14
          | : || || |
Db      359 CPVPSRTNSFNSHQ  372

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```

RESULT 9
US-60-500-337-1679
: Sequence 1679, Application US/60500337
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
: TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL001483
: CURRENT APPLICATION NUMBER: US/60/500,337
: CURRENT FILING DATE: 2003-09-05
: NUMBER OF SEQ. ID NOS: 123188
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 1679
: LENGTH: 1088
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-500-337-1679

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Query Match	33.1%	Score 40	DB 7	Length 1088
Best Local Similarity	50.0%	Pred. No.	2.3e+02	
Matches 7	Conservative	1	Mismatches 6	Indels 0
				Gaps 0

QY 1 CYFSKKTNDINSHQ 14
: || || ||
Db 400 CPVPSKKTNSFNSHQ 413

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RESULT 10
US-60-500-337-1680
: Sequence 1680, Application US/60500337
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
: TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL001483
: CURRENT APPLICATION NUMBER: US/60/500,337
: CURRENT FILING DATE: 2003-09-05
: NUMBER OF SEQ ID NOS: 123188
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1680
: LENGTH: 1088
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-500-337-1680

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Query Match	33.1%	Score	40	DB	7	Length	1088
Best Local Similarity	50.0%	Pred. No.	2.3e+02				
Matches	7	Conservative	1	Mismatches	6	Indels	0
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QY      1 CYFSKKTNDINSHQ 14
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Db      400 CPVPSRTNSFNHQ 413
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RESULT 11 890-842
US-60-480-890-842
Sequence 842 Application US/60430890
GENERAL INFORMATION
APPLICANT: LI, Martha
APPLICANT: Rudnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: JACKSON, Donald
APPLICANT: Wong, Tai W.

```

; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 842
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-490-890-842

Query Match          33.1%; Score 40; DB 7; Length 1102;
Best Local Similarity 57.1%; Pred. No. 2,3e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      8 NDINSHOTPRKTC 21
Db      798 SDIAHSFNKRKGC 811

RESULT 12
PCT-US03-24575-8
; Sequence 8, Application PC/TUS0324575
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-056C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/24575
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/401,739
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US03-24575-8

Query Match          32.6%; Score 39.5; DB 1; Length 341;
Best Local Similarity 30.3%; Pred. No. 1,1e+02;
Matches 10; Conservative 4; Mismatches 6; Indels 13; Gaps 1;

Qy      1 CYFSKKT-----NDINSHOTPRKTC 20
Db      222 CIFPKKTLNIFVISEKPLLFNGLNSIDSPENET 254

RESULT 13
US-10-425-114A-56465
; Sequence 56465, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56465
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB24-075-Cl1_FLI.pep
; US-10-425-114A-56465
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Query Match          32.6%; Score 39.5; DB 6; Length 621;
Best Local Similarity 40.0%; Pred. No. 1,7e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Qy      2 YFSKKTNDINSHOTPRKTC 21
Db      530 YF-RKTKDVNKRKRPDLSDRTC 548

RESULT 14
US-10-425-114A-44813
; Sequence 44813, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 44813
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701202720_FLI.pep
; US-10-425-114A-44813

Query Match          32.2%; Score 39; DB 6; Length 239;
Best Local Similarity 52.9%; Pred. No. 99;
Matches 0; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      5 KKTNDINSHOTPRKTC 21
Db      163 KKTVDINEPQVCNKGK 179

RESULT 15
US-10-425-114A-58752
; Sequence 58752, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58752
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700209678_FLI.pep
; US-10-425-114A-58752

Query Match          32.2%; Score 39; DB 6; Length 286;
Best Local Similarity 40.0%; Pred. No. 1,1e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      5 KKTNDINSHOTPRK 19
Db      15 KRLHEENSHSTPAKR 29
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Thu Oct 16 09:56:36 2003

us-09-555-115a-10.rapn

Page 5

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-555-115A-11

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SUMMARIES

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102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	102	100.0	
18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	18	19	
US-09-555-115A-12	US-09-555-115A-13	US-09-555-115A-14	US-09-555-115A-15	US-09-555-115A-16	US-09-555-115A-17	US-09-555-115A-18	US-09-555-115A-19	US-09-555-115A-20	US-09-555-115A-21	US-09-555-115A-22	US-09-555-115A-23	US-09-555-115A-24	US-09-555-115A-25	US-09-555-115A-26	US-09-555-115A-27	US-09-555-115A-28	US-09-555-115A-29	US-09-555-115A-30	US-09-555-115A-31	US-09-555-115A-32	US-09-555-115A-33	US-09-555-115A-34	US-09-555-115A-35	US-09-555-115A-36	US-09-555-115A-37	US-09-555-115A-38	US-09-555-115A-39	US-09-555-115A-40	US-09-555-115A-41	US-09-555-115A-42	US-09-555-115A-43	US-09-555-115A-44	US-09-555-115A-45	US-09-555-115A-46	US-09-555-115A-47	US-09-555-115A-48	US-09-555-115A-49	US-09-555-115A-50	US-09-555-115A-51	US-09-555-115A-52	US-09-555-115A-53	US-09-555-115A-54	US-09-555-115A-55	US-09-555-115A-56	US-09-555-115A-57	US-09-555-115A-58	US-09-555-115A-59	US-09-555-115A-60
Sequence 12, Appl	Sequence 13, Appl	Sequence 14, Appl	Sequence 15, Appl	Sequence 16, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 19, Appl	Sequence 20, Appl	Sequence 21, Appl	Sequence 22, Appl	Sequence 23, Appl	Sequence 24, Appl	Sequence 25, Appl	Sequence 26, Appl	Sequence 27, Appl	Sequence 28, Appl	Sequence 29, Appl	Sequence 30, Appl	Sequence 31, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 34, Appl	Sequence 35, Appl	Sequence 36, Appl	Sequence 37, Appl	Sequence 38, Appl	Sequence 39, Appl	Sequence 40, Appl	Sequence 41, Appl	Sequence 42, Appl	Sequence 43, Appl	Sequence 44, Appl	Sequence 45, Appl	Sequence 46, Appl	Sequence 47, Appl	Sequence 48, Appl	Sequence 49, Appl	Sequence 50, Appl	Sequence 51, Appl	Sequence 52, Appl	Sequence 53, Appl	Sequence 54, Appl	Sequence 55, Appl	Sequence 56, Appl	Sequence 57, Appl	Sequence 58, Appl	Sequence 59, Appl	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-555-115A-11

Sequence 11, Application US/09555115A

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136 USWO

CURRENT APPLICATION NUMBER: US/09/555, 115A

CURRENT FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067, 357

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 18

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-555-115A-11

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CYPSSKDNVKGVTGKTC 18

RESULT 2

US-09-555-115A-12
; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CYPSSKDNVKGVTGKTC 18

RESULT 3

US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CYPSSKDNVKGVTGKTC 18

RESULT 4

US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO

; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CYPSSKDNVKGVTGKTC 18

RESULT 5

US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CYPSSKDNVKGVTGKTC 18

RESULT 6

US-09-555-115A-60
; Sequence 60, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
DB 1 CYFSSKDNVGVKVTGKTC 18

RESULT 7

US-08-882-431B-21
; Sequence 21, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-21

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 8

US-08-882-431B-22
; Sequence 22, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines

NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-22

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 9

US-08-882-431B-23
; Sequence 23, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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/
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Charles H. Harris
/ REGISTRATION NUMBER: 34,616
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 619-2065
/ TELEFAX: (301) 619-7714
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 89
/ TYPE: Amino Acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/
US-08-882-431B-23

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 54 CYFSSKDNVKGKVTGKTC 71

RESULT 10
US-10-002-784A-36
/ Sequence 36, Application US/10002784A
/ GENERAL INFORMATION:
/
/33
/ APPLICANT: Ulrich, Robert G.
/ TITLE OF INVENTION: Bacterial Superantigen Vaccines
/ FILE REFERENCE: 003/233/SAP
/ CURRENT APPLICATION NUMBER: US/10/002,784A
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
/ PRIOR FILING DATE: 97-06-25; 98-09-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Apple Macintosh Microsoft Word 6.0
/ SEQ ID NO 36
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: staphylococcal enterotoxin C1
/ FEATURE:
/ OTHER INFORMATION: partial sequence as shown in Figure 3
/
US-10-002-784A-36

Query Match 100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 54 CYFSSKDNVKGKVTGKTC 71

RESULT 11
US-10-002-784A-37
/ Sequence 37, Application US/10002784A
/ GENERAL INFORMATION:
/
/33
/ APPLICANT: Ulrich, Robert G.
/ TITLE OF INVENTION: Bacterial Superantigen Vaccines
/ FILE REFERENCE: 003/233/SAP
/ CURRENT APPLICATION NUMBER: US/10/002,784A
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
/ PRIOR FILING DATE: 97-06-25; 98-09-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Apple Macintosh Microsoft Word 6.0
/ SEQ ID NO 37
/ LENGTH: 89
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/
/ TYPE: PRT
/ ORGANISM: staphylococcal enterotoxin C2
/ FEATURE:
/ OTHER INFORMATION: partial sequence as shown in Figure 3
/
US-10-002-784A-37

Query Match 100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 54 CYFSSKDNVKGKVTGKTC 71

RESULT 12
US-10-002-784A-38
/ Sequence 38, Application US/10002784A
/ GENERAL INFORMATION:
/
/33
/ APPLICANT: Ulrich, Robert G.
/ TITLE OF INVENTION: Bacterial Superantigen Vaccines
/ FILE REFERENCE: 003/233/SAP
/ CURRENT APPLICATION NUMBER: US/10/002,784A
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
/ PRIOR FILING DATE: 97-06-25; 98-09-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Apple Macintosh Microsoft Word 6.0
/ SEQ ID NO 38
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: staphylococcal enterotoxin C3
/ FEATURE:
/ OTHER INFORMATION: partial sequence as shown in Figure 3
/
US-10-002-784A-38

Query Match 100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 54 CYFSSKDNVKGKVTGKTC 71

RESULT 13
US-09-791-537-107560
/ Sequence 107560, Application US/09791537
/ GENERAL INFORMATION:
/ APPLICANT: Bionomix, Inc.
/ APPLICANT: Debe, Derek
/ APPLICANT: Danzer, Joseph
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
/ FILE REFERENCE: 261/210
/ CURRENT APPLICATION NUMBER: US/09/791,537
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 153055
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 107560
/ LENGTH: 234
/ TYPE: PRT
/ ORGANISM: Staphylococcus
/
US-09-791-537-107560

Query Match 100.0%; Score 102; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 88 CYFSSKDNVKGKVTGKTC 105
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RESULT 14

US-08-491-746-27
 ; Sequence 27, Application US/08491746
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
 ; FILE REFERENCE: 09629/006002
 ; CURRENT APPLICATION NUMBER: US/08/491,746
 ; CURRENT FILING DATE: 1995-06-19
 ; EARLIER APPLICATION NUMBER: 08/189,424
 ; EARLIER FILING DATE: 1994-01-31
 ; EARLIER APPLICATION NUMBER: 08/025,144
 ; EARLIER FILING DATE: 1993-03-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: PCT/US91/00342
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-08-491-746-27

Query Match 100.0%; Score 102; DB 8; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
 |||||
 Db 92 CYFSSKDNVKGVTGKTC 109

RESULT 15

US-09-708-008B-28
 ; Sequence 28, Application US/09708008B
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/09/708,008B
 ; CURRENT FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: US/08/896,933
 ; PRIOR FILING DATE: 1997-07-18
 ; PRIOR APPLICATION NUMBER: 08/252,978
 ; PRIOR FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-09-708-008B-28

Query Match 100.0%; Score 102; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
 |||||
 Db 92 CYFSSKDNVKGVTGKTC 109

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-555-115A-11

Perfect score: 102
Sequence: 1 CYPSSKDNVKGKVTGKTC 18

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Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/prodata1/paa/US07_NEW_COMB.pep:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	46	45.1	375	7	US-60-499-964-460
3	46	45.1	375	7	US-60-499-964-461
4	46	45.1	375	7	US-60-499-964-776
5	46	45.1	375	7	US-60-499-964-777
6	46	45.1	375	7	US-60-499-964-778
7	46	45.1	380	1	PCT-US03-28227-4671
8	46	45.1	385	7	US-60-487-610-1723
9	46	45.1	385	7	US-60-499-964-462
10	44	43.1	1403	1	PCT-US03-14382-30
11	44	43.1	1403	1	PCT-US03-14382-30
12	44	43.1	1462	1	PCT-US03-14382-31
13	44	43.1	1462	1	PCT-US03-14382-31
14	42	41.2	253	6	US-10-425-114A-52327
15	42	41.2	257	6	US-10-425-114A-36981
16	42	41.2	253	6	US-10-425-114A-40237
17	42	41.2	333	6	US-10-425-114A-39097
18	42	41.2	333	6	US-10-425-114A-40939
19	42	41.2	418	6	US-10-425-114A-49025
20	41	40.2	246	7	US-60-499-964-414
21	41	40.2	246	7	US-60-499-964-415
22	41	40.2	340	1	PCT-US03-28227-4677
23	41	40.2	357	1	PCT-US03-28227-4674
24	41	40.2	357	1	PCT-US03-28227-4676
25	41	40.2	358	1	PCT-US03-28227-4675
26	41	40.2	358	1	PCT-US03-28227-4678

27	41	40.2	368	7	US-60-487-610-1505	Sequence 1505, Ap
28	41	40.2	382	7	US-60-487-610-1506	Sequence 1506, Ap
29	40	39.2	335	7	US-60-499-964-463	Sequence 463, App
30	40	39.2	348	1	PCT-US03-19153-166	Sequence 166, App
31	40	39.2	375	7	US-60-487-610-1724	Sequence 1724, Ap
32	40	39.2	375	7	US-60-499-964-464	Sequence 464, App
33	40	39.2	429	6	US-10-425-114A-64698	Sequence 64698, A
34	40	39.2	433	6	US-10-425-114A-67284	Sequence 67284, A
35	39.5	38.7	417	6	US-10-389-647-494	Sequence 494, App
36	39	38.2	170	6	US-10-419-462-43	Sequence 43, App1
37	39	38.2	416	5	US-09-897-516A-6844	Sequence 6844, Ap
38	39	38.2	682	7	US-60-493-369-33	Sequence 33, App1
39	39	38.2	682	7	US-60-502-656-59	Sequence 59, App1
40	39	38.2	789	7	US-60-493-369-22	Sequence 22, App1
41	39	38.2	789	7	US-60-493-369-25	Sequence 25, App1
42	39	38.2	789	7	US-60-502-656-60	Sequence 60, App1
43	39	38.2	789	7	US-60-502-656-62	Sequence 62, App1
44	39	38.2	798	7	US-60-487-610-2001	Sequence 2001, Ap
45	39	38.2	798	7	US-60-487-610-2002	Sequence 2002, Ap

ALIGNMENTS

RESULT 1
US-60-487-610-2744
; Sequence 2744, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LAYER PIROSIOS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001463
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2744
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2744.*

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy 1 CYPSSKDNVKGKVTGKTC 18
Db 175 CFPSTGYSANVAKVTPGSTC 196

RESULT 2
US-60-499-964-460
; Sequence 460, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-460

Query Match 45.1%; Score 46; DB 7; Length 375;


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; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PN-0100 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/28227
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/410,260
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/410,259
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 5444
; SOFTWARE: PERL Program
; SEQ ID NO 4671
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 962211.PT69P
PCT-US03-28227-4671

Query Match
Best Local Similarity 45.1%; Score 46; DB 1; Length 380;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGYTGKTC 18
| | | | | | | | | | | | | | | | | |
Db 180 CGFSTGCGSAVNAVAKYTPGSTC 201

RESULT 8
US-60-487-610-1723
; Sequence 1723, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LAYER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1723

Query Match
Best Local Similarity 45.1%; Score 46; DB 7; Length 385;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGYTGKTC 18
| | | | | | | | | | | | | | | | | |
Db 175 CGFSTGCGSAVNAVAKYTPGSTC 196

RESULT 9
US-60-499-964-462
; Sequence 462, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 385
; TYPE: PRT
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```

; ORGANISM: Homo sapiens
US-60-499-964-462

Query Match
Best Local Similarity 45.1%; Score 46; DB 7; Length 385;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGYTGKTC 18
| | | | | | | | | | | | | | | | | |
Db 175 CGFSTGCGSAVNAVAKYTPGSTC 196

RESULT 10
PCT-US03-14382-30
; Sequence 30, Application PC/TUS0314382
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-30

Query Match
Best Local Similarity 43.1%; Score 44; DB 1; Length 1403;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGYTGKTC 18
| | | | | | | | | | | | | | | | | |
Db 95 CLCSEKGLGKTTGKLC 112

RESULT 11
PCT-US03-14382A-30
; Sequence 30, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-30

Query Match
Best Local Similarity 44.4%; Score 44; DB 1; Length 1403;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGYTGKTC 18
| | | | | | | | | | | | | | | | | |
Db 95 CLCSEKGLGKTTGKLC 112

RESULT 12
PCT-US03-14382-31
; Sequence 31, Application PC/TUS0314382
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; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; FILE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-31

Query Match          43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 18
Db 41 CLCSGKGLGKTGKLC 58

RESULT 13
PCT-US03-14382A-31
; Sequence 31, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; FILE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-31

Query Match          43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 18
Db 41 CLCSGKGLGKTGKLC 58

RESULT 14
US-10-425-114A-52327
; Sequence 52327, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52327
; LENGTH: 253
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700872843_FLI.pep
US-10-425-114A-52327

Query Match          41.2%; Score 42; DB 6; Length 253;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 15
Db 118 CVASADNITARMKLG 132

RESULT 15
US-10-425-114A-36981
; Sequence 36981, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36981
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-051-G3_FLI.pep
US-10-425-114A-36981

Query Match          41.2%; Score 42; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 15
Db 120 CVASADNITARMKLG 134

Search completed: October 15, 2003, 17:42:38
Job time : 8.08383 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:57:11 ; Search time 211.042 Seconds
(without alignments)
77.608 Million cell updates/sec

Title: US-09-555-115A-12
Perfect score: 102
Sequence: 1 CFFSSKDNVGVKVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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2:	/cgn2_6/prodata/1/paa/US06_COMB.pep:*
3:	/cgn2_6/prodata/1/paa/US07_COMB.pep:*
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27:	/cgn2_6/prodata/1/paa/US101_COMB.pep:*
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29:	/cgn2_6/prodata/1/paa/US103_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	18	US-09-555-115A-11	Sequence 11, Appl

2	102	100.0	18	US-09-555-115A-12	Sequence 12, Appl
3	102	100.0	18	US-09-555-115A-13	Sequence 13, Appl
4	102	100.0	18	US-09-555-115A-15	Sequence 15, Appl
5	102	100.0	18	US-09-555-115A-16	Sequence 16, Appl
6	102	100.0	18	US-09-555-115A-60	Sequence 60, Appl
7	102	100.0	18	US-08-882-431B-21	Sequence 21, Appl
8	102	100.0	18	US-08-882-431B-22	Sequence 22, Appl
9	102	100.0	18	US-08-882-431B-23	Sequence 23, Appl
10	102	100.0	18	US-10-002-784A-36	Sequence 36, Appl
11	102	100.0	18	US-10-002-784A-37	Sequence 37, Appl
12	102	100.0	18	US-10-002-784A-38	Sequence 38, Appl
13	102	100.0	18	US-09-791-537-107560	Sequence 107560, Appl
14	102	100.0	18	US-08-491-746-27	Sequence 27, Appl
15	102	100.0	18	US-09-708-008B-28	Sequence 28, Appl
16	102	100.0	18	US-08-491-746-26	Sequence 26, Appl
17	102	100.0	18	US-09-708-008B-27	Sequence 27, Appl
18	102	100.0	18	US-09-791-537-52671	Sequence 52671, A
19	102	100.0	18	US-09-791-537-52673	Sequence 52673, A
20	102	100.0	18	US-09-791-537-52675	Sequence 52675, A
21	102	100.0	18	US-09-791-537-52677	Sequence 52677, A
22	102	100.0	18	US-09-791-537-57117	Sequence 57117, A
23	102	100.0	18	US-09-791-537-128386	Sequence 128386, A
24	102	100.0	18	US-09-555-115A-1	Sequence 1, Appl
25	102	100.0	18	US-09-555-115A-2	Sequence 2, Appl
26	102	100.0	18	US-09-555-115A-3	Sequence 3, Appl
27	102	100.0	18	US-09-555-115A-5	Sequence 5, Appl
28	102	100.0	18	US-09-555-115A-6	Sequence 6, Appl
29	102	100.0	18	PCT-US98-16766-14	Sequence 14, Appl
30	102	100.0	18	US-08-882-431A-14	Sequence 14, Appl
31	102	100.0	18	US-08-882-431B-14	Sequence 14, Appl
32	102	100.0	18	US-08-882-431B-14	Sequence 14, Appl
33	102	100.0	18	US-09-751-708A-12	Sequence 12, Appl
34	102	100.0	18	US-09-791-537-93999	Sequence 93999, A
35	102	100.0	18	US-09-791-537-94000	Sequence 94000, A
36	102	100.0	18	US-09-791-537-115863	Sequence 115863, A
37	102	100.0	18	US-09-870-759-12	Sequence 12, Appl
38	102	100.0	18	US-10-002-784A-14	Sequence 14, Appl
39	96	94.1	18	US-09-555-115A-14	Sequence 14, Appl
40	96	94.1	18	US-09-791-537-17768	Sequence 17768, A
41	96	94.1	18	US-09-791-537-52676	Sequence 52676, A
42	96	94.1	18	US-09-555-115A-7	Sequence 7, Appl
43	96	94.1	18	US-09-555-115A-17	Sequence 17, Appl
44	93	91.2	18	US-09-555-115A-17	Sequence 17, Appl
45	93	91.2	18	US-09-791-537-52695	Sequence 52695, A

ALIGNMENTS

RESULT 1
US-09-555-115A-11
Sequence 11, Application US/09555115A
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136 USMO
CURRENT APPLICATION NUMBER: US/09/555, 115A
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-555-115A-11

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 2

US-09-555-115A-12
; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 3

US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 4

US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO

; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 5

US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 6

US-09-555-115A-60
; Sequence 60, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
DB 1 CYFSSKDNVGVKVTGKTC 18

RESULT 7
US-08-882-431B-21
; Sequence 21, Application US/08882431B
; GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide

US-08-882-431B-21

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 8
US-08-882-431B-22

; Sequence 22, Application US/08882431B
; GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide

US-08-882-431B-22

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 9
US-08-882-431B-23

; Sequence 23, Application US/08882431B
; GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
;
US-08-882-431B-23

Query Match      100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
Db      54 CYFSSKDNVKGKVTGKTC 71

RESULT 10
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
;
US-10-002-784A-36

Query Match      100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
Db      54 CYFSSKDNVKGKVTGKTC 71

RESULT 11
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
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; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
;
US-10-002-784A-37

Query Match      100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
Db      54 CYFSSKDNVKGKVTGKTC 71

RESULT 12
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
;
US-10-002-784A-38

Query Match      100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
Db      54 CYFSSKDNVKGKVTGKTC 71

RESULT 13
US-09-791-537-107560
; Sequence 107560, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107560
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus
;
US-09-791-537-107560

Query Match      100.0%; Score 102; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CYFSSKDNVKGKVTGKTC 18
Db      88 CYFSSKDNVKGKVTGKTC 105
```


RESULT 14

US-08-491-746-27
 ; Sequence 27, Application US/08491746
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
 ; FILE REFERENCE: 09629/006002
 ; CURRENT APPLICATION NUMBER: US/08/491,746
 ; CURRENT FILING DATE: 1995-06-19
 ; EARLIER APPLICATION NUMBER: 08/189,424
 ; EARLIER FILING DATE: 1994-01-31
 ; EARLIER APPLICATION NUMBER: 08/025,144
 ; EARLIER FILING DATE: 1993-03-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: PCT/US91/00342
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; NUMBER OF SEQ. ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-08-491-746-27

Query Match

Best local Similarity 100.0%; Score 102; DB 8; Length 238;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
 |||||
 DB 92 CYFSSKDNVKGVTGGKTC 109

RESULT 15

US-09-708-008B-28
 ; Sequence 28, Application US/09708008B
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/09/708,008B
 ; CURRENT FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: US/08/896,933
 ; PRIOR FILING DATE: 1997-07-18
 ; PRIOR APPLICATION NUMBER: 08/252,978
 ; PRIOR FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-09-708-008B-28

Query Match 100.0%; Score 102; DB 21; Length 238;
 Best local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
 |||||
 DB 92 CYFSSKDNVKGVTGGKTC 109

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 8.08383 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-12

Perfect score: 102
Sequence: 1 CYPSSKDNVKGKVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	45.1	375	7 US-60-487-610-2744	Sequence 2744, Ap
2	46	45.1	375	7 US-60-499-964-460	Sequence 460, App
3	46	45.1	375	7 US-60-499-964-461	Sequence 461, App
4	46	45.1	375	7 US-60-499-964-776	Sequence 776, App
5	46	45.1	375	7 US-60-499-964-777	Sequence 777, App
6	46	45.1	375	7 US-60-499-964-778	Sequence 778, App
7	46	45.1	380	1 PCT-US03-28227-4671	Sequence 4671, App
8	46	45.1	385	7 US-60-487-610-1723	Sequence 1723, Ap
9	46	45.1	385	7 US-60-499-964-462	Sequence 462, App
10	44	43.1	1403	1 PCT-US03-14382-30	Sequence 30, App1
11	44	43.1	1403	1 PCT-US03-14382-30	Sequence 30, App1
12	44	43.1	1462	1 PCT-US03-14382-31	Sequence 31, App1
13	44	43.1	1462	1 PCT-US03-14382-31	Sequence 31, App1
14	42	41.2	253	6 US-10-425-114A-52327	Sequence 52327, A
15	42	41.2	253	6 US-10-425-114A-52327	Sequence 52327, A
16	42	41.2	263	6 US-10-425-114A-36981	Sequence 36981, A
17	42	41.2	263	6 US-10-425-114A-40237	Sequence 40237, A
18	42	41.2	343	6 US-10-425-114A-39097	Sequence 39097, A
19	42	41.2	343	6 US-10-425-114A-40939	Sequence 40939, A
20	41	40.2	418	6 US-10-425-114A-49025	Sequence 49025, A
21	41	40.2	246	7 US-60-499-964-414	Sequence 414, App
22	41	40.2	246	7 US-60-499-964-415	Sequence 415, App
23	41	40.2	340	1 PCT-US03-28227-4677	Sequence 4677, App
24	41	40.2	357	1 PCT-US03-28227-4676	Sequence 4676, App
25	41	40.2	358	1 PCT-US03-28227-4675	Sequence 4675, App
26	41	40.2	358	1 PCT-US03-28227-4678	Sequence 4678, App

27	41	40.2	368	7 US-60-487-610-1505	Sequence 1505, Ap
28	41	40.2	382	7 US-60-487-610-1506	Sequence 1506, Ap
29	40	39.2	335	7 US-60-499-964-463	Sequence 463, App
30	40	39.2	348	1 PCT-US03-19153-166	Sequence 166, App
31	40	39.2	375	7 US-60-487-610-1724	Sequence 1724, App
32	40	39.2	375	7 US-60-499-964-464	Sequence 464, App
33	40	39.2	429	6 US-10-425-114A-64698	Sequence 64698, A
34	40	39.2	433	6 US-10-425-114A-67284	Sequence 67284, A
35	39.5	38.7	417	6 US-10-489-647-494	Sequence 494, App1
36	39	38.2	170	6 US-10-419-462-43	Sequence 43, App1
37	39	38.2	416	5 US-09-897-516A-6844	Sequence 6844, App
38	39	38.2	682	7 US-60-493-369-53	Sequence 53, App1
39	39	38.2	682	7 US-60-502-656-59	Sequence 59, App1
40	39	38.2	789	7 US-60-493-369-22	Sequence 22, App1
41	39	38.2	789	7 US-60-493-369-25	Sequence 25, App1
42	39	38.2	789	7 US-60-502-656-60	Sequence 60, App1
43	39	38.2	789	7 US-60-502-656-62	Sequence 62, App1
44	39	38.2	789	7 US-60-487-610-2001	Sequence 2001, App
45	39	38.2	798	7 US-60-487-610-2002	Sequence 2002, App

ALIGNMENTS

RESULT 1 0
US-60-487-610-2744
Sequence 2744, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
LAYER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2744
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-2744

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy 1 CYPSSKDNVKGKVTGKTC 18
Db 175 CCFSTGSGSNVAKYTPGSGTC 196

RESULT 2
US-60-499-964-460
Sequence 460, Application US/60499964
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001481
CURRENT APPLICATION NUMBER: US/60/499,964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 460
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-460
Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18

Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 3

US-60-499-964-461
; Sequence 461, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 461
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-461

Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18

Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 4

US-60-499-964-776
; Sequence 776, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-776

Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18

Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 5

US-60-499-964-777
; Sequence 777, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481

CURRENT APPLICATION NUMBER: US/60/499,964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 777
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-777

Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18

Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 6

US-60-499-964-778
; Sequence 778, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-778

Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18

Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 7

PCT-US03-28227-4671
; Sequence 4671, Application PC/TUS0328227
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
; WRIGHT, Rachel J.; BRUNS, Christopher M.;
; APPLICANT: MARJANOVIC, Miljana M.; SHEN, Fan;
; APPLICANT: HARTSHORNE, ToINETTE A.; SUCHROLDSKI, Martin;
; APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
; APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
; APPLICANT: DELEGREANE, Angelo M.; PANESAR, Iqbal S.;
; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
; STEVENS, Kristian A.; BLANCHARD, John D.;
; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
; APPLICANT: PERALTA, Carey H.; ANDERSON, Scott E.;
; APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
; APPLICANT: WU, Mingham C.; STIVE, Laura L.;
; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
; APPLICANT: VITT, Ursula A.; KIRTON, Edward;
; APPLICANT: XU, Yeming; KWONG, Mary;
; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
; APPLICANT: GLEZEN, Darryl; PATURI, Srikanth;
; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.

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; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PN-0100 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/28227
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/410,260
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/410,259
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 5444
; SOFTWARE: PERL Program
; SEQ ID NO 4671
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 962211.PT69P
PCT-US03-28227-4671

Query Match          45.1%; Score 46; DB 1; Length 380;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy      1  CYFS---SKDNYGKVTGKTC 18
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      180 CGFSTGYGSANVAKVTPGSTC 201

RESULT 8
US-60-487-610-1723
; Sequence 1723, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1723

Query Match          45.1%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy      1  CYFS---SKDNYGKVTGKTC 18
      ||| : ||| ||| |||
      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 9
US-60-499-964-462
; Sequence 462, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 385
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-60-499-964-462

Query Match          45.1%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy      1  CYFS---SKDNYGKVTGKTC 18
      ||| : ||| ||| |||
      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 10
PCT-US03-14382-30
; Sequence 30, Application PC/TUS0314382
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011M01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-30

Query Match          43.1%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
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Qy      1  CYFSSKDNVGYKVTGKTC 18
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      95 CLCSGKGGKVTGKTKLC 112

RESULT 11
PCT-US03-14382A-30
; Sequence 30, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011M01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-30

Query Match          43.1%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy      1  CYFSSKDNVGYKVTGKTC 18
      ||| : ||| ||| |||
      95 CLCSGKGGKVTGKTKLC 112

RESULT 12
PCT-US03-14382-31
; Sequence 31, Application PC/TUS0314382
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; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-31

Query Match      43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVGTGKTC 18
Db      41  CLCGSEKGLGKTGKLC 58

RESULT 13
PCT-US03-14382A-31
; Sequence 31, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-31

Query Match      43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVGTGKTC 18
Db      41  CLCGSEKGLGKTGKLC 58

RESULT 14
US-10-425-114A-52327
; Sequence 52327, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52327
; LENGTH: 253
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURe:
; OTHER INFORMATION: Clone ID: 700872843_FLI.pep
US-10-425-114A-52327

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Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVGTG 15
Db      118  CYASSADNIRMLKG 132

RESULT 15
US-10-425-114A-36981
; Sequence 36981, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36981
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURe:
; OTHER INFORMATION: Clone ID: LIB3170-051-G3_FLI.pep
US-10-425-114A-36981

Query Match      41.2%; Score 42; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVGTG 15
Db      120  CYASSADNIRMLKG 134

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:57:11 : Search time 211.042 Seconds
(without alignments)
77.608 Million cell updates/sec

Title: US-09-555-115A-13

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Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	102	100.0	18	19	US-09-555-115A-11
					Sequence 11, Appl

2	102	100.0	18	19	US-09-555-115A-12	Sequence 12, Appl
3	102	100.0	18	19	US-09-555-115A-13	Sequence 13, Appl
4	102	100.0	18	19	US-09-555-115A-15	Sequence 15, Appl
5	102	100.0	18	19	US-09-555-115A-16	Sequence 16, Appl
6	102	100.0	18	19	US-09-555-115A-60	Sequence 60, Appl
7	102	100.0	89	12	US-08-882-431B-21	Sequence 21, Appl
8	102	100.0	89	12	US-08-882-431B-22	Sequence 22, Appl
9	102	100.0	89	12	US-08-882-431B-23	Sequence 23, Appl
10	102	100.0	89	26	US-10-002-784A-36	Sequence 36, Appl
11	102	100.0	89	26	US-10-002-784A-37	Sequence 37, Appl
12	102	100.0	89	26	US-10-002-784A-38	Sequence 38, Appl
13	102	100.0	234	8	US-09-791-746-27	Sequence 8, Appl
14	102	100.0	238	21	US-09-708-008B-28	Sequence 21, Appl
15	102	100.0	238	21	US-08-491-746-26	Sequence 27, Appl
16	102	100.0	239	21	US-08-491-746-26	Sequence 28, Appl
17	102	100.0	239	21	US-09-708-008B-27	Sequence 29, Appl
18	102	100.0	239	22	US-09-791-537-52671	Sequence 27, Appl
19	102	100.0	239	22	US-09-791-537-52673	Sequence 2, Appl
20	102	100.0	239	22	US-09-791-537-52675	Sequence 2, Appl
21	102	100.0	239	22	US-09-791-537-52677	Sequence 52677, A
22	102	100.0	239	22	US-09-791-537-57117	Sequence 52677, A
23	102	100.0	239	22	US-09-791-537-128386	Sequence 57117, A
24	102	100.0	240	19	US-09-555-115A-1	Sequence 128386, A
25	102	100.0	240	19	US-09-555-115A-2	Sequence 1, Appl
26	102	100.0	240	19	US-09-555-115A-3	Sequence 2, Appl
27	102	100.0	240	19	US-09-555-115A-5	Sequence 3, Appl
28	102	100.0	240	19	US-09-555-115A-6	Sequence 5, Appl
29	102	100.0	266	1	PCT-US98-16766-14	Sequence 6, Appl
30	102	100.0	266	12	US-08-882-431-14	Sequence 14, Appl
31	102	100.0	266	12	US-08-882-431B-14	Sequence 14, Appl
32	102	100.0	266	12	US-08-882-431B-12	Sequence 14, Appl
33	102	100.0	266	12	US-09-751-708A-12	Sequence 12, Appl
34	102	100.0	266	22	US-09-791-537-93999	Sequence 93999, A
35	102	100.0	266	22	US-09-791-537-94000	Sequence 94000, A
36	102	100.0	266	22	US-09-791-537-115863	Sequence 115863, A
37	102	100.0	266	23	US-09-870-759-12	Sequence 12, Appl
38	102	100.0	266	26	US-10-002-784A-14	Sequence 14, Appl
39	96	94.1	18	19	US-09-555-115A-14	Sequence 14, Appl
40	96	94.1	239	22	US-09-791-537-17768	Sequence 17768, A
41	96	94.1	239	22	US-09-791-537-52676	Sequence 52676, A
42	96	94.1	240	19	US-09-555-115A-4	Sequence 4, Appl
43	96	94.1	240	19	US-09-555-115A-7	Sequence 7, Appl
44	93	91.2	18	19	US-09-555-115A-17	Sequence 17, Appl
45	93	91.2	239	22	US-09-791-537-52695	Sequence 52695, A

ALIGNMENTS

RESULT 1

US-09-555-115A-11

Sequence 11, Application US/09555115A

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: #216.1USMO

CURRENT APPLICATION NUMBER: US/09/555, 115A

CURRENT FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067, 357

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 18

TYPE: PRT

ORGANISM: *Staphylococcus aureus*

US-09-555-115A-11

Query Match 100.0%; Score 102; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 1 CYFSSKDNVKGKVTGKTC 18

RESULT 2

US-09-555-115A-12
; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 1 CYFSSKDNVKGKVTGKTC 18

RESULT 3

US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 1 CYFSSKDNVKGKVTGKTC 18

RESULT 4

US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO

; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 1 CYFSSKDNVKGKVTGKTC 18

RESULT 5

US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 1 CYFSSKDNVKGKVTGKTC 18

RESULT 6

US-09-555-115A-60
; Sequence 60, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 87e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 1 CYFSSKDNVGVKVTGKTC 18

RESULT 7

US-08-882-431B-21
; Sequence 21, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-21

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 8

US-08-882-431B-22
; Sequence 22, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines

NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-22

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 9

US-08-882-431B-23
; Sequence 23, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-23

Query Match      100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
        |||
        54 CYFSSKDNVKGKVTGKTC 71

RESULT 10
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-36

Query Match      100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
        |||
        54 CYFSSKDNVKGKVTGKTC 71

RESULT 11
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
```

```
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-37

Query Match      100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
        |||
        54 CYFSSKDNVKGKVTGKTC 71

RESULT 12
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-38

Query Match      100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
        |||
        54 CYFSSKDNVKGKVTGKTC 71

RESULT 13
US-09-791-537-107560
; Sequence 107560, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent version 3.0
; SEQ ID NO 107560
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus
; US-09-791-537-107560

Query Match      100.0%; Score 102; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGKVTGKTC 18
        |||
        88 CYFSSKDNVKGKVTGKTC 105
```

RESULT 14

US-08-491-746-27
; Sequence 27, Application US/08491746;
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
; FILE REFERENCE: 09629/006002
; CURRENT APPLICATION NUMBER: US/08/491,746
; CURRENT FILING DATE: 1995-06-19
; EARLIER APPLICATION NUMBER: 08/189,424
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/025,144
; EARLIER FILING DATE: 1993-03-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: PCT/US91/00342
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-491-746-27

Query Match

100.0%; Score 102; DB 8; Length 238;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
|||||
Db 92 CYFSSKDNVKGVTGKTC 109

RESULT 15

US-09-708-008B-28
; Sequence 28, Application US/09708008B
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-28

Query Match

100.0%; Score 102; DB 21; Length 238;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
|||||
Db 92 CYFSSKDNVKGVTGKTC 109

Search completed: October 15, 2003, 17:41:16
Job time : 212.042 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 8.08383 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-13

Perfect score: 102

Sequence: 1 CYPSSKDNVSKVTGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Pending Patents AA New:
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	45.1	375	7	US-60-487-610-2744
2	46	45.1	375	7	US-60-499-964-460
3	46	45.1	375	7	US-60-499-964-461
4	46	45.1	375	7	US-60-499-964-776
5	46	45.1	375	7	US-60-499-964-777
6	46	45.1	375	7	US-60-499-964-778
7	46	45.1	380	1	PCT-US03-28227-4671
8	46	45.1	385	7	US-60-487-610-1723
9	46	45.1	385	7	US-60-499-964-462
10	44	43.1	1403	1	PCT-US03-14382-30
11	44	43.1	1403	1	PCT-US03-14382-30
12	44	43.1	1462	1	PCT-US03-14382-31
13	44	43.1	1462	1	PCT-US03-14382-31
14	42	41.2	253	6	US-10-425-114A-52327
15	42	41.2	253	6	US-10-425-114A-36981
16	42	41.2	263	6	US-10-425-114A-40237
17	42	41.2	343	6	US-10-425-114A-39097
18	42	41.2	343	6	US-10-425-114A-40939
19	42	41.2	418	6	US-10-425-114A-49025
20	41	40.2	246	7	US-60-499-964-414
21	41	40.2	246	7	US-60-499-964-415
22	41	40.2	340	1	PCT-US03-28227-4677
23	41	40.2	357	1	PCT-US03-28227-4674
24	41	40.2	357	1	PCT-US03-28227-4676
25	41	40.2	358	1	PCT-US03-28227-4675
26	41	40.2	358	1	PCT-US03-28227-4678

27	41	40.2	368	7	US-60-487-610-1505	Sequence 1505, Ap
28	41	40.2	382	7	US-60-487-610-1506	Sequence 1506, Ap
29	40	39.2	335	7	US-60-499-964-463	Sequence 463, App
30	40	39.2	348	1	PCT-US03-19153-166	Sequence 166, App
31	40	39.2	375	7	US-60-487-610-1174	Sequence 1724, Ap
32	40	39.2	375	7	US-60-499-964-464	Sequence 464, App
33	40	39.2	429	6	US-10-425-114A-64698	Sequence 64698, A
34	40	39.2	433	6	US-10-425-114A-67284	Sequence 67284, A
35	39.5	38.7	417	6	US-10-389-647-494	Sequence 494, App
36	39	38.2	170	6	US-10-419-462-43	Sequence 43, App
37	39	38.2	416	5	US-09-897-516A-6844	Sequence 6844, Ap
38	39	38.2	682	7	US-60-493-365-33	Sequence 33, App
39	39	38.2	682	7	US-60-502-656-59	Sequence 59, App
40	39	38.2	789	7	US-60-493-369-22	Sequence 22, App
41	39	38.2	789	7	US-60-493-369-25	Sequence 25, App
42	39	38.2	789	7	US-60-502-656-60	Sequence 60, App
43	39	38.2	789	7	US-60-502-656-62	Sequence 62, App
44	39	38.2	798	7	US-60-487-610-2001	Sequence 2001, Ap
45	39	38.2	798	7	US-60-487-610-2002	Sequence 2002, Ap

ALIGNMENTS

RESULT 1
US-60-487-610-2744
; Sequence 2744, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2744
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2744

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservativity 0; Mismatches 6; Indels 4; Gaps 1;

Cy 1 CYPSSKDNVSKVTGKTC 18
Db 175 CYPSSKDNVSKVTGKTC 196

RESULT 2
US-60-499-964-460
; Sequence 460, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-460
Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 3

US-60-499-964-461
; Sequence 461, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 461
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-461

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 4

US-60-499-964-776
; Sequence 776, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-776

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

US-60-499-964-777
; Sequence 777, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481

RESULT 5
US-60-499-964-777
; Sequence 777, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481

CURRENT APPLICATION NUMBER: US/60/499,964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 777
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-777

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 6

US-60-499-964-778
; Sequence 778, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-778

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 7

PCT-US03-28227-4671
; Sequence 4671, Application PC/TUS0328227
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
; APPLICANT: MARJANOVIC, Marijana M.; SHEN, Fan;
; APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
; APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
; APPLICANT: BLDER, Linda V.; MOONEY, Elizabeth M.;
; APPLICANT: DELBESANE, Angelo M.; PAVESAK, Iqbal S.;
; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
; APPLICANT: RIoux, Pierre; SHEN, Edward J.;
; APPLICANT: WU, Mingham C.; STUVE, Laura L.;
; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
; APPLICANT: VITT, Ursula A.; KIRTON, Edward;
; APPLICANT: XU, Yuming; KWONG, Mary;
; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
; APPLICANT: GIETZEN, Daryl; PATURY, Strikanth;
; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.


```
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; FILE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-31

Query Match      43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGKTC 18
Db      41  CLCGEKGKLGKTKGKLC 58

RESULT 13
PCT-US03-14382A-31
; Sequence 31, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; FILE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-31

Query Match      43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGKTC 18
Db      41  CLCGEKGKLGKTKGKLC 58

RESULT 14
US-10-425-114A-52327
; Sequence 52327, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52327
; LENGTH: 253
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700872843_F11.pep
US-10-425-114A-52327

Query Match      41.2%; Score 42; DB 6; Length 253;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGG 15
Db      118  CYASSADNIRMLKG 132

RESULT 15
US-10-425-114A-36981
; Sequence 36981, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36981
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-051-G3_F11.pep
US-10-425-114A-36981

Query Match      41.2%; Score 42; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGG 15
Db      120  CYASSADNIRMLKG 134

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Job time : 8.08383 secs
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:57:11 ; Search time 211.042 Seconds
(without alignments)
77.608 Million cell updates/sec

Title: US-09-555-115A-14

Perfect score: 100

Sequence: 1 CYFSSKDNVGVKVTGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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26: /cgn2_6/prodata/1/paa/US100_COMB.pep:*
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32: /cgn2_6/prodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	18	US-09-555-115A-14	Sequence 14, Appl

2	100	100.0	239	22	US-09-791-537-17768	Sequence 17768, A
3	100	100.0	239	22	US-09-791-537-52676	Sequence 52676, A
4	100	100.0	240	19	US-09-555-115A-4	Sequence 4, Appl
5	96	96.0	18	19	US-09-555-115A-11	Sequence 11, Appl
6	96	96.0	18	19	US-09-555-115A-12	Sequence 12, Appl
7	96	96.0	18	19	US-09-555-115A-13	Sequence 13, Appl
8	96	96.0	18	19	US-09-555-115A-15	Sequence 15, Appl
9	96	96.0	18	19	US-09-555-115A-16	Sequence 16, Appl
10	96	96.0	18	19	US-09-555-115A-60	Sequence 60, Appl
11	96	96.0	89	12	US-08-882-431B-21	Sequence 21, Appl
12	96	96.0	89	12	US-08-882-431B-22	Sequence 22, Appl
13	96	96.0	89	12	US-08-882-431B-23	Sequence 23, Appl
14	96	96.0	89	12	US-10-002-784A-36	Sequence 36, Appl
15	96	96.0	89	26	US-10-002-784A-37	Sequence 37, Appl
16	96	96.0	89	26	US-10-002-784A-38	Sequence 38, Appl
17	96	96.0	234	22	US-09-791-537-107560	Sequence 107560, A
18	96	96.0	238	8	US-08-491-746-27	Sequence 27, Appl
19	96	96.0	238	21	US-09-708-008B-28	Sequence 28, Appl
20	96	96.0	239	8	US-08-491-746-26	Sequence 26, Appl
21	96	96.0	239	21	US-09-708-008B-27	Sequence 27, Appl
22	96	96.0	239	22	US-09-791-537-52671	Sequence 52671, A
23	96	96.0	239	22	US-09-791-537-52672	Sequence 52672, A
24	96	96.0	239	22	US-09-791-537-52673	Sequence 52673, A
25	96	96.0	239	22	US-09-791-537-52677	Sequence 52677, A
26	96	96.0	239	22	US-09-791-537-57117	Sequence 57117, A
27	96	96.0	239	22	US-09-791-537-128386	Sequence 128386, A
28	96	96.0	240	19	US-09-555-115A-1	Sequence 1, Appl
29	96	96.0	240	19	US-09-555-115A-2	Sequence 2, Appl
30	96	96.0	240	19	US-09-555-115A-3	Sequence 3, Appl
31	96	96.0	240	19	US-09-555-115A-5	Sequence 5, Appl
32	96	96.0	240	19	US-09-555-115A-6	Sequence 6, Appl
33	96	96.0	266	1	PCT-US98-16766-14	Sequence 14, Appl
34	96	96.0	266	12	US-08-882-431A-14	Sequence 14, Appl
35	96	96.0	266	12	US-08-882-431B-14	Sequence 14, Appl
36	96	96.0	266	12	US-09-751-708A-12	Sequence 12, Appl
37	96	96.0	266	22	US-09-791-537-93999	Sequence 93999, A
38	96	96.0	266	22	US-09-791-537-94000	Sequence 94000, A
39	96	96.0	266	22	US-09-791-537-115863	Sequence 115863, A
40	96	96.0	266	23	US-09-870-759-12	Sequence 12, Appl
41	96	96.0	266	26	US-10-002-784A-14	Sequence 14, Appl
42	96	96.0	266	26	US-09-555-115A-7	Sequence 7, Appl
43	90	90.0	18	19	US-09-555-115A-17	Sequence 17, Appl
44	87	87.0	18	19	US-09-791-537-52695	Sequence 52695, A
45	87	87.0	239	22	US-09-791-537-52695	Sequence 52695, A

ALIGNMENTS

RESULT 1

US-09-555-115A-14

Sequence 14, Application US/09555115A

GENERAL INFORMATION:

APPLICANT: Biobach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12116.1USWO

CURRENT APPLICATION NUMBER: US/09/555, 115A

CURRENT FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067, 357

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 18

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-555-115A-14

Query Match 100.0%; Score 100; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTSGKTC 18
Db 1 CYFSSKDNVGVKVTSGKTC 18

RESULT 2

US-09-791-537-17768
; Sequence 17768, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17768
; LENGTH: 239
; TYPE: PRT
; ORGANISM: pdb 1JCKB
US-09-791-537-17768

Query Match 100.0%; Score 100; DB 22; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTSGKTC 18
Db 93 CYFSSKDNVGVKVTSGKTC 110

RESULT 3

US-09-791-537-52676
; Sequence 52676, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52676
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-791-537-52676

Query Match 100.0%; Score 100; DB 22; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTSGKTC 18
Db 93 CYFSSKDNVGVKVTSGKTC 110

RESULT 4

US-09-555-115A-4
; Sequence 4, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01

; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-4

Query Match 100.0%; Score 100; DB 19; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTSGKTC 18
Db 93 CYFSSKDNVGVKVTSGKTC 110

RESULT 5

US-09-555-115A-11
; Sequence 11, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-11

Query Match 96.0%; Score 96; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTSGKTC 18
Db 1 CYFSSKDNVGVKVTSGKTC 18

RESULT 6

US-09-555-115A-12
; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 96.0%; Score 96; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 7

US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match 96.0%; Score 96; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 8

US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match 96.0%; Score 96; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 9

US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match 96.0%; Score 96; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 10

US-09-555-115A-60
; Sequence 60, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60

Query Match 96.0%; Score 96; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 1 CYFSSKDNVGVKVTGKTC 18

RESULT 11

US-08-882-431B-21
; Sequence 21, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-DA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK

STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-21

Query Match 96.0%; Score 96; DB 12; Length 89;
Best Local Similarity 94.4%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYSSKDNVGVKVTSGKTC 18
|||
Db 54 CYSSKDNVGVKVTSGKTC 71

RESULT 12
US-08-882-431B-22
Sequence 22, Application US/08882431B
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-22

Query Match 96.0%; Score 96; DB 12; Length 89;
Best Local Similarity 94.4%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYSSKDNVGVKVTSGKTC 18
|||
Db 54 CYSSKDNVGVKVTSGKTC 71

RESULT 13
US-08-882-431B-23
Sequence 23, Application US/08882431B
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-23

Query Match 96.0%; Score 96; DB 12; Length 89;
Best Local Similarity 94.4%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYSSKDNVGVKVTSGKTC 18
|||
Db 54 CYSSKDNVGVKVTSGKTC 71

RESULT 14

US-10-002-784A-36
 ; Sequence 36, Application US/10002784A
 ; GENERAL INFORMATION:

;/33
 ; APPLICANT: Ulrich, Robert G.
 ; TITLE OF INVENTION: Bacterial Superantigen Vaccines
 ; FILE REFERENCE: 003/233/SAP
 ; CURRENT APPLICATION NUMBER: US/10/002,784A
 ; CURRENT FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
 ; PRIOR FILING DATE: 97-06-25; 98-09-01
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Apple Macintosh Microsoft Word 6.0
 ; SEQ ID NO 36
 ; LENGTH: 89
 ; TYPE: PRT
 ; ORGANISM: staphylococcal enterotoxin C1
 ; FEATURE:
 ; OTHER INFORMATION: partial sequence as shown in Figure 3
 US-10-002-784A-36

Query Match 96.0%; Score 96; DB 26; Length 89;
 Best Local Similarity 94.4%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTSGKTC 18
 |||||
 DB 54 CYFSSKDNVKGKVTGKTC 71

RESULT 15

US-10-002-784A-37
 ; Sequence 37, Application US/10002784A
 ; GENERAL INFORMATION:

;/33
 ; APPLICANT: Ulrich, Robert G.
 ; TITLE OF INVENTION: Bacterial Superantigen Vaccines
 ; FILE REFERENCE: 003/233/SAP
 ; CURRENT APPLICATION NUMBER: US/10/002,784A
 ; CURRENT FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
 ; PRIOR FILING DATE: 97-06-25; 98-09-01
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Apple Macintosh Microsoft Word 6.0
 ; SEQ ID NO 37
 ; LENGTH: 89
 ; TYPE: PRT
 ; ORGANISM: staphylococcal enterotoxin C2
 ; FEATURE:
 ; OTHER INFORMATION: partial sequence as shown in Figure 3
 US-10-002-784A-37

Query Match 96.0%; Score 96; DB 26; Length 89;
 Best Local Similarity 94.4%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTSGKTC 18
 |||||
 DB 54 CYFSSKDNVKGKVTGKTC 71

Search completed: October 15, 2003, 17:41:16
 Job time : 211.042 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 : Search time 8.08383 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-14

Perfect score: 100

Sequence: 1 CYFSSKDNVGVKTSKTC 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Pending Patents AA New:*
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	47	47.0	375	7 US-60-487-610-2744	Sequence 2744, App
2	47	47.0	375	7 US-60-499-964-460	Sequence 460, App
3	47	47.0	375	7 US-60-499-964-461	Sequence 461, App
4	47	47.0	375	7 US-60-499-964-776	Sequence 776, App
5	47	47.0	375	7 US-60-499-964-777	Sequence 777, App
6	47	47.0	375	7 US-60-499-964-778	Sequence 778, App
7	47	47.0	380	1 PCT-US03-28227-4671	Sequence 4671, App
8	47	47.0	385	7 US-60-487-610-1723	Sequence 1723, App
9	47	47.0	385	7 US-60-499-964-462	Sequence 462, App
10	44	44.0	253	6 US-10-425-114A-52327	Sequence 52327, A
11	44	44.0	257	6 US-10-425-114A-36981	Sequence 36981, A
12	44	44.0	263	6 US-10-425-114A-40237	Sequence 40237, A
13	44	44.0	343	6 US-10-425-114A-39097	Sequence 39097, A
14	44	44.0	343	6 US-10-425-114A-40939	Sequence 40939, A
15	43	43.0	682	7 US-60-493-369-33	Sequence 33, App1
16	43	43.0	682	7 US-60-502-656-59	Sequence 59, App1
17	43	43.0	789	7 US-60-493-369-22	Sequence 22, App1
18	43	43.0	789	7 US-60-493-369-25	Sequence 25, App1
19	43	43.0	789	7 US-60-502-656-60	Sequence 60, App1
20	43	43.0	789	7 US-60-502-656-62	Sequence 62, App1
21	43	43.0	798	7 US-60-487-610-2001	Sequence 2001, App
22	43	43.0	798	7 US-60-487-610-2002	Sequence 2002, App
23	43	43.0	798	7 US-60-487-610-2003	Sequence 2003, App
24	43	43.0	798	7 US-60-493-369-19	Sequence 19, App1
25	43	43.0	798	7 US-60-493-369-24	Sequence 24, App1
26	43	43.0	798	7 US-60-493-369-27	Sequence 27, App1

27	43	43.0	798	7 US-60-493-369-28	Sequence 28, App1
28	43	43.0	798	7 US-60-493-369-32	Sequence 32, App1
29	43	43.0	798	7 US-60-493-369-34	Sequence 34, App1
30	43	43.0	798	7 US-60-502-656-54	Sequence 54, App1
31	43	43.0	798	7 US-60-502-656-58	Sequence 58, App1
32	43	43.0	798	7 US-60-502-656-61	Sequence 61, App1
33	43	43.0	798	7 US-60-502-656-68	Sequence 68, App1
34	43	43.0	798	7 US-60-502-656-70	Sequence 70, App1
35	43	43.0	801	7 US-60-493-369-20	Sequence 20, App1
36	43	43.0	801	7 US-60-493-369-23	Sequence 23, App1
37	43	43.0	801	7 US-60-493-369-31	Sequence 31, App1
38	43	43.0	801	7 US-60-502-656-55	Sequence 55, App1
39	43	43.0	801	7 US-60-502-656-64	Sequence 64, App1
40	43	43.0	801	7 US-60-502-656-69	Sequence 69, App1
41	43	43.0	819	7 US-60-493-369-17	Sequence 17, App1
42	43	43.0	819	7 US-60-493-369-26	Sequence 26, App1
43	43	43.0	819	7 US-60-493-369-30	Sequence 30, App1
44	43	43.0	819	7 US-60-502-656-56	Sequence 56, App1
45	43	43.0	819	7 US-60-502-656-57	Sequence 57, App1

ALIGNMENTS

RESULT 1
US-60-487-610-2744
Sequence 2744, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487, 610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2744
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-2744

Query Match 47.0%; Score 47; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 2.7;
Matches 12; Conservativity 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVKTSKTC 18
DB 175 CFFSTGYGSAVNAVAKVTPGSTC 196

RESULT 2
US-60-499-964-460
Sequence 460, Application US/60499964
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
FILE REFERENCE: CL001481
CURRENT APPLICATION NUMBER: US/60/499, 964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 460
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-460

Query Match 47.0%; Score 47; DB 7; Length 375;

Best Local Similarity	54.5%;	Pred. No. 2.7;	
Matches	12; Conservative	0; Mismatches	6; Indels
			4; Gaps
			1;

QY 1 CYFS---SKDNVGKVTSGKTC 18
175 CGFSTGYGSAVNNAKVTTPGSTC 196
Db

RESULT 3
US-60-499-964-461

```

? GENERAL INFORMATION:
? APPLICANT: CARGILL, Michele
? TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
? TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
? TITLE OF INVENTION: DETECTION AND USES THEREOF
? FILE REFERENCE: CL001481
? CURRENT APPLICATION NUMBER: US/60/499,964
? CURRENT FILING DATE: 2003-09-04
? NUMBER OF SEQ ID NOS: 30431
? SOFTWARE: FastSeq For Windows Version 4.0
? SEQ ID NO 461
? LENGTH: 375
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-60-499-964-461

```

Query Match	47.0%;	Score 47;	DB 7;	Length 375;
Best Local Similarity	54.5%;	Pred. No. 2.7;		
Matches 12;	Conservative 0;	Mismatches 6;	Indels 4;	Gaps 1

QY 1 CYFS---SKDNVGKVTSGKTC 18
175 CGFSTGYGSANVAKVTPGSTC 196
DB

RESULT 4
US-60-499-964-776
; Sequence 776, Application US/60499964

```

1  APPLICANT CARGILL, Michele
2  TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
3  TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
4  TITLE OF INVENTION: DETECTION AND USES THEREOF
5  FILE REFERENCE: CLO01481
6  CURRENT APPLICATION NUMBER: US/60/499,964
7  CURRENT FILING DATE: 2003-09-04
8  NUMBER OF SEQ ID NOS: 30431
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 776
11
12 LENGTH: 375
13
14 TYPE: PRT
15
16 ORGANISM: Homo sapiens
17
18 US-60-499-964-776

```

Query Match	47.0%;	Score 47;	DB 7;	Length 375;
Best Local Similarity	54.5%;	Pred. No. 2.7;		
Matches 12;	Conservative 0;	Mismatches 6;	Indels 4;	Gaps 1

QY 1 CYFS---SKDNVGKVTSGKTC 18
| | | | | | | | | |
Db 1.75 CGFSTGYGSANVAKVTTPGSTC 196

```

; RESULT 5
; US-60-499-364-777
; Sequence 777, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481

```

```

; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777

```

Query Match	47.04;	Score 47;	DB 7;	Length 375;
Best Local Similarity	54.58;	Pred. No. 2.7;		
Matches 12;	Conservative 0;	Mismatches 6;	Indels 4;	Gaps 1.

Qy 1 CYFS---SKDNVGKVTSGKTC 18
175 CGFSTGYGSANVNAKVTTPGSTC 196
Db

RESULT 6
US-60-499-964-778

```

? GENERAL INFORMATION.
? APPLICANT: CARGILL, Michele
? TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
? TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
? TITLE OF INVENTION: DETECTION AND USES THEREOF
? FILE REFERENCE: CL001481
? CURRENT APPLICATION NUMBER: US/60/499,964
? CURRENT FILING DATE: 2003-09-04
? NUMBER OF SEQ. ID NOS: 30431
? SOFTWARE: FASTSEQ For Windows Version 4.0
? SEQ. ID NO 778
? LENGTH: 375
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-60-499-964-778

```

Query Match	47.0%	Score 47	DB 7	length 375
Best Local	54.5%	Pred. No. 2.7		
Matches 12	Conservative 0	Mismatches 6	Indels 4	Gaps 1

QY 1 CYFS---SKDNVGKVTSGKTC 18
175 CGFSTGYGSANVAKVTPGSTC 196
Db

RESULT 7
PCT-US03-28227-4671

APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARCANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STIVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GLEITZEN, Darryl; PATURY, Srikenth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charilyn J.

;; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: PN-0100 PCT
;; CURRENT APPLICATION NUMBER: PCT/US03/28227
;; CURRENT FILING DATE: 2003-09-12
;; PRIOR APPLICATION NUMBER: US 60/410,260
;; PRIOR FILING DATE: 2002-09-12
;; PRIOR APPLICATION NUMBER: US 60/410,259
;; PRIOR FILING DATE: 2002-09-12
;; NUMBER OF SEQ ID NOS: 5444
;; SOFTWARE: PERL Program
;; SEQ ID NO 4671
;; LENGTH: 380
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No: 962211.PT69P
PCT-US03-28227-4671

Query Match 47.0%; Score 47; DB 1; Length 380;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CYFS---SKDNVGYTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 180 CGFSTGYGSAVNVAKYTPGSTC 201

RESULT 8
US-60-487-610-1723
;; Sequence 1723, Application US/60487610
;; GENERAL INFORMATION:
;; APPLICANT: CARGILL, Michele
;; APPLICANT: HUANG, Hongjin
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;; FILE REFERENCE: CL001469
;; CURRENT APPLICATION NUMBER: US/60/487,610
;; CURRENT FILING DATE: 2003-07-17
;; NUMBER OF SEQ ID NOS: 97101
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1723
;; LENGTH: 385
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-487-610-1723

Query Match 47.0%; Score 47; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CYFS---SKDNVGYTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 175 CGFSTGYGSAVNVAKYTPGSTC 196

RESULT 9
US-60-499-964-462
;; Sequence 462, Application US/60499964
;; GENERAL INFORMATION:
;; APPLICANT: CARGILL, Michele
;; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
;; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
;; FILE REFERENCE: CL001481
;; CURRENT APPLICATION NUMBER: US/60/499,964
;; CURRENT FILING DATE: 2003-09-04
;; NUMBER OF SEQ ID NOS: 30431
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 462
;; LENGTH: 385
;; TYPE: PRT

;; ORGANISM: Homo sapiens
US-60-499-964-462

Query Match 47.0%; Score 47; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CYFS---SKDNVGYTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 175 CGFSTGYGSAVNVAKYTPGSTC 196

RESULT 10
US-10-425-114A-52327
;; Sequence 52327, Application US/10425114A
;; GENERAL INFORMATION:
;; APPLICANT: Liu, Jingdong
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Screen, Steven E
;; APPLICANT: Tabaska, Jack E
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53313)B
;; CURRENT APPLICATION NUMBER: US/10/425,114A
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 73128
;; SEQ ID NO 52327
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; OTHER INFORMATION: Clone ID: 700872843_FLI.pep
US-10-425-114A-52327

Query Match 44.0%; Score 44; DB 6; Length 253;
Best Local Similarity 46.7%; Pred. No. 5.6;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGYTSG 15
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Db 118 CYASSADNIAFMLKG 132

RESULT 11
US-10-425-114A-36981
;; Sequence 36981, Application US/10425114A
;; GENERAL INFORMATION:
;; APPLICANT: Liu, Jingdong
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Screen, Steven E
;; APPLICANT: Tabaska, Jack E
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53313)B
;; CURRENT APPLICATION NUMBER: US/10/425,114A
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 73128
;; SEQ ID NO 36981
;; LENGTH: 257
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; OTHER INFORMATION: Clone ID: LIB3170-051-G3_FLI.pep
US-10-425-114A-36981

Query Match 44.0%; Score 44; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 5.7;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSG 15
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Db 120 CVASSADNIARMLKG 134

RESULT 12

US-10-425-114A-40237
; Sequence 40237, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovailic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40237
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701109042_FLI.pep
US-10-425-114A-40237

Query Match 44.0%; Score 44; DB 6; Length 263;
Best Local Similarity 46.7%; Pred. No. 5.9;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSG 15
||| ||| : : :
Db 137 CVASSADNIARMLKG 151

RESULT 13

US-10-425-114A-39097
; Sequence 39097, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovailic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39097
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-052-C9_FLI.pep
US-10-425-114A-39097

Query Match 44.0%; Score 44; DB 6; Length 343;
Best Local Similarity 46.7%; Pred. No. 7.9;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSG 15
||| ||| : : :
Db 206 CVASSADNIARMLKG 220

RESULT 14
US-10-425-114A-40939

; Sequence 40939, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovailic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40939
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-084-A12_FLI.pep
US-10-425-114A-40939

Query Match 44.0%; Score 44; DB 6; Length 343;
Best Local Similarity 46.7%; Pred. No. 7.9;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSG 15
||| ||| : : :
Db 206 CVASSADNIARMLKG 220

RESULT 15
US-60-493-369-33
; Sequence 33, Application US/60493369
; GENERAL INFORMATION:
; APPLICANT: Bruce DOMON
; APPLICANT: Tao HE
; APPLICANT: Aiqun LI
; APPLICANT: Xiaolong ZHANG
; APPLICANT: Karen KETCHUM
; APPLICANT: Ian MCCAFFERY
; TITLE OF INVENTION: PANCREATIC DISEASES TARGETS AND USE
; FILE REFERENCE: CL001476
; CURRENT APPLICATION NUMBER: US/60/493,369
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-493-369-33

Query Match 43.0%; Score 43; DB 7; Length 682;
Best Local Similarity 38.9%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSGKTC 18
||| ||| : : :
Db 479 CVCRRKDNTEIISGKFC 496

Search completed: October 15, 2003, 17:42:39
Job time : 8.08383 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: October 15, 2003, 16:57:11 ; Search time 211.042 Seconds
(without alignments)
77.608 Million cell updates/sec

Title: US-09-555-115A-15
Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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32: /cgn2_6/ptodata/1/paa/US60 COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	18	19	US-09-555-115A-11
					Sequence 11, Appl

2	102	100.0	18	19	US-09-555-115A-12	Sequence 12, Appl
3	102	100.0	18	19	US-09-555-115A-13	Sequence 13, Appl
4	102	100.0	18	19	US-09-555-115A-15	Sequence 15, Appl
5	102	100.0	18	19	US-09-555-115A-16	Sequence 16, Appl
6	102	100.0	18	19	US-09-555-115A-60	Sequence 60, Appl
7	102	100.0	18	12	US-08-882-431B-21	Sequence 21, Appl
8	102	100.0	89	12	US-08-882-431B-22	Sequence 22, Appl
9	102	100.0	89	12	US-08-882-431B-23	Sequence 23, Appl
10	102	100.0	89	26	US-10-002-784A-36	Sequence 36, Appl
11	102	100.0	89	26	US-10-002-784A-37	Sequence 37, Appl
12	102	100.0	89	26	US-10-002-784A-38	Sequence 38, Appl
13	102	100.0	234	22	US-09-791-537-107560	Sequence 107560, Appl
14	102	100.0	238	8	US-08-491-746-27	Sequence 27, Appl
15	102	100.0	238	21	US-09-708-008B-28	Sequence 28, Appl
16	102	100.0	239	8	US-08-491-746-26	Sequence 26, Appl
17	102	100.0	239	21	US-09-708-008B-27	Sequence 27, Appl
18	102	100.0	239	22	US-09-791-537-52671	Sequence 52671, A
19	102	100.0	239	22	US-09-791-537-52673	Sequence 52673, A
20	102	100.0	239	22	US-09-791-537-52675	Sequence 52675, A
21	102	100.0	239	22	US-09-791-537-52677	Sequence 52677, A
22	102	100.0	239	22	US-09-791-537-57117	Sequence 57117, A
23	102	100.0	239	22	US-09-791-537-128386	Sequence 128386, A
24	102	100.0	240	19	US-09-555-115A-1	Sequence 1, Appl
25	102	100.0	240	19	US-09-555-115A-2	Sequence 2, Appl
26	102	100.0	240	19	US-09-555-115A-3	Sequence 3, Appl
27	102	100.0	240	19	US-09-555-115A-5	Sequence 5, Appl
28	102	100.0	240	19	US-09-555-115A-6	Sequence 6, Appl
29	102	100.0	266	1	PCT-US98-16766-14	Sequence 14, Appl
30	102	100.0	266	12	US-08-882-431-14	Sequence 14, Appl
31	102	100.0	266	12	US-08-882-431B-14	Sequence 14, Appl
32	102	100.0	266	12	US-08-882-431B-1	Sequence 1, Appl
33	102	100.0	266	12	US-09-751-708A-12	Sequence 12, Appl
34	102	100.0	266	22	US-09-791-537-93999	Sequence 93999, A
35	102	100.0	266	22	US-09-791-537-94000	Sequence 94000, A
36	102	100.0	266	22	US-09-791-537-115863	Sequence 115863, A
37	102	100.0	266	23	US-09-870-759-12	Sequence 12, Appl
38	102	100.0	266	26	US-10-002-784A-14	Sequence 14, Appl
39	96	94.1	18	19	US-09-555-115A-14	Sequence 14, Appl
40	96	94.1	239	22	US-09-791-537-17768	Sequence 17768, A
41	96	94.1	239	22	US-09-791-537-52676	Sequence 52676, A
42	96	94.1	240	19	US-09-555-115A-4	Sequence 4, Appl
43	96	94.1	240	19	US-09-555-115A-7	Sequence 7, Appl
44	93	91.2	18	19	US-09-555-115A-17	Sequence 17, Appl
45	93	91.2	239	22	US-09-791-537-52695	Sequence 52695, A

ALIGNMENTS

RESULT 1
US-09-555-115A-11
; Sequence 11, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136 USXO
; CURRENT APPLICATION NUMBER: US/09/555, 115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-11

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVKGVTGKTC 18
Db 1 CFFSSKDNVKGVTGKTC 18

RESULT 2

US-09-555-115A-12
; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:

; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVKGVTGKTC 18
Db 1 CFFSSKDNVKGVTGKTC 18

RESULT 3

US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:

; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVKGVTGKTC 18
Db 1 CFFSSKDNVKGVTGKTC 18

RESULT 4

US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO

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; CURRENT APPLICATION NUMBER: US/09/555,115A

; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVKGVTGKTC 18
Db 1 CFFSSKDNVKGVTGKTC 18

RESULT 5

US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:

; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVKGVTGKTC 18
Db 1 CFFSSKDNVKGVTGKTC 18

RESULT 6

US-09-555-115A-60
; Sequence 60, Application US/09555115A
; GENERAL INFORMATION:

; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60

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Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8 7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
|||
Db 1 CYFSSKDNVGVGTGKTC 18

RESULT 7

US-08-882-431B-21
; Sequence 21, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-21

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
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Db 54 CYFSSKDNVGVGTGKTC 71

RESULT 8

US-08-882-431B-22
; Sequence 22, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines

NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
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; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
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; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-22

Query Match 100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
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Db 54 CYFSSKDNVGVGTGKTC 71

RESULT 9

US-08-882-431B-23
; Sequence 23, Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Charles H. Harris
;   REGISTRATION NUMBER: 34,616
;   REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 619-2065
;   TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 89
;     TYPE: Amino Acid
;     STRANDEDNESS: Unknown
;     TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-23

Query Match
Best Local Similarity 100.0%; Score 102; DB 12; Length 89;
Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
Db 54 CYFSSKDNVGVKVTGGKTC 71

RESULT 10
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-36

Query Match
Best Local Similarity 100.0%; Score 102; DB 26; Length 89;
Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
Db 54 CYFSSKDNVGVKVTGGKTC 71

RESULT 11
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
```

```

; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-37

Query Match
Best Local Similarity 100.0%; Score 102; DB 26; Length 89;
Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
Db 54 CYFSSKDNVGVKVTGGKTC 71

RESULT 12
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-38

Query Match
Best Local Similarity 100.0%; Score 102; DB 26; Length 89;
Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10CYFSSKDNVGVKVTGGKTC 18
Db 54 CYFSSKDNVGVKVTGGKTC 71

RESULT 13
US-09-791-537-107560
; Sequence 107560, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107560
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus
; US-09-791-537-107560

Query Match
Best Local Similarity 100.0%; Score 102; DB 22; Length 234;
Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
Db 88 CYFSSKDNVGVKVTGGKTC 105
```

RESULT 14

US-08-491-746-27
 ; Sequence 27, Application US/08491746
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
 ; FILE REFERENCE: 09629/006002
 ; CURRENT APPLICATION NUMBER: US/08/491,746
 ; FILING DATE: 1995-06-19
 ; EARLIER APPLICATION NUMBER: 08/189,424
 ; EARLIER FILING DATE: 1994-01-31
 ; EARLIER APPLICATION NUMBER: 08/025,144
 ; EARLIER FILING DATE: 1993-03-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: PCT/US91/00342
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; NUMBER OF SEQ. ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-08-491-746-27

Query Match

100.0%; Score 102; DB 8; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1 CYFSSKDNVKGKTC 18
 |||||

Db

92 CYFSSKDNVKGKTC 109

RESULT 15

US-09-708-008B-28
 ; Sequence 28, Application US/09708008B
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/09/708,008B
 ; FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: US/08/896,933
 ; PRIOR FILING DATE: 1997-07-18
 ; PRIOR APPLICATION NUMBER: 08/252,978
 ; PRIOR FILING DATE: 1994-06-02
 ; NUMBER OF SEQ. ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-09-708-008B-28

Query Match

100.0%; Score 102; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1 CYFSSKDNVKGKTC 18
 |||||

Db

92 CYFSSKDNVKGKTC 109

Search completed: October 15, 2003, 17:41:16
 Job time : 211.042 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 8.0883 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-15
Perfect score: 102
Sequence: 1 CYPSSKDNVSKVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*
1: /cgn2_6/ptodaca/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodaca/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodaca/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodaca/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodaca/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodaca/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodaca/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	45.1	375	7	US-60-487-610-2744
2	46	45.1	375	7	US-60-499-964-460
3	46	45.1	375	7	US-60-499-964-461
4	46	45.1	375	7	US-60-499-964-776
5	46	45.1	375	7	US-60-499-964-777
6	46	45.1	375	7	US-60-499-964-778
7	46	45.1	380	1	PCT-US03-28227-4671
8	46	45.1	385	7	US-60-487-610-1723
9	46	45.1	385	7	US-60-499-964-462
10	44	43.1	1403	1	PCT-US03-14382-30
11	44	43.1	1403	1	PCT-US03-14382A-30
12	44	43.1	1462	1	PCT-US03-14382-31
13	44	43.1	1462	1	PCT-US03-14382A-31
14	42	41.2	253	6	US-10-425-114A-52327
15	42	41.2	257	6	US-10-425-114A-36981
16	42	41.2	263	6	US-10-425-114A-40237
17	42	41.2	343	6	US-10-425-114A-39097
18	42	41.2	343	6	US-10-425-114A-40939
19	42	41.2	418	6	US-10-425-114A-49025
20	41	40.2	246	7	US-60-499-964-414
21	41	40.2	246	7	US-60-499-964-415
22	41	40.2	340	1	PCT-US03-28227-4677
23	41	40.2	357	1	PCT-US03-28227-4674
24	41	40.2	357	1	PCT-US03-28227-4676
25	41	40.2	358	1	PCT-US03-28227-4675
26	41	40.2	358	1	PCT-US03-28227-4678

27	41	40.2	368	7	US-60-487-610-1505	Sequence 1505, Ap
28	41	40.2	382	7	US-60-487-610-1506	Sequence 1506, Ap
29	40	39.2	335	7	US-60-499-964-463	Sequence 463, App
30	40	39.2	348	1	PCT-US03-19153-166	Sequence 166, App
31	40	39.2	375	7	US-60-487-610-1724	Sequence 1724, Ap
32	40	39.2	375	7	US-60-499-964-464	Sequence 464, App
33	40	39.2	429	6	US-10-425-114A-64698	Sequence 64698, A
34	40	39.2	433	6	US-10-425-114A-67284	Sequence 67284, A
35	39.5	38.7	417	6	US-10-389-647-494	Sequence 494, App
36	39	38.2	170	6	US-10-419-462-43	Sequence 43, App
37	39	38.2	416	5	US-09-897-516A-6844	Sequence 6844, Ap
38	39	38.2	682	7	US-60-493-369-33	Sequence 33, App
39	39	38.2	682	7	US-60-502-656-59	Sequence 59, App
40	39	38.2	789	7	US-60-493-369-22	Sequence 22, App
41	39	38.2	789	7	US-60-493-369-25	Sequence 25, App
42	39	38.2	789	7	US-60-502-656-60	Sequence 60, App
43	39	38.2	789	7	US-60-502-656-62	Sequence 62, App
44	39	38.2	798	7	US-60-487-610-2001	Sequence 2001, Ap
45	39	38.2	798	7	US-60-487-610-2002	Sequence 2002, Ap

ALIGNMENTS

```
RESULT 1
US-60-487-610-2744
; Sequence 2744, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LAYER FIROSIS IN HEPATITIS C VIRUS- INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2744
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2744

Query Match          45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy      1  CYPSSKDNVSKVTGKTC 18
Db      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 2
US-60-499-964-460
; Sequence 460, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-460

Query Match          45.1%; Score 46; DB 7; Length 375;
```

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 3

US-60-499-964-461
; Sequence 461, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 461
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-461

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 4

US-60-499-964-776
; Sequence 776, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-776

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 5

US-60-499-964-777
; Sequence 777, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481

CURRENT APPLICATION NUMBER: US/60/499,964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 777
LENGTH: 385
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-777

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 6

US-60-499-964-778
; Sequence 778, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-778

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 7

PCT-US03-28227-4671
; Sequence 4671, Application PC/TUS0328227
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
; APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
; APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOWOLSKI, Martin;
; APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
; APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
; APPLICANT: DELESEANE, Angelo M.; PANESAR, Iqbal S.;
; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
; APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
; APPLICANT: WU, Mingham C.; STUVE, Laura L.;
; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
; APPLICANT: VITT, Ursula A.; KIRTON, Edward;
; APPLICANT: XU, Yuming; KWONG, Mary;
; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
; APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.

```

; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PN-0100 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/28227
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/410,260
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/410,259
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 5444
; SOFTWARE: PERL Program
; SEQ ID NO 4671
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 962211.PT69P
PCT-US03-28227-4671

```

```

Query Match          45.1%; Score 46; DB 1; Length 380;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

```

```

QY      1  CYFS---SKDNVGVKVTGKTC 18
      |||  |||  |||  |||  |||
Db      180  CGFSTGYGSAVNVAKVTPGSGTC 201

```

```

RESULT 8
US-60-487-610-1723
; Sequence 1723, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1723

```

```

Query Match          45.1%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

```

```

QY      1  CYFS---SKDNVGVKVTGKTC 18
      |||  |||  |||  |||  |||
Db      175  CGFSTGYGSAVNVAKVTPGSGTC 196

```

```

RESULT 9
US-60-499-964-462
; Sequence 462, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 385
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-60-499-964-462

```

```

Query Match          45.1%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

```

```

QY      1  CYFS---SKDNVGVKVTGKTC 18
      |||  |||  |||  |||  |||
Db      175  CGFSTGYGSAVNVAKVTPGSGTC 196

```

```

RESULT 10
PCT-US03-14382-30
; Sequence 30, Application PC/TUS0314382
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-30

```

```

Query Match          43.1%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 13e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      1  CYFSKDNVGVKVTGKTC 18
      |||  |||  |||  |||  |||
Db      95  CLCSGKGLGKTTGKKLC 112

```

```

RESULT 11
PCT-US03-14382A-30
; Sequence 30, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-30

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Best Local Similarity 44.4%; Pred. No. 13e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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PCT-US03-14382-31
; Sequence 31, Application PC/TUS0314382

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; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-31

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Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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Db      41  CLCGSEKGLGKTGKLC 58

RESULT 13
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; Sequence 31, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-31

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Best Local Similarity 44.4%; Pred. No. 1.4e+02;
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; Sequence 52327, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52327
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700872843_FLI.pep
US-10-425-114A-52327

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RESULT 15
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; Sequence 36981, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36981
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-051-G3_FLI.pep
US-10-425-114A-36981

Query Match      41.2%; Score 42; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGG 15
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Search completed: October 15, 2003, 17:42:39
Job time : 8.08383 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2003, 16:57:11 : Search time 211.042 Seconds
(without alignments)
77.608 Million cell updates/sec

Title: US-09-555-115A-16

Perfect score: 102
Sequence: 1 CYPSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	102	100.0	18	US-09-555-115A-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1 0

US-09-555-115A-11

Sequence 11, Application US/09555115A

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136.1USXO

CURRENT APPLICATION NUMBER: US/09/555, 115A

CURRENT FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067,357

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 18

TYPE: PRT

ORGANISM: *Staphylococcus aureus*

US-09-555-115A-11

Query Match 100.0%; Score 102; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  CYFSSKDNVGVKGKTC 18

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; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match      100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CYFSSKDNVGVKGKTC 18
Db      1  CYFSSKDNVGVKGKTC 18

RESULT 3
US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match      100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CYFSSKDNVGVKGKTC 18
Db      1  CYFSSKDNVGVKGKTC 18

RESULT 4
US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
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; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match      100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CYFSSKDNVGVKGKTC 18
Db      1  CYFSSKDNVGVKGKTC 18

RESULT 5
US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match      100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CYFSSKDNVGVKGKTC 18
Db      1  CYFSSKDNVGVKGKTC 18

RESULT 6
US-09-555-115A-60
; Sequence 60, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60
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Query Match 100.0%; Score 102; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKGTGKTC 18
|||||
Db 1 CYFSSKDNVGVKGTGKTC 18

RESULT 7
US-08-882-431B-21

; Sequence 21, Application US/08882431B
; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,

; APPLICANT: Mark A. Olson

; TITLE OF INVENTION: Bacterial Superantigen

; TITLE OF INVENTION: Vaccines

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles H. Harris

; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/882,431B

; FILING DATE: June 25, 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

; REGISTRATION NUMBER: 34,616

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 89

; TYPE: Amino Acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; MOLECULE TYPE: Peptide

; US-08-882-431B-21

QY 1 CYFSSKDNVGVKGTGKTC 18
|||||
Db 54 CYFSSKDNVGVKGTGKTC 71

RESULT 8
US-08-882-431B-22

; Sequence 22, Application US/08882431B
; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,

; APPLICANT: Mark A. Olson

; TITLE OF INVENTION: Bacterial Superantigen

; TITLE OF INVENTION: Vaccines

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles H. Harris

; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/882,431B

; FILING DATE: June 25, 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

; REGISTRATION NUMBER: 34,616

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 89

; TYPE: Amino Acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; MOLECULE TYPE: Peptide

; US-08-882-431B-22

QY 1 CYFSSKDNVGVKGTGKTC 18
|||||
Db 54 CYFSSKDNVGVKGTGKTC 71

RESULT 9
US-08-882-431B-23

; Sequence 23, Application US/08882431B
; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,

; APPLICANT: Mark A. Olson

; TITLE OF INVENTION: Bacterial Superantigen

; TITLE OF INVENTION: Vaccines

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles H. Harris

; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/882,431B

; FILING DATE: June 25, 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-23

Query Match          100.0%; Score 102; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
        |||
        54  CYFSSKDNVGVKVTGKTC 71

RESULT 10
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-36

Query Match          100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
        |||
        54  CYFSSKDNVGVKVTGKTC 71

RESULT 11
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
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; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-37

Query Match          100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
        |||
        54  CYFSSKDNVGVKVTGKTC 71

RESULT 12
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-38

Query Match          100.0%; Score 102; DB 26; Length 89;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
        |||
        54  CYFSSKDNVGVKVTGKTC 71

RESULT 13
US-09-791-537-107560
; Sequence 107560, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107560
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus
; US-09-791-537-107560

Query Match          100.0%; Score 102; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
        |||
        88  CYFSSKDNVGVKVTGKTC 105
```


RESULT 14

US-08-491-746-27
 ; Sequence 27, Application US/08491746
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: METHOD OF CANCER TREATMENT
 ; FILE REFERENCE: 09629/006002
 ; CURRENT APPLICATION NUMBER: US/08/491,746
 ; CURRENT FILING DATE: 1995-06-19
 ; EARLIER APPLICATION NUMBER: 08/189,424
 ; EARLIER FILING DATE: 1994-01-31
 ; EARLIER APPLICATION NUMBER: 08/025,144
 ; EARLIER FILING DATE: 1993-03-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: PCT/US91/00342
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-08-491-746-27

Query Match

100.0%; Score 102; DB 8; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
 |||||
 Db 92 CYFSSKDNVKGVTGKTC 109

RESULT 15

US-09-708-008B-28
 ; Sequence 28, Application US/09708008B
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/09/708,008B
 ; CURRENT FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: US/08/896,933
 ; PRIOR FILING DATE: 1997-07-18
 ; PRIOR APPLICATION NUMBER: 08/252,978
 ; PRIOR FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureas
 US-09-708-008B-28

Query Match 100.0%; Score 102; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
 |||||
 Db 92 CYFSSKDNVKGVTGKTC 109

Search completed: October 15, 2003, 17:41:17
 Job time : 212.042 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 8.08383 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-16
Perfect score: 102
Sequence: 1 CYPSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	45.1	375	7	US-60-487-610-2744
2	46	45.1	375	7	US-60-499-964-460
3	46	45.1	375	7	US-60-499-964-461
4	46	45.1	375	7	US-60-499-964-776
5	46	45.1	375	7	US-60-499-964-777
6	46	45.1	375	7	US-60-499-964-778
7	46	45.1	380	1	PCT-US03-28227-4671
8	46	45.1	385	7	US-60-487-610-1723
9	46	45.1	385	7	US-60-499-964-462
10	44	43.1	1403	1	PCT-US03-14382-30
11	44	43.1	1403	1	PCT-US03-14382-30
12	44	43.1	1462	1	PCT-US03-14382-31
13	44	43.1	1462	1	PCT-US03-14382-31
14	42	41.2	253	6	US-10-425-114A-52327
15	42	41.2	257	6	US-10-425-114A-36981
16	42	41.2	263	6	US-10-425-114A-40237
17	42	41.2	343	6	US-10-425-114A-39097
18	42	41.2	343	6	US-10-425-114A-40939
19	42	41.2	418	6	US-10-425-114A-49025
20	41	40.2	246	7	US-60-499-964-414
21	41	40.2	246	7	US-60-499-964-415
22	41	40.2	340	1	PCT-US03-28227-4677
23	41	40.2	357	1	PCT-US03-28227-4674
24	41	40.2	357	1	PCT-US03-28227-4676
25	41	40.2	358	1	PCT-US03-28227-4675
26	41	40.2	358	1	PCT-US03-28227-4678

27	41	40.2	368	7	US-60-487-610-1505	Sequence 1505, Ap
28	41	40.2	382	7	US-60-487-610-1506	Sequence 1506, Ap
29	40	39.2	335	7	US-60-499-964-463	Sequence 463, App
30	40	39.2	348	1	PCT-US03-19153-166	Sequence 166, App
31	40	39.2	375	7	US-60-487-610-1724	Sequence 1724, Ap
32	40	39.2	375	7	US-60-499-964-464	Sequence 464, App
33	40	39.2	429	6	US-10-425-114A-64698	Sequence 64698, A
34	40	39.2	433	6	US-10-425-114A-67284	Sequence 67284, A
35	39.5	38.7	417	6	US-10-389-647-494	Sequence 494, App
36	39	38.2	170	6	US-10-419-462-43	Sequence 43, App
37	39	38.2	416	5	US-09-897-516A-6844	Sequence 6844, Ap
38	39	38.2	682	7	US-60-493-369-33	Sequence 33, App
39	39	38.2	682	7	US-60-502-656-59	Sequence 59, App
40	39	38.2	789	7	US-60-493-369-22	Sequence 22, App
41	39	38.2	789	7	US-60-493-369-25	Sequence 25, App
42	39	38.2	789	7	US-60-502-656-60	Sequence 60, App
43	39	38.2	789	7	US-60-502-656-62	Sequence 62, App
44	39	38.2	798	7	US-60-487-610-2001	Sequence 2001, Ap
45	39	38.2	798	7	US-60-487-610-2002	Sequence 2002, Ap

ALIGNMENTS

RESULT 1
US-60-487-610-2744 Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487, 610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2744
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-2744

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Oy 1 CYPSSKDNVKGVTGKTC 18
Db 175 CFPSTGGSANVAKTTPGSTC 196

RESULT 2
US-60-499-964-460 Application US/60499964
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
FILE REFERENCE: CL001481
CURRENT APPLICATION NUMBER: US/60/499, 964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 460
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-460

Query Match 45.1%; Score 46; DB 7; Length 375;

Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGVTKGKTC 18
Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 3

US-60-499-964-461
; Sequence 461, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 461
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-461

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGVTKGKTC 18
Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 4

US-60-499-964-776
; Sequence 776, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-776

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGVTKGKTC 18
Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 5

US-60-499-964-777
; Sequence 777, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481

CURRENT APPLICATION NUMBER: US/60/499,964
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 30431
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 777
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-60-499-964-777

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGVTKGKTC 18
Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 6

US-60-499-964-778
; Sequence 778, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 778
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-778

Query Match 45.1%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGVTKGKTC 18
Db 175 CGFSTGYGSANVAVKATPGSTC 196

RESULT 7

PCT-US03-28227-4671
; Sequence 4671, Application PC/TUS0328227
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
; APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
; APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
; APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
; APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
; APPLICANT: DELGEMANE, Angelo M.; PANESAR, Iqbal S.;
; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
; APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
; APPLICANT: WU, Mingham C.; STUVE, Laura L.;
; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
; APPLICANT: VITT, Ureula A.; KIRTON, Edward;
; APPLICANT: XU, Yuming; KWONG, Mary;
; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
; APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.

```

; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PN-0100 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/28227
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/410,260
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/410,259
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 5444
; SOFTWARE: PERL Program
; SEQ ID NO 4671
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 962211.PT69P
PCT-US03-28227-4671

Query Match          45.1%; Score 46; DB 1; Length 380;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYFS----SKDNVKGVTGKTC 18
        |||  |||  |||  |||  |||
Db      180  CGFSTGYGSANVNAKVTGPGSTC 201

RESULT 8
US-60-487-610-1723
; Sequence 1723, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1723

Query Match          45.1%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYFS----SKDNVKGVTGKTC 18
        |||  |||  |||  |||  |||
Db      175  CGFSTGYGSANVNAKVTGPGSTC 196

RESULT 9
US-60-499-964-462
; Sequence 462, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 385
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-60-499-964-462

Query Match          45.1%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYFS----SKDNVKGVTGKTC 18
        |||  |||  |||  |||  |||
Db      175  CGFSTGYGSANVNAKVTGPGSTC 196

RESULT 10
PCT-US03-14382-30
; Sequence 30, Application PC/TUS0314382
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-30

Query Match          43.1%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGVTGKTC 18
        |||  |||  |||  |||  |||
Db      95  CLCSGKGGKGTGKTLK 112

RESULT 11
PCT-US03-14382A-30
; Sequence 30, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-30

Query Match          43.1%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGVTGKTC 18
        |||  |||  |||  |||  |||
Db      95  CLCSGKGGKGTGKTLK 112

RESULT 12
PCT-US03-14382-31
; Sequence 31, Application PC/TUS0314382
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; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
;   TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382-31

Query Match      43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVTKGKTC 18
Db      41  CLCGSEKGLGKTKGKLC 58

RESULT 13
PCT-US03-14382A-31
; Sequence 31, Application PC/TUS0314382A
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
;   TITLE OF INVENTION: ANTIVIRAL AGENTS
; FILE REFERENCE: 12804-011W01
; CURRENT APPLICATION NUMBER: PCT/US03/14382A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 60/378,711
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1462
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-14382A-31

Query Match      43.1%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVTKGKTC 18
Db      41  CLCGSEKGLGKTKGKLC 58

RESULT 14
US-10-425-114A-52327
; Sequence 52327, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;   TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52327
; LENGTH: 253
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: 0
; OTHER INFORMATION: Clone ID: 700872843_FLI.pep
US-10-425-114A-52327

Query Match      41.2%; Score 42; DB 6; Length 253;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVTKG 15
Db      118  CYASSADNIRMLKG 132

RESULT 15
US-10-425-114A-36981
; Sequence 36981, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;   TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36981
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: 0
; OTHER INFORMATION: Clone ID: LIB3170-051-G3_FLI.pep
US-10-425-114A-36981

Query Match      41.2%; Score 42; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVTKG 15
Db      120  CYASSADNIRMLKG 134

Search completed: October 15, 2003, 17:42:40
Job time : 9.08383 secs
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Thu Oct 16 09:57:27 2003

GenCore version 5.1.5
 (c) 1993 - 2003
 All alignments
 Copyright (c) 1993 - 2003
 100 Million cell updates/sec

OM protein - protein search, using SW
 October 15, 2003
 0.5
 Run on: US-09-918778 residues
 5728757

Perfect score: 100000000
 Sequence: 100% chosen parameters: 5728757
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 Matching first 45 summaries

5 Pending Patents AA Main:*

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32:	/cgn2_6/prodata/1/paa/US056_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match Length	DB	ID	Description
1	104	100.0	18	19	US-09-555-115A-17

2	104	100.0	239	22	US-09-791-537-52695	Sequence 52695, A
3	98	94.2	240	19	US-09-555-115A-8	Sequence 8, Appl1
4	93	89.4	18	19	US-09-555-115A-11	Sequence 11, Appl1
5	93	89.4	18	19	US-09-555-115A-12	Sequence 12, Appl1
6	93	89.4	18	19	US-09-555-115A-13	Sequence 13, Appl1
7	93	89.4	18	19	US-09-555-115A-15	Sequence 15, Appl1
8	93	89.4	18	19	US-09-555-115A-16	Sequence 16, Appl1
9	93	89.4	18	19	US-09-555-115A-17	Sequence 17, Appl1
10	93	89.4	89	12	US-08-882-431B-21	Sequence 21, Appl1
11	93	89.4	89	12	US-08-882-431B-22	Sequence 22, Appl1
12	93	89.4	89	12	US-08-882-431B-23	Sequence 23, Appl1
13	93	89.4	89	12	US-10-002-784A-36	Sequence 36, Appl1
14	93	89.4	89	26	US-10-002-784A-37	Sequence 37, Appl1
15	93	89.4	89	26	US-10-002-784A-38	Sequence 38, Appl1
16	93	89.4	234	22	US-09-791-537-107560	Sequence 107560, A
17	93	89.4	238	8	US-08-491-746-27	Sequence 27, Appl1
18	93	89.4	238	8	US-09-708-008B-28	Sequence 28, Appl1
19	93	89.4	239	8	US-08-491-746-26	Sequence 26, Appl1
20	93	89.4	239	21	US-09-708-008B-27	Sequence 27, Appl1
21	93	89.4	239	22	US-09-791-537-52671	Sequence 52671, A
22	93	89.4	239	22	US-09-791-537-52672	Sequence 52672, A
23	93	89.4	239	22	US-09-791-537-52673	Sequence 52673, A
24	93	89.4	239	22	US-09-791-537-52675	Sequence 52675, A
25	93	89.4	239	22	US-09-791-537-52677	Sequence 52677, A
26	93	89.4	239	22	US-09-791-537-52679	Sequence 52679, A
27	93	89.4	240	19	US-09-555-115A-1	Sequence 1, Appl1
28	93	89.4	240	19	US-09-555-115A-2	Sequence 2, Appl1
29	93	89.4	240	19	US-09-555-115A-3	Sequence 3, Appl1
30	93	89.4	240	19	US-09-555-115A-5	Sequence 5, Appl1
31	93	89.4	240	19	US-09-555-115A-6	Sequence 6, Appl1
32	93	89.4	266	12	PCT-US98-16766-14	Sequence 14, Appl1
33	93	89.4	266	12	US-08-882-431A-14	Sequence 14, Appl1
34	93	89.4	266	12	US-08-882-431A-14	Sequence 14, Appl1
35	93	89.4	266	12	US-08-882-431B-14	Sequence 14, Appl1
36	93	89.4	266	22	US-09-751-708A-12	Sequence 12, Appl1
37	93	89.4	266	22	US-09-791-537-93999	Sequence 93999, A
38	93	89.4	266	22	US-09-791-537-94000	Sequence 94000, A
39	93	89.4	266	22	US-09-791-537-115863	Sequence 115863, A
40	93	89.4	266	22	US-09-870-759-12	Sequence 12, Appl1
41	93	89.4	266	26	US-10-002-784A-14	Sequence 14, Appl1
42	87	83.7	18	19	US-09-555-115A-14	Sequence 14, Appl1
43	87	83.7	239	22	US-09-791-537-17768	Sequence 17768, A
44	87	83.7	239	22	US-09-791-537-52676	Sequence 52676, A
45	87	83.7	240	19	US-09-555-115A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
 US-09-555-115A-17
 ; Sequence 17, Application US/09555115A
 ; GENERAL INFORMATION:
 ; APPLICANT: Bohach, Gregory I.
 ; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
 ; FILE REFERENCE: 12136, USWO
 ; CURRENT APPLICATION NUMBER: US/09/555, 115A
 ; CURRENT FILING DATE: 2000-08-01
 ; PRIOR APPLICATION NUMBER: PCT/US98/25107
 ; PRIOR FILING DATE: 1998-12-01
 ; PRIOR APPLICATION NUMBER: US 60/067, 357
 ; PRIOR FILING DATE: 1997-12-02
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 17
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: *Staphylococcus aureus*
 US-09-555-115A-17

Query Match 100.0%; Score 104; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 56-08; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

OY 1 CCFSSKDNVKGVTGKTC 18
DB 1 CCFSSKDNVKGVTGKTC 18

RESULT 2

US-09-791-537-52695
Sequence 52695, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 52695
LENGTH: 239
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-791-537-52695

Query Match 100.0%; Score 104; DB 22; Length 239;
Best Local Similarity 100.0%; Pred. No. 6,4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCFSSKDNVKGVTGKTC 18
DB 93 CCFSSKDNVKGVTGKTC 110

RESULT 3

US-09-555-115A-8
Sequence 8, Application US/09555115A
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PCT APPLICATION NUMBER: PCT/US98/25107
PCT FILING DATE: 1998-12-01
APPLICATION NUMBER: US 60/067,357
FILING DATE: 1997-12-02
ID NOS: 66
PatentIn version 3.1

Query Match 99.4%; Score 93; DB 19; Length 240;
Best Local Similarity 99.4%; Pred. No. 2,2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCFSSKDNVKGVTGKTC 18
DB 93 CCFSSKDNVKGVTGKTC 110

US-09-555-115A-11
Sequence 11, Application US/09555115A
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PCT APPLICATION NUMBER: PCT/US98/25107
PCT FILING DATE: 1998-12-01
APPLICATION NUMBER: US 60/067,357
FILING DATE: 1997-12-02
ID NOS: 66
PatentIn version 3.1

APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PCT APPLICATION NUMBER: PCT/US98/25107
PCT FILING DATE: 1998-12-01
APPLICATION NUMBER: US 60/067,357
FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-555-115A-11

Query Match 89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2,2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCFSSKDNVKGVTGKTC 18
DB 1 CCFSSKDNVKGVTGKTC 18

US-09-555-115A-12
Sequence 12, Application US/09555115A
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PCT APPLICATION NUMBER: PCT/US98/25107
PCT FILING DATE: 1998-12-01
APPLICATION NUMBER: US 60/067,357
FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2,2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCFSSKDNVKGVTGKTC 18
DB 1 CCFSSKDNVKGVTGKTC 18

US-09-555-115A-13
Sequence 13, Application US/09555115A
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PCT APPLICATION NUMBER: PCT/US98/25107
PCT FILING DATE: 1998-12-01
APPLICATION NUMBER: US 60/067,357
FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 18


```

; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

```

```

Query Match      89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CCFSSKDNVGVKVTGKTC 18
DB      1 CCFSSKDNVGVKVTGKTC 18

```

```

RESULT 7
US-09-555-115A-15
; Sequence 15: Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555.115A
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

```

```

Query Match      89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CCFSSKDNVGVKVTGKTC 18
DB      1 CCFSSKDNVGVKVTGKTC 18

```

```

RESULT 8
US-09-555-115A-16
; Sequence 16: Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555.115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

```

```

Query Match      89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CCFSSKDNVGVKVTGKTC 18
DB      1 CCFSSKDNVGVKVTGKTC 18

```

```

US-09-555-115A-16

```

```

Query Match      89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CCFSSKDNVGVKVTGKTC 18
DB      1 CCFSSKDNVGVKVTGKTC 18

```

```

RESULT 9
US-09-555-115A-60
; Sequence 60: Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555.115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-60

```

```

Query Match      89.4%; Score 93; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CCFSSKDNVGVKVTGKTC 18
DB      1 CCFSSKDNVGVKVTGKTC 18

```

```

RESULT 10
US-08-882-431B-21
; Sequence 21: Application US/08882431B
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-UA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide

```


Db 54 CFFSSKDNVKGVTGKTC 71

```

RESULT 14
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-37

```

Query Match 89.4%; Score 93; DB 26; Length 89;
 Best Local Similarity 94.4%; Pred. No. 1.1e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFFSSKDNVKGVTGKTC 18
 Db 54 CFFSSKDNVKGVTGKTC 71

```

RESULT 15
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-38

```

Query Match 89.4%; Score 93; DB 26; Length 89;
 Best Local Similarity 94.4%; Pred. No. 1.1e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFFSSKDNVKGVTGKTC 18
 Db 54 CFFSSKDNVKGVTGKTC 71

Search completed: October 15, 2003, 17:41:17
 Job time : 211.042 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 8.08183 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115A-17
Sequence: 1 CCFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	48.1	2835	1 PCT-US03-26780-2570	Sequence 2570, Ap
2	48.5	46.6	220	6 US-10-425-114A-39278	Sequence 39278, A
3	47	45.2	1596	1 PCT-US03-26780-3489	Sequence 3489, Ap
4	46	44.2	375	7 US-60-487-610-2744	Sequence 2744, Ap
5	46	44.2	375	7 US-60-489-964-460	Sequence 460, Ap
6	46	44.2	375	7 US-60-499-964-461	Sequence 461, App
7	46	44.2	375	7 US-60-499-964-776	Sequence 776, App
8	46	44.2	375	7 US-60-499-964-777	Sequence 777, App
9	46	44.2	375	7 US-60-499-964-778	Sequence 778, App
10	46	44.2	380	1 PCT-US03-28227-4671	Sequence 4671, Ap
11	46	44.2	385	7 US-60-487-610-1723	Sequence 1723, Ap
12	46	44.2	385	7 US-60-499-964-462	Sequence 462, App
13	46	44.2	1431	1 PCT-US03-26780-3049	Sequence 3049, Ap
14	46	43.3	645	1 PCT-US03-26780-2856	Sequence 2856, Ap
15	44	42.3	1403	1 PCT-US03-14382-30	Sequence 30, App1
16	44	42.3	1403	1 PCT-US03-14382A-30	Sequence 30, App1
17	44	42.3	1462	1 PCT-US03-14382-31	Sequence 31, App1
18	44	42.3	1462	1 PCT-US03-14382A-31	Sequence 31, App1
19	44	42.3	2141	1 PCT-US03-26780-2951	Sequence 2951, Ap
20	44	42.3	2148	1 PCT-US03-26780-2972	Sequence 2972, Ap
21	43	41.3	337	1 PCT-US03-26780-3385	Sequence 3385, Ap
22	43	41.3	2027	1 PCT-US03-26780-3056	Sequence 3056, Ap
23	43	41.3	2322	1 PCT-US03-26780-2711	Sequence 2711, Ap
24	42	40.4	240	1 PCT-US03-26780-2735	Sequence 2735, Ap
25	42	40.4	371	6 US-10-425-114A-44237	Sequence 44237, A
26	42	40.4	764	1 PCT-US03-26780-3612	Sequence 3612, Ap

27	42	40.4	951	1 PCT-US03-26780-2941	Sequence 2941, Ap
28	42	40.4	1878	1 PCT-US03-26780-2738	Sequence 2738, Ap
29	41	39.4	210	1 PCT-US03-26780-2966	Sequence 2966, Ap
30	41	39.4	246	7 US-60-489-964-414	Sequence 414, App
31	41	39.4	246	7 US-60-489-964-415	Sequence 415, App
32	41	39.4	340	1 PCT-US03-28227-4677	Sequence 4677, Ap
33	41	39.4	357	1 PCT-US03-28227-4674	Sequence 4674, Ap
34	41	39.4	357	1 PCT-US03-28227-4676	Sequence 4676, Ap
35	41	39.4	358	1 PCT-US03-28227-4678	Sequence 4678, Ap
36	41	39.4	358	1 PCT-US03-28227-4675	Sequence 4675, Ap
37	41	39.4	368	7 US-60-487-610-1505	Sequence 1505, Ap
38	41	39.4	432	7 US-60-487-610-1506	Sequence 1506, Ap
39	41	39.4	439	6 US-10-425-114A-51052	Sequence 51052, A
40	41	39.4	678	1 PCT-US03-26780-3281	Sequence 3281, Ap
41	41	39.4	783	1 PCT-US03-26780-3282	Sequence 3282, Ap
42	41	39.4	933	1 PCT-US03-26780-3508	Sequence 3508, Ap
43	41	39.4	1008	1 PCT-US03-26780-2719	Sequence 2719, Ap
44	41	39.4	1222	1 PCT-US03-26780-2499	Sequence 2499, Ap
45	41	39.4	1358	1 PCT-US03-26780-2993	Sequence 2993, Ap

ALIGNMENTS

RESULT 1
PCT-US03-26780-2570
Sequence 2570, Application PC/TUS0326780
GENERAL INFORMATION:
APPLICANT: FIVEPRIME THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
FILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PCT/US03/26780
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: 60/406,616
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,579
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,655
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,642
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,640
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,588
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,576
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,646
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3700
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2570
LENGTH: 2835
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-26780-2570
Query Match 48.1%; Score 50; DB 1; Length 2835;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Oy 1 CCFSSKDNVKGVTGKTC 18
Db 1011 CCAAGGTATATGGTC 1028
RESULT 2

US-10-425-114A-39278
; Sequence 39278, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39278
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700452123_FLI.pep
US-10-425-114A-39278

Query Match 46.6%; Score 48.5; DB 6; Length 220;
Best Local Similarity 37.0%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

OY 1 CCFSSKXN-----VGKVTGKTC 18
Db 160 CCWSSSDGFLCSFPRSVSKLNGLSLC 186

RESULT 3
PCT-US03-26780-3489
; Sequence 3489, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3489
; LENGTH: 1596
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26780-3489

Query Match 45.2%; Score 47; DB 1; Length 1596;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;

Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
OY 1 CCFSSKXNKGKVTGKTC 18
Db 606 CCTTCGGAGAGATGTTTC 623

RESULT 4
US-60-487-610-2744
; Sequence 2744, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2744
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2744

Query Match 44.2%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

OY 1 CCFSS---SKDNVGKVTGKTC 18
Db 175 CGFTGYGSANVAKVTPTGSTC 196

RESULT 5
US-60-499-964-460
; Sequence 460, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-460

Query Match 44.2%; Score 46; DB 7; Length 375;
Best Local Similarity 54.5%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

OY 1 CCFSS---SKDNVGKVTGKTC 18
Db 175 CGFTGYGSANVAKVTPTGSTC 196

RESULT 6
US-60-499-964-461
; Sequence 461, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CL001481

; CURRENT APPLICATION NUMBER: US/60/499,964
 ; CURRENT FILING DATE: 2003-09-04
 ; NUMBER OF SEQ ID NOS: 30431
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 461
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-499-964-461

Query Match 44.2%; Score 46; DB 7; Length 375;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFS----SKDNVKGVTGKTC 18
 Db 175 CGFSTGYGSANVNAKVTGPGSTC 196

RESULT 7
 US-60-499-964-776
 ; Sequence 776, Application US/60499964
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
 ; FILE REFERENCE: C0001481
 ; CURRENT APPLICATION NUMBER: US/60/499,964
 ; CURRENT FILING DATE: 2003-09-04
 ; NUMBER OF SEQ ID NOS: 30431
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 776
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-499-964-776

Query Match 44.2%; Score 46; DB 7; Length 375;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFS----SKDNVKGVTGKTC 18
 Db 175 CGFSTGYGSANVNAKVTGPGSTC 196

RESULT 8
 US-60-499-964-777
 ; Sequence 777, Application US/60499964
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
 ; FILE REFERENCE: C0001481
 ; CURRENT APPLICATION NUMBER: US/60/499,964
 ; CURRENT FILING DATE: 2003-09-04
 ; NUMBER OF SEQ ID NOS: 30431
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 777
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-499-964-777

Query Match 44.2%; Score 46; DB 7; Length 375;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFS----SKDNVKGVTGKTC 18
 Db 175 CGFSTGYGSANVNAKVTGPGSTC 196

RESULT 9
 US-60-499-964-778
 ; Sequence 778, Application US/60499964
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
 ; FILE REFERENCE: C0001481
 ; CURRENT APPLICATION NUMBER: US/60/499,964
 ; CURRENT FILING DATE: 2003-09-04
 ; NUMBER OF SEQ ID NOS: 30431
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 778
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-499-964-778

Query Match 44.2%; Score 46; DB 7; Length 375;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFS----SKDNVKGVTGKTC 18
 Db 175 CGFSTGYGSANVNAKVTGPGSTC 196

RESULT 10
 PCT-US03-28227-4671
 ; Sequence 4671, Application PC/TUS0328227
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
 ; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
 ; APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
 ; APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
 ; APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
 ; APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
 ; APPLICANT: DELLEGANE, Angelo M.; PANESAR, Iqbal S.;
 ; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
 ; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
 ; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
 ; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
 ; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
 ; APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
 ; APPLICANT: WU, Mingham C.; STUVE, Laura L.;
 ; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
 ; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
 ; APPLICANT: VITT, Ursula A.; KIRTON, Edward;
 ; APPLICANT: XU, Yuming; KWONG, Mary;
 ; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
 ; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
 ; APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
 ; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
 ; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: P0100 PCT
 ; CURRENT APPLICATION NUMBER: PCT/US03/28227
 ; CURRENT FILING DATE: 2003-09-12
 ; PRIOR APPLICATION NUMBER: US 60/410,260
 ; PRIOR FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 60/410,259
 ; PRIOR FILING DATE: 2002-09-12
 ; NUMBER OF SEQ ID NOS: 5444
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 4671
 ; LENGTH: 380
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 962211.PT69P

PCT-US03-28227-4671

Query Match 44.2%; Score 46; DB 1; Length 380;
Best Local Similarity 54.5%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFS----SKDNVGVTKGKTC 18
Db 180 CGFSTGSAVAVVAVKVTPESTC 201

RESULT 11

US-60-487-610-1723
; Sequence 1723, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1723

Query Match 44.2%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 68;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
Qy 1 CCFS----SKDNVGVTKGKTC 18
Db 175 CGFSTGSAVAVVAVKVTPESTC 196

RESULT 12

US-60-499-964-462
; Sequence 462, Application US/60499964
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN DRUG-METABOLIZING ENZYMES, METHODS OF
; FILE REFERENCE: CLO01481
; CURRENT APPLICATION NUMBER: US/60/499,964
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 30431
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-499-964-462

Query Match 44.2%; Score 46; DB 7; Length 385;
Best Local Similarity 54.5%; Pred. No. 68;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFS----SKDNVGVTKGKTC 18
Db 175 CGFSTGSAVAVVAVKVTPESTC 196

RESULT 13

PCT-US03-26780-3049
; Sequence 3049, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.

;; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
;; FILE REFERENCE: 08940.0014-00304
;; CURRENT APPLICATION NUMBER: PCT/US03/26780
;; CURRENT FILING DATE: 2003-08-28
;; PRIOR APPLICATION NUMBER: 60/406,616
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,579
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,655
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,642
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,640
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,588
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,576
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,646
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,666
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: 60/406,653
;; PRIOR FILING DATE: 2002-08-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3700
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 3049
;; LENGTH: 1431
;; TYPE: PRT
;; ORGANISM: Homo sapiens
PCT-US03-26780-3049

Query Match 44.2%; Score 46; DB 1; Length 1431;
Best Local Similarity 44.4%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CCFSKDNVGVTKGKTC 18
Db 599 CCTCGATGAGCATGATC 616

RESULT 14

PCT-US03-26780-2856
; Sequence 2856, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29

Remaining Prior Application data removed - See File Wrapper or PALM.
 : NUMBER OF SEQ ID NOS: 3700
 : SOFTWARE: Patent version 3.2
 : SEQ ID NO 2856
 : LENGTH: 645
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 PCT-US03-26780-2856

Query Match 43.3%; Score 45; DB 1; Length 645;
 Best Local Similarity 44.4%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CCFSSKDNVGVKGKTC 18
 ||::|||
 Db 578 CCCMAAATGTGTGATC 595

RESULT 15
 PCT-US03-14382-30
 : Sequence 30, Application PC/TUS0314382
 : GENERAL INFORMATION:
 : APPLICANT: Emory University
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
 : TITLE OF INVENTION: ANTIVIRAL AGENTS
 : FILE REFERENCE: 12804-011W01
 : CURRENT APPLICATION NUMBER: PCT/US03/14382
 : CURRENT FILING DATE: 2003-05-07
 : PRIOR APPLICATION NUMBER: US 60/378,711
 : NUMBER OF SEQ ID NOS: 501
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 30
 : LENGTH: 1403
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 PCT-US03-14382-30

Query Match 42.3%; Score 44; DB 1; Length 1403;
 Best Local Similarity 44.4%; Pred. No. 4.4e+02;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CCFSSKDNVGVKGKTC 18
 ||::|||
 Db 95 CLCGEKGKGTGKTC 112

Search completed: October 15, 2003, 17:42:40
 Job time : 8.08383 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 24.6287 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-1_COPY_98_106
Perfect score: 47
Sequence: 1 KDNVGVKVTG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	18	AA106249	Staphylococcal gro
2	47	100.0	18	ABG71377	Staphylococcal ent
3	47	100.0	18	ABG71379	Staphylococcal ent
4	47	100.0	18	ABG71380	Staphylococcal ent
5	47	100.0	238	AA13208	Staphylococcal ent
6	47	100.0	238	AA145016	Staphylococcal ent
7	47	100.0	238	AA167343	Staphylococcus aur
8	47	100.0	238	AA176239	Staphylococcus aur
9	47	100.0	239	AA13207	Staphylococcal ent

10	47	100.0	239	AA145015	Staphylococcal ent
11	47	100.0	239	AA106255	Staphylococcal gro
12	47	100.0	239	AA106256	Staphylococcal gro
13	47	100.0	239	AA106257	Staphylococcal gro
14	47	100.0	239	AA106258	Staphylococcal gro
15	47	100.0	239	AA106251	Staphylococcal gro
16	47	100.0	239	AA106252	Staphylococcal gro
17	47	100.0	239	AA106253	Staphylococcal gro
18	47	100.0	239	AA167342	Staphylococcus aur
19	47	100.0	239	AA176238	Staphylococcus aur
20	47	100.0	240	ABG71367	Staphylococcal ent
21	47	100.0	240	ABG71368	Staphylococcal ent
22	47	100.0	240	ABG71369	Staphylococcal ent
23	47	100.0	240	ABG71371	Staphylococcal ent
24	47	100.0	240	ABG71372	Staphylococcal ent
25	47	100.0	240	ABG71373	Staphylococcal ent
26	47	100.0	240	ABG71374	Staphylococcal ent
27	47	100.0	266	AA170108	Staphylococcal ent
28	47	100.0	266	AB179507	Staphylococcal SEC
29	41	87.2	18	AA106250	Staphylococcal gro
30	41	87.2	18	ABG71378	Staphylococcal ent
31	41	87.2	239	AA106254	Staphylococcal gro
32	41	87.2	240	ABG71370	Staphylococcal ent
33	37	78.7	185	AA1061568	C glutamicum prote
34	37	78.7	299	AA106436	Arabidopsis thalia
35	37	78.7	312	AA1062524	Arabidopsis thalia
36	37	78.7	312	AA106435	Arabidopsis thalia
37	37	78.7	319	AA1062530	Arabidopsis thalia
38	37	78.7	335	AA1062529	Arabidopsis thalia
39	37	78.7	340	AA106434	Arabidopsis thalia
40	37	78.7	342	AA1062523	Arabidopsis thalia
41	37	78.7	358	AA1062522	Arabidopsis thalia
42	37	78.7	360	AA1062528	Arabidopsis thalia
43	37	78.7	855	AB165227	Bifidobacterium lo
44	36	76.6	630	AB168655	Novel human diagno
45	35	74.5	142	AA1035446	Haemophilus influe

ALIGNMENTS

RESULT 1	0	*
AA106249		
ID	AA106249	standard; Peptide: 18 AA.
AC	AA106249;	
XX		
DT	23-AUG-1999	(first entry)
XX		
DE	Staphylococcal group C enterotoxin disulfide loop.	
XX		
KW	Enterotoxin; SEC1; SEC2; SEC3 FRI 913; SEC3 4446; SEC-Bovine;	
KW	SEC-Ovine; toxin; disulfide loop; protein engineering.	
XX		
OS	Staphylococcus aureus.	
XX		
PN	W09927889-A2.	
XX		
PD	10-JUN-1999.	
XX		
PF	01-DEC-1998; 98WO-US25107.	
XX		
PR	02-DEC-1997; 97US-0067357.	
XX		
PA	(IDAH-) IDAHO RES FOUND INC.	
XX		
PI	Bohach GI;	
XX		
DR	WPI: 1999-358008/30.	
XX		
DR	N-PSDB; AAX58884.	
XX		
PT	Non-toxic modified staphylococcal enterotoxins	
XX		

PS Disclosure; Page 3; 25pp; English.
XX
CC This peptide corresponds to the disulphide loop, i.e. amino acids
CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,
CC SEC3 FRI 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AA06251-53
CC and AA06255-58) . The invention relates to pyrogenic toxins, such as
CC staphylococcal enterotoxins, modified in the disulphide loop region.
CC Typically, the modification involves deletions within the disulphide
CC loop region of SEC (see AA06261). The modified toxins retain useful
CC biological properties, such as the ability to induce cytokine
CC production, but have substantially reduced toxicity compared to the
CC corresponding unmodified native toxin. Emetic response inducing
CC activity and fever inducing activity are typically decreased by at
CC least about 100-fold, while LD50 (in Dutch belted rabbits) is at
CC least 100-fold higher than the native toxin.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGRKVTG 9
|||
6 KDNVGRKVTG 14

Db

RESULT 2
ABG71377 standard; Peptide; 18 AA.
XX
XX ABG71377;
XX
DT 29-JAN-2003 (first entry)
XX
XX Staphylococcal enterotoxin disulphide loop region.
XX
DE Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
XX emetic response-inducing activity; staphylococcal enterotoxin;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KW SEC1; SEC2; SEC3-FRI913; SEC-4446; SEC-bovine.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200283169-A1.
XX
XX 24-OCT-2002.
PD
XX
XX 11-APR-2002; 2002WO-US11619.
PF
XX
XX 13-APR-2001; 2001US-283720P.
PR
XX
XX (IDAH-) IDAHO RES FOUND INC.
PA
XX
XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
PI
XX
XX WPI; 2003-058608/05.
DR
XX
XX New modified staphylococcal enterotoxin derived from a native disulphide
XX loop-containing pyrogenic toxin, useful for non-specifically enhancing
XX an immune function and as a vaccine against toxic shock syndrome or
XX food poisoning -
XX
XX Disclosure; Fig 15; 67pp; English.
XX
XX The invention relates to a modified pyrogenic toxin derived from a native
XX disulphide loop-containing pyrogenic toxin where the modified toxin
XX comprises a disulphide loop having no more than 10 amino acids. The
XX modified toxin has a fever-inducing activity or an emetic
XX response-inducing activity decreased by about 100-fold in comparison to a
XX native toxin. The modified pyrogenic toxin, that is a staphylococcal
XX enterotoxin, is useful for non-specifically enhancing an immune function
XX and for vaccination against diseases such as toxic shock syndrome and
XX for vaccination against diseases such as toxic shock syndrome and

CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC disulphide loop region, occurring in several enterotoxins.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGRKVTG 9
|||
6 KDNVGRKVTG 14

Db

RESULT 3
ABG71379 standard; Peptide; 18 AA.
XX
XX ABG71379;
XX
XX 29-JAN-2003 (first entry)
DT
XX
XX Staphylococcal enterotoxin SEC-ovine disulphide loop region.
XX
DE Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
XX emetic response-inducing activity; staphylococcal enterotoxin;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KW SEC-ovine.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200283169-A1.
XX
XX 24-OCT-2002.
PD
XX
XX 11-APR-2002; 2002WO-US11619.
PF
XX
XX 13-APR-2001; 2001US-283720P.
PR
XX
XX (IDAH-) IDAHO RES FOUND INC.
PA
XX
XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
PI
XX
XX WPI; 2003-058608/05.
DR
XX
XX New modified staphylococcal enterotoxin derived from a native disulphide
XX loop-containing pyrogenic toxin, useful for non-specifically enhancing
XX an immune function and as a vaccine against toxic shock syndrome or
XX food poisoning -
XX
XX Disclosure; Fig 15; 67pp; English.
XX
XX The invention relates to a modified pyrogenic toxin derived from a native
XX disulphide loop-containing pyrogenic toxin where the modified toxin
XX comprises a disulphide loop having no more than 10 amino acids. The
XX modified toxin has a fever-inducing activity or an emetic
XX response-inducing activity decreased by about 100-fold in comparison to a
XX native toxin. The modified pyrogenic toxin, that is a staphylococcal
XX enterotoxin, is useful for non-specifically enhancing an immune function
XX and for vaccination against diseases such as toxic shock syndrome and
XX food poisoning. This sequence represents a staphylococcal enterotoxin
XX disulphide loop region.
XX
XX Sequence 18 AA;

Query Match 100.0%; Score 47; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGRKVTG 9
|||
6 KDNVGRKVTG 14

Db

```

RESULT 4
ABG71380
ID ABG71380 standard; Peptide; 18 AA.
XX
XX
AC ABG71380;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin C1 (SECI) protein fragment.
XX
KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin; SECI;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
XX
OS Staphylococcus aureus.
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PE 11-APR-2002; 2002WO-US11619.
XX
PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX
DR N-PSDB; ABS56822.
XX
PT New modified staphylococcal enterotoxin derived from a native disulphide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning.
XX
PS Example 1; Fig 1; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC protein fragment.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 47; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDNVGRKVTG 9
Db 6 KDNVGRKVTG 14

```

```

OS Staphylococcus aureus.
XX
XX WO9110680-A.
XX
XX 25-JUL-1991.
XX
XX 17-JAN-1991; 91WO-US00342.
XX
XX 17-JAN-1990; 90US-046577.
XX
XX (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
XX WPI; 1991-237984/32.
XX
XX Treating cancer with enterotoxin from Staphylococcus aureus -
XX administered by IV injection, having same tumoricidal activity
XX as Staphylococcal protein A without potential toxic reactions
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX SEC3 was isolated and purified from S.aureus. It can be used for
XX treating cancer, activating cytokine mediators and procoagulant
XX systems, augmenting natural killer cell cytotoxicity, etc. The
XX enterotoxin can be administered intravenously, optionally with
XX ibuprofen to attenuate toxic reaction to SEC3. Synthetic
XX polypeptides having structural homology to Staphylococcal exotoxins
XX are claimed, provided the homology includes statistically
XX significant sequence homology, alignment of Cysteine residues and
XX similar hydrophathy profiles.
XX See AAR13203-R13211.
XX
SQ Sequence 238 AA;
XX
Query Match 100.0%; Score 47; DB 12; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDNVGRKVTG 9
Db 97 KDNVGRKVTG 105

```

```

RESULT 6
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
XX AAR45016;
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEC3.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
XX WO9324136-A1.
XX
XX 09-DEC-1993.
XX
XX 01-JUN-1993; 93WO-US05213.
XX
XX 01-JUN-1992; 92US-0891718.
XX
XX (STON/) STONE J L.
XX (TERM/) TERMAN D S.
XX
XX Stone JL, Terman DS;
XX

```

DR WP1; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A pertussis system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 238 AA;

Query Match 100.0%; Score 47; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGRKVTG 9
|||||||
Db 97 KDNVGRKVTG 105

RESULT 7
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
AC AAB67343;
XX
DT 23-APR-2001 (first entry)
DE Staphylococcus aureus enterotoxin C3 protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
PD 30-JAN-2001.
XX
PE 30-OCT-1998; 98US-0183437.
XX
PR 31-JAN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416330.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91WO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
PA (TERM/) TERMAN D S.
PI Terman DS;
XX
WP1; 2001-158657/16.
XX
PT Tumor cell capable of stimulating antitumor immune reactivity in vitro
PT or in vivo comprises exogenous nucleic acid encoding a superantigen
PT and a costimulatory molecule -
XX
PS Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumor cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and
CC expresses an exogenous nucleic acid molecule encoding a superantigen
CC or its active fragment and an exogenous nucleic acid molecule
CC encoding a costimulatory molecule that activates T cells in

CC	conjunction with an antigenic stimulus. The invention may be used
CC	for cancer therapy by stimulating an anticancer immune response
CC	in vivo or ex vivo.
XX	
SQ	Sequence 238 AA;
OY	1 KDNYGKVTG 9
D6	97 KDNYGKVTG 105
RESULT 8	
ABB76239	
ID	ABB76239 standard; Protein; 238 AA.
XX	
AC	ABB76239;
DT	
XX	09-AUG-2002 (first entry)
XX	
DE	Staphylococcus aureus enterotoxin C3.
XX	
KW	Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
KW	antitumour; therapy.
XX	
OS	Staphylobococcus aureus.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 208
FT	/note= "given as 'O' in the specification"
XX	
PN	US2002051765-A1.
XX	
PD	02-MAY-2002.
XX	
PF	19-DEC-2000; 2000US-0741503.
XX	
PR	31-JAN-1994; 94US-0189424.
PR	19-JUN-1995; 95US-0491746.
PR	03-OCT-1989; 89US-0416530.
PR	17-JAN-1990; 90US-0466577.
PR	17-JAN-1991; 91WO-US00342.
PR	01-JUN-1992; 92US-0891718.
PR	02-MAR-1993; 93US-0025144.
XX	
PA	(TERM/) TERMAN D S.
XX	
PI	Terman DS;
XX	
DR	WPI; 2002-415198/44.
PT	
PT	Reagent for treating cancer without the need for e.g. radiotherapy,
PT	comprises a specific V beta subset of T cells sensitized to a growing
PT	tumor and stimulated with superantigens -
XX	
PS	Disclosure; Fig 2; 17pp; English.
XX	
XX	The present sequence is the protein sequence of enterotoxin C3
CC	(SEC3) of Staphylococcus aureus. Similarity is shown, in several
CC	stretches of sequence, between staphylococcal enterotoxins,
CC	streptococcal pyrogenic exotoxins and staphylococcal exfoliative
CC	toxins (see ABB76234-44). In the present invention, synthetic
CC	polypeptides useful in tumour therapy and in blocking or destroying
CC	autoreactive T and B lymphocyte populations are characterised by
CC	substantial structural homology to staphylococcal enterotoxin A and
CC	enterotoxin B, and to streptococcal pyrogenic exotoxins, with
CC	statistically significant sequence homology and similarity (Z value
CC	of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
CC	6) to include alignment of cysteine residues and similar hydrophathy
CC	profiles. These superantigens are used to treat solid tumours,

CC including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient
 CC with one or more superantigens *ex vivo* to generate stimulated cells,
 CC selecting a specific V beta subset of cells, and reintroducing
 CC these cells into the patient to induce an *in vivo* therapeutic,
 CC tumoricidal reaction.

XX Sequence 238 AA;

Query Match 100.0%; Score 47; DB 23; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVKVTG 9
 |||||
 DB 97 KDNVGVKVTG 105

RESULT 9

AAR13207
 ID AAR13207 standard; Protein; 239 AA.

XX AAR13207;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin C1.

XX SEC1; cancer treatment; pyrogen; tumouricide.

XX Staphylococcus aureus.

OS WO9110680-A.

PD 25-JUL-1991.

PF 17-JAN-1991; 91WO-US00342.

PR 17-JAN-1990; 90US-0466577.

PA (TERM/) TERMAN D S.

PI Terman DS;

XX WPI; 1991-237984/32.

XX Treating cancer with enterotoxin from Staphylococcus aureus -

PT administered by IV injection, having same tumoricidal activity

XX as Staphylococcal protein A without potential toxic reactions

XX Disclosure; Fig 1; 74pp; English.

CC SEC1 was isolated and purified from *S. aureus*. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEC1. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophathy profiles.
 CC See AAR13203-R13211.

XX Sequence 239 AA;

Query Match 100.0%; Score 47; DB 12; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVKVTG 9
 |||||
 DB 98 KDNVGVKVTG 106

RESULT 10

AAR45015
 ID AAR45015 standard; protein; 239 AA.

XX AAR45015;

DT 25-MAR-2003 (updated)

DT 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SEC1.

XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;

XX autoimmune disease; toxicity; Protein A; perfusion system.

OS Staphylococcus aureus.

PN WO9324136-A1.

PD 09-DEC-1993.

PF 01-JUN-1993; 93WO-US05213.

PR 01-JUN-1992; 92US-0891718.

XX (STON/) STONE J L.

PA (TERM/) TERMAN D S.

PI Stone JL, Terman DS;

XX WPI; 1993-405416/50.

XX Use of staphylococcal enterotoxin(s) and homologues - for

PT treating cancer in a patient or for the treatment of auto-immune

XX diseases

XX Disclosure; Fig 1; 90pp; English.

XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)

XX which may be used in the methods of the invention for treating cancer

XX in a patient. These SEs, and homologues of them, can be used as

XX tumouricidal agents for treating cancers and autoimmune disease.

XX They exhibit tumouricidal activity and toxicity identical to that

XX observed for the Protein A perfusion system. They may be administered

XX by i.v. injection.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 239 AA;

Query Match 100.0%; Score 47; DB 14; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVKVTG 9
 |||||
 DB 98 KDNVGVKVTG 106

RESULT 11

AAV06255
 ID AAV06255 standard; Protein; 239 AA.

XX AAV06255;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-MNCopeland.

XX Enterotoxin; SEC-MNCopeland; toxin; disulfide loop;

XX protein engineering.

OS Staphylococcus aureus.

```

XX Key Location/Qualifiers
FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC-MNCoPeland. The invention relates to pyrogenic
XX toxins, such as staphylococcal enterotoxins, modified in the
XX disulfide loop region. Typically, the modification involves
XX deletions within the disulfide loop region of SEC (see AAY06261).
XX The modified toxins retain useful biological properties, such as
XX the ability to induce cytokine production, but have substantially
XX reduced toxicity compared to the corresponding unmodified native
XX toxin. Emetic response inducing activity and fever inducing
XX activity are typically decreased by at least about 100-fold, while
XX LD50 (in Dutch Belted rabbits) is at least 100-fold higher than
XX the native toxin.
XX
XX SQ Sequence 239 AA;
XX
XX Query Match 100.0%; Score 47; DB 20; Length 239;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KDNVGRKVTG 9
XX |||||
XX 98 KDNVGRKVTG 106
XX
XX Db
XX
XX RESULT 12
XX AAY06256
XX ID AAY06256 standard; Protein; 239 AA.
XX
XX AAY06256;
XX
XX 23-AUG-1999 (first entry)
XX
XX Staphylococcal group C enterotoxin SEC-4446.
XX
XX Enterotoxin; SEC-4446; toxin; disulfide loop;
XX protein engineering.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX

```

```

XX Bohach GI;
XX
XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC-4446. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX Belted rabbits) is at least 100-fold higher than the native toxin.
XX
XX SQ Sequence 239 AA;
XX
XX Query Match 100.0%; Score 47; DB 20; Length 239;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KDNVGRKVTG 9
XX |||||
XX 98 KDNVGRKVTG 106
XX
XX Db
XX
XX RESULT 13
XX AAY06257
XX ID AAY06257 standard; Protein; 239 AA.
XX
XX AAY06257;
XX
XX 23-AUG-1999 (first entry)
XX
XX Staphylococcal group C enterotoxin SEC-bovine.
XX
XX Enterotoxin; SEC-bovine; toxin; disulfide loop;
XX protein engineering.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC-bovine. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX

```


CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.
XX
SQ Sequence 239 AA;

Query Match 100.0%; Score 47; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDNVGVKVTG 9
Db 98 KDNVGVKVTG 106

RESULT 14
AA06258
ID AA06258 standard; Protein; 239 AA.

AC AAY06258;
XX
XX 23-AUG-1999 (first entry)
DT
XX

DE Staphylococcal group C enterotoxin SEC-ovine.

XX Enterotoxin; SEC-ovine; toxin; disulfide loop;
KW protein engineering.
XX

OS Staphylococcus aureus.

XX
XX Key Location/Qualifiers
FT Disulfide-bond 93..110

PN MO9927889-A2.

XX 10-JUN-1999.

PD 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

PR (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI, 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC-ovine. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX Belted rabbits) is at least 100-fold higher than the native toxin.
XX
SQ Sequence 239 AA;

Query Match 100.0%; Score 47; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDNVGVKVTG 9

Db 98 KDNVGVKVTG 106

RESULT 15
AA06251
ID AA06251 standard; Protein; 239 AA.

AC AAY06251;

XX 23-AUG-1999 (first entry)
DT
XX

DE Staphylococcal group C enterotoxin SEC1.

XX Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.

XX Staphylococcus aureus.

XX
XX Key Location/Qualifiers
FT Disulfide-bond 93..110

PN MO9927889-A2.

XX 10-JUN-1999.

PD 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

PR (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI, 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC1. The invention relates to pyrogenic toxins, such
XX as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX Belted rabbits) is at least 100-fold higher than the native toxin.
XX
SQ Sequence 239 AA;

Query Match 100.0%; Score 47; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDNVGVKVTG 9
Db 98 KDNVGVKVTG 106

Search completed: October 15, 2003, 16:56:51
Job time : 25.7287 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:51:46 ; Search time 6.8982 Seconds
(without alignments)
55.202 Million cell updates/sec

Title: US-09-555-115A-1_COPY_98_106

Perfect score: 47

Sequence: 1 KDNVGVKVTG 9

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	89	4	US-09-144-776B-21
2	47	100.0	89	4	US-09-144-776B-22
3	47	100.0	89	4	US-09-144-776B-23
4	47	100.0	238	3	US-08-896-933-28
5	47	100.0	238	4	US-09-314-235-28
6	47	100.0	239	3	US-08-896-933-27
7	47	100.0	239	4	US-09-314-235-27
8	47	100.0	266	4	US-09-144-776B-14
9	35	74.5	141	4	US-09-732-210-544
10	35	74.5	141	4	US-09-732-210-551
11	35	74.5	4536	4	US-09-180-422B-27
12	35	74.5	4563	4	US-09-108-006C-1
13	33	70.2	115	1	US-08-152-922A-7
14	33	70.2	170	4	US-09-252-991A-59047
15	33	70.2	385	2	US-08-892-715-2
16	33	70.2	385	2	US-09-145-947-2
17	33	70.2	385	4	US-09-265-642-2
18	33	68.1	193	2	US-08-900-407-3
19	32	66.1	342	4	US-09-328-352-4605
20	32	66.1	440	4	US-09-328-352-7336
21	32	66.1	820	4	US-09-252-991A-30204
22	31	66.0	92	2	US-07-728-215-41
23	31	66.0	92	4	US-08-938-085A-41
24	31	66.0	92	4	US-10-072-844-41
25	31	66.0	197	4	US-09-107-532A-5816
26	31	66.0	320	3	US-09-092-437-2
27	31	66.0	339	4	US-09-044-781A-2

28	31	66.0	427	3	US-08-969-125-9	Sequence 9, Appl1
29	31	66.0	554	3	US-09-167-299-4	Sequence 4, Appl1
30	31	66.0	615	3	US-09-462-844-3	Sequence 3, Appl1
31	31	66.0	620	4	US-09-311-626B-6	Sequence 6, Appl1
32	31	66.0	734	4	US-09-328-352-4412	Sequence 4412, Ap
33	31	66.0	793	4	US-09-313-942-30	Sequence 30, Appl
34	31	66.0	784	4	US-09-313-942-32	Sequence 32, Appl
35	30.5	64.9	1213	1	US-08-188-582-20	Sequence 20, Appl
36	30.5	64.9	1213	1	US-08-646-715-20	Sequence 20, Appl
37	30	63.8	48	3	US-08-776-059-21	Sequence 21, Appl
38	30	63.8	120	3	US-08-751-359-25	Sequence 25, Appl
39	30	63.8	120	4	US-08-907-146-25	Sequence 25, Appl
40	30	63.8	141	4	US-09-732-210-543	Sequence 543, App
41	30	63.8	141	4	US-09-732-210-549	Sequence 549, App
42	30	63.8	146	3	US-08-751-359-15	Sequence 15, Appl
43	30	63.8	146	4	US-08-907-146-15	Sequence 15, Appl
44	30	63.8	159	2	US-08-810-655A-10	Sequence 10, Appl
45	30	63.8	161	4	US-09-325-932A-187	Sequence 187, App

ALIGNMENTS

RESULT 1
US-09-144-776B-21
Sequence 21, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21
Query Match 100.0%; Score 47; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVG 9
|||||
Db 59 KDNVGVKVG 67

RESULT 2

US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-2065
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-144-776B-22

Query Match 100.0%; Score 47; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVG 9
|||||
Db 59 KDNVGVKVG 67

RESULT 3

US-09-144-776B-23
; Sequence 23, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson

Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-144-776B-23

Query Match 100.0%; Score 47; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVG 9
|||||
Db 59 KDNVGVKVG 67

RESULT 4

US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-28

Query Match 100.0%; Score 47; DB 3; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
|||||

Db 97 KDNVGVKVTG 105

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235

; Patent No. 6338845

; GENERAL INFORMATION:

; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
AND RELATED COMPOUNDS

; FILE REFERENCE: 09629/005004

; CURRENT FILING DATE: 1999-05-18

; EARLIER APPLICATION NUMBER: 08/896,933

; EARLIER FILING DATE: 1997-07-18

; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02

; EARLIER APPLICATION NUMBER: 07/891,718

; EARLIER FILING DATE: 1992-06-01

; EARLIER APPLICATION NUMBER: US91/00342

; EARLIER FILING DATE: 1991-01-17

; EARLIER APPLICATION NUMBER: 07/466,577

; EARLIER FILING DATE: 1990-01-17

; EARLIER APPLICATION NUMBER: 07/416,530

; EARLIER FILING DATE: 1989-10-03

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 28

; LENGTH: 238

; TYPE: PRT

; ORGANISM: Staphylococcus aureas

US-09-314-235-28

Query Match 100.0%; Score 47; DB 4; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
|||||

Db 97 KDNVGVKVTG 105

RESULT 6

US-08-896-933-27

; Sequence 27, Application US/08896933

; Patent No. 6221351

; GENERAL INFORMATION:

; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
AND RELATED COMPOUNDS

; FILE REFERENCE: 09629/005002

; CURRENT FILING DATE: 1999-05-18

; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 27

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Staphylococcus aureas

US-08-896-933-27

Query Match 100.0%; Score 47; DB 3; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
|||||

Db 98 KDNVGVKVTG 106

RESULT 7

US-09-314-235-27

; Sequence 27, Application US/09314235

; Patent No. 6338845

; GENERAL INFORMATION:

; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
AND RELATED COMPOUNDS

; FILE REFERENCE: 09629/005004

; CURRENT FILING DATE: 1999-05-18

; EARLIER APPLICATION NUMBER: 08/896,933

; EARLIER FILING DATE: 1997-07-18

; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02

; EARLIER APPLICATION NUMBER: 07/891,718

; EARLIER FILING DATE: 1992-06-01

; EARLIER APPLICATION NUMBER: US91/00342

; EARLIER FILING DATE: 1991-01-17

; EARLIER APPLICATION NUMBER: 07/466,577

; EARLIER FILING DATE: 1990-01-17

; EARLIER APPLICATION NUMBER: 07/416,530

; EARLIER FILING DATE: 1989-10-03

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 27

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Staphylococcus aureas

US-09-314-235-27

Query Match 100.0%; Score 47; DB 4; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
|||||

Db 98 KDNVGVKVTG 106

RESULT 8

US-09-144-776B-14

; Sequence 14, Application US/09144776B

; Patent No. 6399332

; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,
Mark A. Olson

; TITLE OF INVENTION: Bacterial Superantigen
Vaccines

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

ADDRESS: Charles H. Harris

STREET: US Army WMC -504 Scott Street

MCWR-JA (Charles H. Harris-Patent
Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7714
TELEFAX: (301) 619-2065
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match 100.0%; Score 47; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKTG 9
DB 125 KDNVGVKTG 133

RESULT 9
US-09-732-210-544
Sequence 544, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Miltanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 544
LENGTH: 141
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-732-210-544

Query Match 74.5%; Score 35; DB 4; Length 141;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDNVGVKT 8
DB 94 KDNVGVKT 101

RESULT 10
US-09-732-210-551
Sequence 551, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Miltanck, Cindy A.
APPLICANT: Seale, Jeffrey W.

APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 551
LENGTH: 141
TYPE: PRT
ORGANISM: Serratia marcescens
US-09-732-210-551

Query Match 74.5%; Score 35; DB 4; Length 141;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDNVGVKT 8
DB 94 KDNVGVKT 101

RESULT 11
US-09-180-422B-27
Sequence 27, Application US/09180422B
Patent No. 6444644
GENERAL INFORMATION:
APPLICANT: BRUCKDORFER, KARL R
ETTELAI, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED FROM APOLIPOPROTEIN B-100
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27

Query Match 74.5%; Score 35; DB 4; Length 4536;
Best Local Similarity 77.8%; Pred. No. 5.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVGVKTG 9

Db 4044 KDNVKGATG 4052

RESULT 12

US-09-108-006C-1
; Sequence 1, Application US/09108006C
; Patent No. 6524613
; GENERAL INFORMATION:
; APPLICANT: Steer, Clifford J.
; Kren, Betsy T.
; Bandyopadhyay, Paramita
; Roy-Chowdhury, Jayanta
; TITLE OF INVENTION: Hepatocellular Chimeraplaecy
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kimeragen, Inc.
; STREET: 300 Pleasant Run
; CITY: Newtown
; STATE: PA
; COUNTRY: USA
; ZIP: 18940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108.006C
; FILING DATE: 30-Jun-1992
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,288
; FILING DATE: 30-Apr-1997
; APPLICATION NUMBER: 60/054,837
; FILING DATE: 05-Aug-1997
; APPLICATION NUMBER: 60/064,996
; FILING DATE: 10-Nov-1997
; APPLICATION NUMBER: 60/074,497
; FILING DATE: 12-Feb-1998
; APPLICATION NUMBER: PCT US 98/08834
; FILING DATE: 30-Apr-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Fiebel, Thomas
; REGISTRATION NUMBER: 29258
; REFERENCE/DOCKET NUMBER: 7991-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-504-4444
; TELEFAX: 215-504-4545
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4563 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-108-006C-1

Query Match 74.5%; Score 35; DB 4; Length 4563;
Best Local Similarity 77.8%; Pred. No. 5.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KDNVKGATG 9
Db 4071 KDNVKGATG 4079

RESULT 13
US-08-152-922A-7
; Sequence 7, Application US/08152922A
; Patent No. 5395614

GENERAL INFORMATION:

APPLICANT: Knapp, Bernhard
APPLICANT: Hundt, Erika
APPLICANT: Enders, Burkhard
APPLICANT: Kueper, Hans
TITLE OF INVENTION: Protective Plasmodium Falciparum
TITLE OF INVENTION: Hybrid Proteins which Contain Part-Sequences of the Malaria
TITLE OF INVENTION: Antigens HRP1 and SERP, the Preparation and Use Thereof
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,922A
FILING DATE: 16-Nov-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/806,471
FILING DATE: 13-Dec-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1143-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-152-922A-7

Query Match 70.2%; Score 33; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVKGATG 7
Db 93 KDNVKGATG 99

RESULT 14
US-09-252-991A-29047
; Sequence 29047, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29047
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29047

Query Match 70.2%; Score 33; DB 4; Length 170;
 Best Local Similarity 55.6%; Pred. No. 54;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KDNVGVKTG 9
 Db 121 KDNVGRATG 129

RESULT 15

US-08-892-715-2
 ; Sequence 2, Application US/08892715
 ; Patent No. 5922853
 ; GENERAL INFORMATION:
 ; APPLICANT: HANSBURY, MICHAEL J
 ; APPLICANT: JACKSON, JEFFREY R
 ; TITLE OF INVENTION: A HUMAN PELOTA HOMOLOG
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RATNER & PRESTIA
 ; STREET: P.O. BOX 980
 ; CITY: VALLEY FORGE
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: PASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/892,715
 ; FILING DATE: 15-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PRESTIA, PAUL F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GH-70144
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 385 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-892-715-2

Query Match 70.2%; Score 33; DB 2; Length 385;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KDNVGVKT 8
 Db 10 KDNVGVKT 17

Search completed: October 15, 2003, 17:08:28
 Job time : 7.8982 secs

2003

Thu Oct 16 09:57:33

GenCore version 5.1.6
(c) 1993 - 2003
Run time 13.6347 Seconds
Output alignments
Copyright using SW mo357 Million cell updates/sec

OM protein - protein search,
October 15, 2003, 12:05
Run on:
US-09-555-28416 residues

Title: score: 1 KDY chosen parameters: 600653
Perfect: 47
Sequence: 47
Scoring table: 0000000
Match 0%
Sum Match 100%
Searched 45 summaries

Top Published Applications AA:

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep.*
9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep.*
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14: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep.*
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18: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	89	US-10-002-784A-36	Sequence 36, Appl
2	47	100.0	89	US-10-002-784A-37	Sequence 37, Appl
3	47	100.0	89	US-10-002-784A-38	Sequence 38, Appl
4	47	100.0	266	US-08-882-431-14	Sequence 14, Appl
5	47	100.0	266	US-08-870-759-12	Sequence 12, Appl
6	47	100.0	266	US-09-751-708A-12	Sequence 12, Appl
7	47	100.0	266	US-10-002-784A-14	Sequence 14, Appl
8	37	78.7	185	US-09-738-626-5322	Sequence 5322, Ap
9	35	74.5	142	US-09-815-242-11039	Sequence 11039, A
10	35	74.5	4563	US-09-870-759-128	Sequence 128, App
11	35	74.5	4563	US-09-802-640-32	Sequence 32, Appl
12	35	74.5	514	US-09-751-708A-128	Sequence 128, App
13	34	72.3	514	US-10-339-351-1	Sequence 1, Appl
14	33	70.2	385	US-10-023-895A-2	Sequence 2, Appl
15	33	70.2	440	US-09-738-626-6376	Sequence 6376, Ap

16	33	70.2	1639	US-10-087-464-10	Sequence 10, Appl
17	32	68.1	228	US-09-738-626-5016	Sequence 5016, Ap
18	32	68.1	319	US-10-156-761-10519	Sequence 10519, A
19	32	68.1	751	US-09-864-761-38419	Sequence 38419, A
20	32	68.1	866	US-10-032-585-7745	Sequence 7745, Ap
21	32	68.1	1979	US-10-205-823-419	Sequence 419, App
22	31	66.0	92	US-10-072-841-41	Sequence 41, Appl
23	31	66.0	319	US-10-091-007-44	Sequence 2, Appl
24	31	66.0	320	US-09-740-452-2	Sequence 44, Appl
25	31	66.0	320	US-09-815-242-13278	Sequence 13278, A
26	31	66.0	320	US-09-815-242-13621	Sequence 13621, A
27	31	66.0	320	US-09-825-561A-82	Sequence 82, Appl
28	31	66.0	407	US-09-769-744A-44	Sequence 44, Appl
29	31	66.0	426	US-10-140-372-4	Sequence 4, Appl
30	31	66.0	426	US-10-036-568-2	Sequence 2, Appl
31	31	66.0	426	US-10-036-568-4	Sequence 4, Appl
32	31	66.0	431	US-10-156-761-8533	Sequence 8533, Ap
33	31	66.0	461	US-09-764-868-765	Sequence 765, App
34	31	66.0	552	US-10-032-585-7342	Sequence 7342, Ap
35	31	66.0	604	US-10-303-664A-57	Sequence 57, Appl
36	31	66.0	615	US-09-899-482-3	Sequence 3, Appl
37	31	66.0	620	US-10-124-880-6	Sequence 6, Appl
38	31	66.0	776	US-09-935-868-36	Sequence 36, Appl
39	31	66.0	776	US-09-935-868-40	Sequence 40, Appl
40	31	66.0	776	US-09-935-868-44	Sequence 44, Appl
41	31	66.0	776	US-10-287-035-36	Sequence 36, Appl
42	31	66.0	776	US-10-287-035-40	Sequence 40, Appl
43	31	66.0	776	US-10-287-035-44	Sequence 44, Appl
44	31	66.0	778	US-09-935-868-46	Sequence 46, Appl
45	31	66.0	778	US-09-935-868-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-002-784A-36
Sequence 36, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 36
LENGTH: 89
TYPE: PRT
ORGANISM: stephilotoccal enterotoxin C1
FEATURE:
OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match 100.0%; Score 47; DB 15; Length 89;
Best Local Similarity 100.0%; Pred No. 0.1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
Oy 1 KDNVGVKVTG 9
Db 59 KDNVGVKVTG 67

RESULT 2
US-10-002-784A-37
Sequence 37, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33

APPLICANT: Ulrich, Robert G.
 TITLE OF INVENTION: Bacterial Superantigen Vaccines
 FILE REFERENCE: 003/233/SAP
 CURRENT APPLICATION NUMBER: US/10/002,784A
 CURRENT FILING DATE: 2001-11-26
 PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
 PRIOR FILING DATE: 97-06-25; 98-09-01
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ ID NO: 37
 LENGTH: 89
 TYPE: PRT
 ORGANISM: staphylococcal enterotoxin C2
 FEATURE:
 OTHER INFORMATION: partial sequence as shown in Figure 3
 US-10-002-784A-37

Query Match 100.0%; Score 47; DB 15; Length 89;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
 DB 59 KDNVKGKVTG 67

RESULT 3
 US-10-002-784A-38
 Sequence 38, Application US/10002784A
 Publication No. US20030036644A1
 GENERAL INFORMATION:
 /33
 APPLICANT: Ulrich, Robert G.
 TITLE OF INVENTION: Bacterial Superantigen Vaccines
 FILE REFERENCE: 003/233/SAP
 CURRENT APPLICATION NUMBER: US/10/002,784A
 CURRENT FILING DATE: 2001-11-26
 PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
 PRIOR FILING DATE: 97-06-25; 98-09-01
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ ID NO: 38
 LENGTH: 89
 TYPE: PRT
 ORGANISM: staphylococcal enterotoxin C3
 FEATURE:
 OTHER INFORMATION: partial sequence as shown in Figure 3

Query Match 100.0%; Score 47; DB 15; Length 89;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
 DB 59 KDNVKGKVTG 67

RESULT 4
 US-08-882-431-14
 Sequence 14, Application US/08/882,431
 Publication 14, Application US/08/882,431
 GENERAL INFORMATION:
 /33
 APPLICANT: Ulrich, Robert G.
 TITLE OF INVENTION: Bacterial Superantigen Vaccines
 FILE REFERENCE: 003/233/SAP
 CURRENT APPLICATION NUMBER: US/10/002,784A
 CURRENT FILING DATE: 2001-11-26
 PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
 PRIOR FILING DATE: 97-06-25; 98-09-01
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ ID NO: 38
 LENGTH: 89
 TYPE: PRT
 ORGANISM: staphylococcal enterotoxin C3
 FEATURE:
 OTHER INFORMATION: partial sequence as shown in Figure 3

Query Match 100.0%; Score 47; DB 15; Length 89;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/882,431
 FILING DATE: June 25, 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Moran, John
 REGISTRATION NUMBER: 26,313
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 266
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 US-08-882-431-14

Query Match 100.0%; Score 47; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
 DB 125 KDNVKGKVTG 133

RESULT 5
 US-09-870-759-12
 Sequence 12, Application US/09870759
 Patent No. US20020177551A1
 GENERAL INFORMATION:
 /33
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 12
 LENGTH: 266
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-870-759-12

Query Match 100.0%; Score 47; DB 10; Length 266;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
 DB 125 KDNVKGKVTG 133

RESULT 6
 US-09-751-708A-12
 Sequence 12, Application US/09751708A
 Publication No. US20030157113A1

```

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-12

```

```

Query Match          100.0%; Score 47; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KDNVGVKVTG 9
Db      125 KDNVGVKVTG 133

```

```

RESULT 7
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US2003003644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scaphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

```

```

Query Match          100.0%; Score 47; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KDNVGVKVTG 9
Db      125 KDNVGVKVTG 133

```

```

RESULT 8
US-09-738-626-5322
; Sequence 5322, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MITOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

```

```

; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5322
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5322

```

```

Query Match          78.7%; Score 37; DB 10; Length 185;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 DNVGVKVTG 9
Db      100 DNVGVKVTG 107

```

```

RESULT 9
US-09-815-242-11039
; Sequence 11039, Application US/09815242
; Patent No. US2002006159A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11039
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11039

```

```

Query Match          74.5%; Score 35; DB 9; Length 142;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KDNVGVKVT 8
Db      95 KDNVGVKVT 102

```

```
RESULT 10
US-09-870-759-128
; Sequence 128, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-128

Query Match          74.5%; Score 35; DB 10; Length 4563;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 4071 KDNVPRKATG 4079

RESULT 11
US-09-802-640-32
; Sequence 32, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsel Aruna
; APPLICANT: Kleya Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-32

Query Match          74.5%; Score 35; DB 11; Length 4563;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 4071 KDNVPRKATG 4079

RESULT 12
US-09-751-708A-128
; Sequence 128, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
```

```
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-128

Query Match          74.5%; Score 35; DB 12; Length 4563;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 4071 KDNVPRKATG 4079

RESULT 13
US-10-339-351-1
; Sequence 1, Application US/10339351
; Publication No. US20030148417A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: No. US20030148417A1 cacao endoproteinases and their use in the
; TITLE OF INVENTION: production of cocoa flavour
; FILE REFERENCE: 80265-6707
; CURRENT APPLICATION NUMBER: US/10/339,351
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: EP 00114861.8
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Theobroma cacao
US-10-339-351-1

Query Match          72.3%; Score 34; DB 12; Length 514;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVGKVTG 9
DB 374 ENVGKATG 381

RESULT 14
US-10-023-895A-2
; Sequence 2, Application US/10023895A
; Publication No. US20020164734A1
; GENERAL INFORMATION:
; APPLICANT: Jackson et al.
; TITLE OF INVENTION: Human Pelota Homolog
; FILE REFERENCE: PF563D2
; CURRENT APPLICATION NUMBER: US/10/023,895A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/145,947
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 08/892,715
; PRIOR FILING DATE: 1997-07-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: human
US-10-023-895A-2

Query Match          70.2%; Score 33; DB 14; Length 385;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 KDNVGRVT 8
 Db 10 KDNAGQVT 17

RESULT 15

US-09-738-626-6376
 ; Sequence 6376, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAMA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 6376
 ; LENGTH: 440
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-6376

Query Match 70.2%; Score 33; DB 10; Length 440;
 Best Local Similarity 55.6%; Pred. No. 2.5e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGRVTG 9
 Db 150 RENVGRVSG 158

Search completed: October 15, 2003, 17:46:57
 Job time: 14.6347 secs

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Thu Oct 16 09:57:36 2003

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 Version 6.84431 Seconds
 Alignment updates/sec

OM protein - protein search, using sw model
 Run on: October 15, 2003, 16:47:37
 US-09-555-115a-1
 Parameters: 283308

Title: perfect score:
 Sequence: BLAST
 Scoring table: summaries

Searched: total num:
 Minimum: Number of results predicted by chance to have a
 Mean or equal to the score of the result being printed,
 N analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB	ID	Description
1	47	100.0	266	1	ENSAC1	enterotoxin C-1 pr
2	47	100.0	266	1	A60114	enterotoxin C-2 pr
3	47	100.0	266	2	S11885	enterotoxin C3 -S
4	37	78.7	274	2	T13010	hypothetical prote
5	37	78.7	1272	2	C96637	hypothetical prote
6	36	76.6	779	1	B42375	endopeptidase Ia (
7	35	74.5	142	1	RSSE11	ribosomal protein
8	35	74.5	142	2	AG0474	ribosomal protein
9	35	74.5	142	2	AG0456	50S ribosomal prot
10	35	74.5	499	2	AE3514	glutamate synthase
11	35	74.5	500	2	A53658	prostaglandin-I sy
12	35	74.5	709	2	C87258	fatty oxidation co
13	35	74.5	738	2	AH3571	3-hydroxybutyryl-C
14	35	74.5	808	2	B97303	hypothetical prote
15	35	74.5	1778	2	UT0382	apolipoprotein B -
16	35	74.5	2629	1	LPHUB	apolipoprotein B -
17	35	74.5	4563	1	LPHUB	apolipoprotein B-1
18	34	72.3	89	2	AF1141	hypothetical prote
19	34	72.3	89	2	AF1149	hypothetical prote
20	34	72.3	432	2	AI1932	two-component resp
21	34	72.3	487	2	C97188	lysine decarboxyla
22	34	72.3	1156	2	B69444	chromosome segrega
23	34	72.3	1583	2	T00727	myosin heavy chain
24	33	70.2	67	2	C83925	hypothetical prote
25	33	70.2	72	2	S28793	major merizoite su
26	33	70.2	79	2	G86722	hypothetical prote
27	33	70.2	233	2	A25814	glycoprotein 185 -
28	33	70.2	281	2	B54458	major merizoite su
29	33	70.2	297	2	C89792	hypothetical prote

30	33	70.2	319	2	AH2451	hypothetical prote
31	33	70.2	327	2	F87544	UDP-glucose 4-epim
32	33	70.2	339	2	D75473	prolipoprotein dia
33	33	70.2	401	2	AE0257	probable phage pro
34	33	70.2	430	2	A87634	peptidase, M20/M25
35	33	70.2	445	2	S07724	translation elonga
36	33	70.2	569	2	AI1347	hypothetical prote
37	33	70.2	573	2	AE1718	hypothetical prote
38	33	70.2	601	2	E95863	alcohol dehydrogen
39	33	70.2	638	2	S37085	polyadenylate-bind
40	33	70.2	639	2	AB1538	amidase homolog 1
41	33	70.2	703	2	D81365	carbon starvation
42	33	70.2	725	2	T17732	helicase-like prot
43	33	70.2	739	2	B82552	phage-related prot
44	33	70.2	739	2	F82769	phage-related tail
45	33	70.2	1060	2	S06286	major merizoite su

ALIGNMENTS

RESULT 1

ENSAC1

C:Species: Staphylococcus aureus

C:Date: 15-Nov-1984 #sequence_revison 05-Jan-1996 #text_change 18-Jun-1999

C:Accession: S06356; A01816

R:Bohach, G.A.; Schlievert, P.M.

Mol. Gen. Genet. 209, 15-20, 1987

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to

A:Reference number: S06356; MUID:88038352; PMID:2823067

A:Accession: S06356

A:Molecule type: DNA

A:Residues: 1-266 <BOH>

A:Cross-references: EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567

R:Schmidt, J.J.; Spero, L.

J. Biol. Chem. 258, 6300-6306, 1983

A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.

A:Reference number: A01816; MUID:83213327; PMID:6189824

A:Accession: A01816

A:Molecule type: protein

A:Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>

C:Gene: entC1

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-266/Product: enterotoxin C-1 #status experimental <MAT>

F:120-137/Distillate bonds: #status experimental

Query Match 100.0%; Score 47; DB 1; Length 266;

Best Local Similarity 100.0%; Pred. No. 0.14; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVTG 9

Db 125 KDNVGVKVTG 133

RESULT 2

A60114

enterotoxin C-2 precursor - Staphylococcus aureus

N:Alternate names: enterotoxin C-3 precursor

C:Species: Staphylococcus aureus

C:Date: 10-Nov-1992 #sequence_revison 10-Nov-1992 #text_change 16-Jul-1999

C:Accession: A60114; B60114; A33866

R:Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2252, 1989

A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins

A:Reference number: A60114; MUID:89277549; PMID:2543637

A:Accession: A60114

A:Status: not compared with conceptual translation

	Query Match	Score 47;	DB 2;	Length 266;
	Best Local Similarity	100.0%;	Pred. No. 0.14;	
Matches	9; conservative	0;	Mismatches	0; Indels 0; Gaps 0
QY	1 KDNVGVKVTG 9			
D8	125 KDNVGVKVTG 133			

Genet. 220, 329-333, 1990

primary
DNA
N<HOV>
T130_GB:X51661; NID:g46570; PIDN:CMA35972.1; PID:g46571
C/DpoIh3cToxin B
C/Specter-
C/Dates: 100.0%; Score 47; DB 2; Length 266;
R/Acc: 13 Aug 87; Pred. No. 0.14; Mismatches 0; Gaps 0;
Substition: 113010
A/Related: N.; T13010
A/Accession to the Robert.
A/Molecule number:
A/Residue type: T13010
A/Cross-ref type: 217586
C/Expres-ref: 1 274 DNA
A/GeneRef: 1 274 DNA
A/GeneRef: 1 274 DNA
A/Map position: ATP:T24C20.90
A/Intons: 62/1; 84/1; 133/1; 171/1; 201/1; 271/3
sis thaliana
(cross)
1-1999 #text_change 22-Oct-1999
F.; Catcolico, L.; Attiguenave, F.; Sa
GSPDB:GN1999
BAC clon

RESULT
C96637

hypothetical protein FILP17.13 [imported] - Arabidopsis thaliana
C|Species: Arabidopsis thaliana (mouse-ear cress)
C|Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C|Accession: C96637
R|Title: [Rothlopfis, A.; Ecker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huiskar, L.](#)
N|Date 408, 816-820, 2000
A|Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maltli, R.; Mazzilli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A|Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A|Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A|Reference number: A86141; MUID:21016719; PMID:11130712
A|Accession: C96637
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-1272 <STO>
A|Cross-References: GB:AE005173; NID:g2443887; PIDN:AA871480.1; GSPDB:GN00141
C|Genetics:
A|Gene: FILP17.13
A|Map position: 1

Query Match	78.7%;	Score 37;	DB 2;	Length 1272;
Best Local Similarity	87.5%;	Pred. No. 65;		
Matches	7;	Mismatches	0;	Gaps 0;
	Conservative			

Qy	2	DNVGKVTG	9
		:	
Db	661	DSVGKVTG	668

RESULT 6
B42375
endopeptidase Ia (EC 3.4.21.53) [validated] - *Bacillus brevis*
N:Alternate names: ATP-dependent proteinase lon; ATP-dependent serine proteinase Ia
M:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: *Bacillus brevis*
C>Date: 09-Apr-1999 #sequence revision 09-Apr-1999 #ext_change 19-Jan-2001
C:Accession: B42375; 139874; J00901
R:Ito, K.; Uda, S.; Yamagata, H.
J. Bacteriol 174, 2281-2287, 1992
A:Title: Cloning, characterization, and inactivation of the *Bacillus brevis* lon gene.
A:Reference number: B42375; MUID:92202157; PMID:1551846
A:Accession: B42375
A:Molecule type: DNA
A:Residues: 1-779 <ITG>
A:Cross-references: GB:D00863; NID:G216293; PIDN:BAA00737.1; PID:g402504
A:Experimental source: strain HPD31
C:Comment: This allosteric enzyme catalyzes the hydrolysis of large proteins in the presence of ATP.
C:Genetics:
A:Gene: lon
A:Start codon: TTG
C:Function:
A:Description: responsible for degradation of abnormal polypeptides [validated, MUID:92202157]
C:Superfamily: ATP-dependent serine proteinase Ia
C:Keywords: allosteric regulation; ATP; DNA binding; heat shock; hydrolase; nucleotide binding site
F:335-362/Region: nucleotide-binding motif A (P-loop)
F:418-423/Region: nucleotide-binding motif B
E:678/Active site Ser #status predicted

Query Match 76.6%; Score 36; DB 1; Length 779;
Best Local Similarity 77.8%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KDNVGVKVTG 9
Db 591 KDVGVSVTG 599

RESULT 7

R5SE11

ribosomal protein L11 - *Serratia marcescens*C/Species: *Serratia marcescens*

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

C/Accession: S01967

R/SOR, F.; Nomura, M.

Mol. Gen. Genet. 210, 52-59, 1987

A/Title: Cloning and DNA sequence determination of the L11 ribosomal protein operon of *S. marcescens*

A/Reference number: S01967; PMID:88121705; PMID:3323840

A/Accession: S01967

A/Molecule type: DNA

A/Residues: 1-142 <SOR>

A/Cross-references: EMBL:X12584; NID:947255; PIDN:CAA31095.1; PID:947256

C/Genetics:

A/Genes: rplK

C/Superfamily: *Escherichia coli* ribosomal protein L11

C/Keywords: protein biosynthesis; ribosome

Query Match 74.5%; Score 35; DB 1; Length 142;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDNVGVKVT 8
Db 95 KDNVGVKVT 102

RESULT 8

A64074 ribosomal protein L11 - *Haemophilus influenzae* (strain Rd KW20)C/Species: *Haemophilus influenzae*

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 13-Aug-1999

C/Accession: A64074

R./Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.H.; Gocayne, J.D.; Scott, J.; Shetty, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, D.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.

A/Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A/Reference number: A64000; PMID:95350630; PMID:7542800

A/Accession: A64074

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-142 <TRIG>

A/Cross-references: GB:U32734; GB:U42023; NID:91573498; PIDN:AA022175.1; PID:91573500; T

C/Superfamily: *Escherichia coli* ribosomal protein L11

C/Keywords: protein biosynthesis; ribosome

Query Match 74.5%; Score 35; DB 2; Length 142;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDNVGVKVT 8
Db 95 KDNVGVKVT 102

RESULT 9

AG0456 ribosomal protein L11 [imported] - *Yersinia pestis* (strain CO92)C/Species: *Yersinia pestis*

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C/Accession: AG0456
R./Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; et al., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, J.

Nature 413, 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001, PMID:21470413; PMID:11586360

A/Accession: AG0456

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-142 <KUR>

A/Cross-references: GB:AL590842; PIDN:CA093219.1; PID:915981667; GSPDB:GN00175

C/Genetics:

A/Genes: rplK

C/Superfamily: *Escherichia coli* ribosomal protein L11

Query Match 74.5%; Score 35; DB 2; Length 142;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDNVGVKVT 8
Db 95 KDNVGVKVT 102

RESULT 10

AE3514

glutamate synthase (NADPH) (EC 1.4.1.13) [imported] - *Brucella melitensis* (strain 16M)C/Species: *Brucella melitensis*

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

C/Accession: AE3514

R./DeVincenzo, V.G.; Kaput, V.; Redkar, R.J.; Petra, G.; Mujer, C.; Los, T.; Ivanova, I.

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A/Reference number: AD3252; PMID:11756688

A/Accession: AE3514

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-499 <KUR>

A/Cross-references: GB:AE008918; PIDN:AA153280.1; PID:917984162; GSPDB:GN00191

A/Experimental source: strain 16M

C/Genetics:

A/Genes: BMEI10039

A/Map position: II

C/Superfamily: glutamate synthase small chain

C/Keywords: oxidoreductase

Query Match 74.5%; Score 35; DB 2; Length 499;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVTG 9
Db 13 ENNVGVKVTG 21

RESULT 11

A53658 prostaglandin-I synthase (EC 5.3.99.4) - bovine

N/Alternate names: prostacyclin synthase

C/Species: *Bos primigenius taurus* (cattle)

C/Date: 26-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000

C/Accession: A53658; J02350; PC2227; PC2016

R./Hara, S.; Miyata, A.; Yokoyama, C.; Inoue, H.; Brugger, R.; Lottepeich, F.; Ullrich, V.

J. Biol. Chem. 269, 19897-19903, 1994

A/Title: Isolation and molecular cloning of prostacyclin synthase from bovine endothelial

A/Reference number: A53658; PMID:94327536; PMID:8051072

A/Accession: A53658

A/Molecule type: mRNA

A/Residues: 1-500 <HAR>

A/Cross-references: GB:D30718; NID:9538522; PIDN:BA06383.1; PID:9538523

A/Experimental source: aortic endothelium

R; Pereira, B.; Wu, K.K.; Wang, L.H.
Biochem. Biophys. Res. Commun. 203, 59-66, 1994
A;Title: Molecular cloning and characterization of bovine prostacyclin synthase.
A;Reference number: J02350; MUID:94354863; PMID:8074709
A;Accession: J02350
A;Molecule type: mRNA
A;Residues: 1-191, 'N', 193-352, 'P', 354-406, 'T', 408-500 <PER>
A;Cross-references: GB:J34208; NID:G508425; PIDN:AAA53674.1; PID:G508426
A;Accession: PC2227
A;Molecule type: Protein
A;Residues: 1-15;28-39;82-91;163-183 <PE2>
A;Experimental source: aorta
R; Pereira, B.; Wu, K.K.; Wang, L.H.
Biochem. Biophys. Res. Commun. 197, 1041-1048, 1993
A;Title: Bovine prostacyclin synthase: Purification and isolation of partial cDNA.
A;Reference number: PC2016; MUID:94107296; PMID:8280118
A;Accession: PC2016
A;Molecule type: mRNA
A;Residues: 1-38 <PE3>
A;Experimental source: aorta
C;Comment: This enzyme catalyzes the conversion of prostaglandin H2 to prostaglandin I2.
C;Superfamily: human cytochrome P450 CYP7A1; cytochrome P450 homology
C;Keywords: chromoprotein; heme; intramolecular oxidoreductase; iron; isomerase; membrat
F;1-500/Product: prostaglandin-1 synthase #status predicted <MAT>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.5%; Score 35; DB 2; Length 500;
Best Local Similarity 77.8%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVGVTVG 9
|||
Db 227 KDRVGVTVG 235

RESULT 12
C87258
fatty oxidation complex, alpha subunit (imported) - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: C87258
R;Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Brnolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87258
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-709 <STO>
A;Cross-references: GB:AE005673; NID:G13421173; PIDN:AAK22063.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0076
C;Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA de

Query Match 74.5%; Score 35; DB 2; Length 709;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVGVTVG 9
|||
Db 510 DNVGVTVG 517

RESULT 13
AH3571
3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3) [imported] - Brucella melitensis (strain 16M
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C;Accession: AH3571
R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leles

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3552; PMID:11756688
A;Accession: AH3571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-738 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53739.1; PID:G17984664; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME10497
A;Map position: 11
C;Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA de
C;Keywords: isomerase

Query Match 74.5%; Score 35; DB 2; Length 738;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNVGVTVG 9
|||
Db 96 DNVGVTVG 103

RESULT 14
B97303
hypothetical protein CAC3279 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97303
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-808 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81213.1; PID:G15026356; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3279

Query Match 74.5%; Score 35; DB 2; Length 808;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVGVTVG 9
|||
Db 442 DNVGVTVG 449

RESULT 15
J070382
apolipoprotein B - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
C;Accession: J070382; I46567; I46568
R;Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Haefler-Rapacz, J.; Attie, A.D.; Rapacz
Gene 70, 213-229, 1988
A;Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atheroscl
A;Reference number: J070382; MUID:89108006; PMID:2905687
A;Accession: J070382
A;Molecule type: DNA
A;Residues: 1-1778 <MAE>
R;Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Haefler-Rapacz, J.O.; Attie, A.D.; Rap
Gene 69, 213-229, 1988
A;Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atheroscl
A;Reference number: I46567
A;Accession: I46567
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA

A:Residues: 1-8,'S',10-238 <MA2>
A:Cross-references: GB:M22646; NID:g164366; PIDN:AAA30996.1; PID:g164369
A:Accession: 146568
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 239-1778 <MA3>
A:Cross-references: GB:M22647; NID:g164367; PIDN:AAA30997.1; PID:g164370
C:Comment: Apolipoprotein B is the predominant protein component of the low-density lipoprotein
C:Genetics:
A:Gene: apob
A:Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3
A>Note: the list of introns may be incomplete
C:Superfamily: apolipoprotein B
C:Keywords: atherosclerosis; cholesterol metabolism; LDL; lipid binding; lipoprotein

Query Match 74.5%; Score 35; DB 2; Length 1778;
Best Local Similarity 77.8%; Pred.No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
Db 1274 KDNVGVKVTG 1282

Search completed: October 15, 2003, 17:06:15
Job time : 9.8431 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 3.66467 Seconds
(Without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115a-1_COPY_98_106
Perfect score: 47
Sequence: 1 KDNVGVKVTG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	266	1	ETC1 STAU
2	47	100.0	266	1	ETC2 STAU
3	47	100.0	266	1	ETC3 STAU
4	36	76.6	779	1	LON BRECH
5	35	74.5	141	1	RL11 HARIN
6	35	74.5	141	1	RL11 SERMA
7	35	74.5	500	1	PTG1 BOVIN
8	35	74.5	673	1	FXR2 MOUSE
9	35	74.5	4563	1	APB HUMAN
10	34	72.3	89	1	V537 LISMO
11	34	72.3	89	1	V537 LISIN
12	34	72.3	357	1	MURG CLOPE
13	33	70.2	169	1	CAPI DIDI
14	33	70.2	233	1	MSP1 PLAFD
15	33	70.2	281	1	MSP1 PLAFN
16	33	70.2	445	1	EP1A_EUGR
17	33	70.2	1630	1	MSP1 PLAFK
18	33	70.2	1639	1	MSP1 PLAFW
19	33	70.2	1682	1	MSP1 PLAF3
20	33	70.2	1701	1	MSP1 PLAFM
21	33	70.2	1701	1	MSP1 PLAFM
22	33	70.2	1726	1	MSP1 PLAFM
23	33	70.2	1726	1	MSP1 PLAFM
24	33	70.2	6669	1	NEBU_HUMAN
25	32	68.1	182	1	SODC DEIRA
26	32	68.1	184	1	RL6 THEMMA
27	32	68.1	193	1	HS27 CHICK
28	32	68.1	224	1	MT04 URICA
29	32	68.1	242	1	RS4E_MERTH
30	32	68.1	350	1	SYM4_CAEEL
31	32	68.1	771	1	CTPG_MYCTU
32	32	68.1	802	1	SYFB_RHILIO
33	31	66.0	87	1	SYNC_SACDO

34	31	66.0	183	1	YS4L_CAEEL
35	31	66.0	343	1	G3P_SULTO
36	31	66.0	370	1	PNK3_HUMAN
37	31	66.0	370	1	PNK3_MOUSE
38	31	66.0	399	1	FTSW_BUCAL
39	31	66.0	424	1	IT31_MOUSE
40	31	66.0	427	1	IT31_HUMAN
41	31	66.0	457	1	LIP1_MYOCO
42	31	66.0	510	1	LIP1_MOUSE
43	31	66.0	548	1	PNK1_MOUSE
44	31	66.0	554	1	SYNC_YEAST
45	31	66.0	568	1	DONS_DROME

ALIGNMENTS

RESULT 1	ETC1 STAU	STANDARD;	PRT;	266 AA.
AC	P01553			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Enterotoxin type C-1 precursor (SEC1).			
GN	ENTC1.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8038352; PubMed=2823067;			
RA	Bohach G.A., Schlievert P.M.;			
RT	"Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic toxins.";			
RL	Mol. Gen. Genet. 209:15-20(1987).			
RN	[2]			
RP	SEQUENCE OF 28-266.			
RX	MEDLINE=83213327; PubMed=6189824;			
RA	Schmidt J.J., Spero L.;			
RL	"The complete amino acid sequence of staphylococcal enterotoxin C1.";			
CC	J. Biol. Chem. 258:6300-6306(1983).			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION			
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.			
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN			
CC	FAMILY.			
CC	-----			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X05815; CAA29260.1; -.			
DR	PIR; S06356; ENSACI.			
DR	HSSP; P34071; ISE2.			
DR	InterPro; IPR006177; Bctrl tox.			
DR	InterPro; IPR006123; Staph/Strep toxin.			
DR	InterPro; IPR006126; Staph/Strep tox.			
DR	InterPro; IPR006173; Staph_tox OB.			
DR	Pfam; PF02876; Staph_Strep_tox OB.			
DR	Pfam; PF01123; Staph_Strep_toxin; 1.			
DR	PRINTS; PR00279; BACTRILTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Enterotoxin; Toxin; Signal; Superantigen.			
FT	SIGNAL	1	27	
FT	CHAIN	28	266	ENTEROTOXIN TYPE C-1.
FT	DISULFID	120	137	
FT	CONFLICT	177	177	D -> N (IN REF. 2).

```

SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;
Query Match 100.0%; Score 47; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVYTG 9
Db 125 KDNVGVYTG 133

RESULT 2
ETC2 STAAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Enterotoxin type C-2 precursor (SEC2).
GN ENTC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bobach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RL enterotoxins C1 and C2."
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; PubMed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Brehm R.D., Tranter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RL Staphylococcus aureus reveals a zinc-binding site."
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F., Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RL enterotoxins."
RN [4]
RP Nat. Struct. Biol. 2:680-686(1995).
RN [5]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=9734373; PubMed=9191070;
RA Schach E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RL enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RN [6]
RP J. Mol. Biol. 266:270-280(1997).
RN [7]
RP -1- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC PIR; A60114; A60114.
DR PDB; 1STE; 23-DEC-96.
DR PDB; 1SE2; 08-MAR-96.
DR PDB; 1COV; 19-SEP-01.
DR PDB; 1I4P; 19-SEP-01.
DR PDB; 1I4Q; 19-SEP-01.
DR PDB; 1I4R; 19-SEP-01.
DR PDB; 1I4X; 19-SEP-01.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_08.
DR Pfam; PF02876; Staph_stp_tox_C; 1.

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DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
FT HELIX 35 37
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 55
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 79
FT TURN 83 86
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 109 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 128 129
FT STRAND 136 139
FT STRAND 142 144
FT TURN 146 147
FT STRAND 149 149
FT HELIX 151 153
FT STRAND 156 164
FT TURN 165 166
FT STRAND 167 176
FT STRAND 178 178
FT STRAND 180 182
FT HELIX 183 198
FT STRAND 208 216
FT TURN 218 219
FT STRAND 222 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 256 263
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVYTG 9
Db 125 KDNVGVYTG 133

RESULT 3
ETC2 STAAU 0 STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN ENTC3 OR SAV2009 OR SA1817.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N115), and
OS Staphylococcus aureus.

```

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 RX NCBI_TaxID=158878, 158879, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M050 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Mizumori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Hattori M., Ogasawara N., Hayashi H., Yoshino C., Shiba T.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackert S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT sequence comparison of all three type C staphylococcal
 RT enterotoxins";
 RL Mol. Gen. Genet. 220:329-333(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=970641178; PubMed=8906797;
 RA Fields B.A., Matchodi E.L., Li H., Yeern X., Stauffer C.V.,
 RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen";
 RL Nature 384:188-192(1996).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: AP003364; BAB58171.1; -
 CC EMBL: AP003135; BAB43097.1; -
 CC EMBL: X51661; CAA35972.1; -
 CC PIR: S11885; S11885.
 CC PDB: 1JCK; 12-NOV-97.
 CC PDB: 1KLG; 02-AUG-02.
 CC PDB: 1KLU; 14-AUG-02.
 CC InterPro: IPR006177; Bcst1 tox.
 CC InterPro: IPR006123; Staph/Strep toxin.
 CC InterPro: IPR006126; Staph/Strep tox.
 CC InterPro: IPR006173; Staph_tox_OB.
 CC Pfam: PF02876; Staph_Scrlp_tox_C; 1.
 CC Pfam: PF01123; BACTRLTOXIN.
 CC PRINTS: PR00279; BACTRLTOXIN.
 CC PROSITE: PS00277; STAPH STREP TOXIN 1; 1.
 CC PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
 CC Enterotoxin Toxin; Signal; Superantigen; 3D-structure;
 KW Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137
 SQ SEQUENCE 266 AA; 30671 MW; SED8A32D11FFCA59 CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVTG 9
 Db 125 KDNVGVKVTG 133
 RESULT 4
 ID LON BRECH STANDARD; PRT; 779 AA.
 AC P36772;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP-dependent protease La (EC 3.4.21.53).
 GN LON.
 OS Brevibacillus choshinensis.
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
 OX NCBI_TaxID=54911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPD31;
 RX MEDLINE=92202157; PubMed=1551846;
 RA Ito K., Ueda S., Yamagata H.;
 RT "Cloning, characterization, and inactivation of the Bacillus brevis
 RT LON gene";
 RL J. Bacteriol. 174:2281-2287(1992).
 CC -1- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN
 CC PRESENCE OF ATP. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED
 CC IN THE PROTEIN SUBSTRATE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin,
 CC casein and denatured serum albumin, in presence of ATP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16.
 CC -----
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 CC -----
 CC EMBL: D00863; BAA00737.1; -
 CC MEROPS: S16.001; -
 CC InterPro: IPR001593; AAA_ATPase.
 CC InterPro: IPR003958; AAA_ATPase_cent.
 CC InterPro: IPR001270; Chaprin_c1pA/B.
 CC InterPro: IPR003111; LON.
 CC InterPro: IPR001984; Lon_endopep.
 CC InterPro: IPR004815; Lon_fam.
 CC Pfam: PR00004; AAA; 1.
 CC Pfam: PR02190; LON; 1.
 CC Pfam: PF05362; Lon_C; 1.
 CC PRINTS: PR00300; CLP/PROTEASEA.
 CC PRINTS: PR00830; ENDOLAPTASE.
 CC SMART: SM00382; AAA; 1.
 CC SMART: SM00464; LON; 1.
 CC TIGRfam: TIGR00763; lon; 1.
 CC PROSITE: PS01046; LON_SER; 1.
 KW Hydrolase; Serine protease; ATP-binding.
 FT NP BIND 355 362
 FT ACT SITE 678 678 ATP (POTENTIAL).
 FT ACT SITE 678 678 BY SIMILARITY.
 SQ SEQUENCE 779 AA; 87421 MW; 625E0DA9B98941B5 CRC64;
 Query Match 76.8%; Score 36; DB 1; Length 779;
 Best Local Similarity 77.8%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KDNVGVKVTG 9
 Db 591 KDNVGVKVTG 599
 RESULT 5

RL11_HAEIN
ID RL11_HAEIN STANDARD; PRT; 141 AA.
AC P44351;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK OR RPL11 OR H10517.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=55350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kellavagge A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Furman J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; U32734; AAC2175.1; -;
DR PIR; A64074; A64074.
DR HSSP; P56210; 1FOW.
DR TIGR; H10517; -;
DR InterPro; IPR000911; Ribosomal_L11.
DR InterPro; IPR006519; Ribosomal_L11bac.
DR Pfam; PF00298; Ribosomal_L11; 1.
DR Pfam; PF03946; Ribosomal_L11_N; 1.
DR ProDom; PD001367; Ribosomal_L11; 1.
DR SMART; SM00649; RL11; 1.
DR TIGRFAMs; TIGR01632; L11_bact; 1.
DR PROSITE; PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; Methylation; RNA-binding; Complete proteome.
FT INIT MET 0 BY SIMILARITY.
FT MOD_RES 3 1 METHYLATION (TRI-) (BY SIMILARITY).
FT MOD_RES 3 3 METHYLATION (TRI-) (BY SIMILARITY).
FT MOD_RES 39 39 METHYLATION (TRI-) (BY SIMILARITY).
SQ SEQUENCE 141 AA; 14772 MW; A2AE370E18E1DECF CRC64;
Query Match 74.5%; Score 35; DB 1; Length 141;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO1011; PubMed=3323840;
RX MEDLINE=88121705; PubMed=7542800;
RA Sor F., Nomura M.;
RT Cloning and DNA sequence determination of the l11 ribosomal protein
RT operon of Serratia marcescens and protein vulgaris: translational
RT feedback regulation of the Escherichia coli l11 operon by
RT heterologous l1 proteins.
RL Mol. Gen. Genet. 210:52-59(1987).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; X12584; CAA31095.1; -;
DR PIR; S01967; RSSE11.
DR HSSP; P56210; 1FOW.
DR TIGR; H10517; -;
DR InterPro; IPR000911; Ribosomal_L11.
DR InterPro; IPR006519; Ribosomal_L11bac.
DR Pfam; PF00298; Ribosomal_L11; 1.
DR Pfam; PF03946; Ribosomal_L11_N; 1.
DR ProDom; PD001367; Ribosomal_L11; 1.
DR SMART; SM00649; RL11; 1.
DR TIGRFAMs; TIGR01632; L11_bact; 1.
DR PROSITE; PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; RNA-binding.
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 141 AA; 14777 MW; B32DEB1186F6382 CRC64;
Query Match 74.5%; Score 35; DB 1; Length 141;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
PTGI_BOVIN STANDARD; PRT; 500 AA.
ID PTGI_BOVIN
AC Q29626; Q28841;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prostacyclin synthase (EC 5.3.99.4) (Prostaglandin 12 synthase).
GN PTGIS OR CYP8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Aorta;
RX MEDLINE=94327536; PubMed=8051072;
RA Hara S., Miyata A., Yokoyama C., Inoue H., Brugger R., Lottspeich F.,

OY 1 KDNVGVKVTG 9
| | | | |
Db 6 KDNVGVKVTG 14

RESULT 2

US-09-555-115A-12
; Sequence 12, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-12

Query Match 100.0%; Score 47; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVKVTG 9
| | | | |
Db 6 KDNVGVKVTG 14

RESULT 3

US-09-555-115A-13
; Sequence 13, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-13

Query Match 100.0%; Score 47; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVKVTG 9
| | | | |
Db 6 KDNVGVKVTG 14

RESULT 4

US-09-555-115A-15
; Sequence 15, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO

; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-15

Query Match 100.0%; Score 47; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

US-09-555-115A-16
; Sequence 16, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-16

Query Match 100.0%; Score 47; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KDNVGVKVTG 9
| | | | |
Db 6 KDNVGVKVTG 14

RESULT 6

US-09-555-115A-17
; Sequence 17, Application US/09555115A
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-555-115A-17

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 15, 2003, 16:57:11 ; Search time 105.521 Seconds
(without alignments)
77.608 Million cell updates/sec

Title: US-09-555-115A-1_COPY_98_106

Perfect score: 1 KDNVGRVGTG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA Main:*

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32: /cgn2_6/prodata/1/paa/US109_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	47	100.0	18	US-09-555-115A-11	Sequence 11, Appl

2	47	100.0	18	US-09-555-115A-12	Sequence 12, Appl
3	47	100.0	18	US-09-555-115A-13	Sequence 13, Appl
4	47	100.0	18	US-09-555-115A-15	Sequence 15, Appl
5	47	100.0	18	US-09-555-115A-16	Sequence 16, Appl
6	47	100.0	18	US-09-555-115A-17	Sequence 17, Appl
7	47	100.0	18	US-09-555-115A-60	Sequence 60, Appl
8	47	100.0	18	US-08-882-431B-21	Sequence 21, Appl
9	47	100.0	18	US-08-882-431B-22	Sequence 22, Appl
10	47	100.0	18	US-08-882-431B-23	Sequence 23, Appl
11	47	100.0	18	US-10-002-784A-36	Sequence 36, Appl
12	47	100.0	18	US-10-002-784A-37	Sequence 37, Appl
13	47	100.0	18	US-10-002-784A-38	Sequence 38, Appl
14	47	100.0	24	US-09-791-537-107560	Sequence 107560,
15	47	100.0	238	US-08-491-746-27	Sequence 27, Appl
16	47	100.0	238	US-09-708-008B-28	Sequence 28, Appl
17	47	100.0	239	US-08-491-746-26	Sequence 26, Appl
18	47	100.0	239	US-09-708-008B-27	Sequence 27, Appl
19	47	100.0	239	US-09-791-537-52671	Sequence 52671, A
20	47	100.0	239	US-09-791-537-52673	Sequence 52673, A
21	47	100.0	239	US-09-791-537-52675	Sequence 52675, A
22	47	100.0	239	US-09-791-537-52677	Sequence 52677, A
23	47	100.0	239	US-09-791-537-52695	Sequence 52695, A
24	47	100.0	239	US-09-791-537-57117	Sequence 57117, A
25	47	100.0	239	US-09-791-537-128386	Sequence 128386,
26	47	100.0	240	US-09-555-115A-1	Sequence 1, Appl
27	47	100.0	240	US-09-555-115A-2	Sequence 2, Appl
28	47	100.0	240	US-09-555-115A-3	Sequence 3, Appl
29	47	100.0	240	US-09-555-115A-5	Sequence 5, Appl
30	47	100.0	240	US-09-555-115A-7	Sequence 7, Appl
31	47	100.0	240	US-09-555-115A-8	Sequence 8, Appl
32	47	100.0	240	PCT-US98-16766-14	Sequence 14, Appl
33	47	100.0	266	US-08-882-431A-14	Sequence 14, Appl
34	47	100.0	266	US-08-882-431A-14	Sequence 14, Appl
35	47	100.0	266	US-08-882-431A-14	Sequence 14, Appl
36	47	100.0	266	US-08-882-431B-14	Sequence 14, Appl
37	47	100.0	266	US-09-751-708A-12	Sequence 12, Appl
38	47	100.0	266	US-09-751-708A-12	Sequence 12, Appl
39	47	100.0	266	US-09-791-537-93999	Sequence 93999, A
40	47	100.0	266	US-09-791-537-94000	Sequence 94000, A
41	47	100.0	266	US-09-791-537-115863	Sequence 115863,
42	47	100.0	266	US-10-002-784A-14	Sequence 12, Appl
43	47	87.2	18	US-09-555-115A-14	Sequence 14, Appl
44	47	87.2	239	US-09-791-537-17768	Sequence 17768, A
45	47	87.2	239	US-09-791-537-52676	Sequence 52676, A

ALIGNMENTS

RESULT 1

US-09-555-115A-11

Sequence 11, Application US/09555115A

GENERAL INFORMATION: Honach, Gregory I.

APPLICANT: Honach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136.1USMO

CURRENT APPLICATION NUMBER: US/09/555,115A

PRIOR FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067,357

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 18

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-555-115A-11

Query Match 100.0%; Score 47; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.098;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3430R1C1
;; CURRENT FILING DATE: 2002-07-11
;; CURRENT APPLICATION NUMBER: US/10/194,486
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-194-486-269

Query Match      86.0%; Score 37; DB 6; Length 1300;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCGKTC 6
Db      82 CCGTTC 87

RESULT 11
US-10-125-923A-451
;; Sequence 451, Application US/10125923A
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C79
;; CURRENT APPLICATION NUMBER: US/10/125,923A
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;; CURRENT FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 451
;; LENGTH: 1743
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-125-923A-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCGKTC 6
Db      1187 CCGATC 1192

RESULT 12
US-10-205-892-451
;; Sequence 451, Application US/10205892
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C517
;; CURRENT APPLICATION NUMBER: US/10/205,892
;; CURRENT FILING DATE: 2002-07-26
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
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;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 451
;; LENGTH: 1743
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-205-892-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCGKTC 6
DB      1187 CCGATC 1192

RESULT 13
US-10-174-575-451
;; Sequence 451, Application US/10174575
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3430R1C35
;; CURRENT APPLICATION NUMBER: US/10/174,575
;; CURRENT FILING DATE: 2002-06-18
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 451
;; LENGTH: 1743
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-174-575-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CCGKTC 6
DB      1187 CCGATC 1192

RESULT 14
US-10-174-575A-451
;; Sequence 451, Application US/10174575A
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3430R1C35
;; CURRENT APPLICATION NUMBER: US/10/174,575A
;; CURRENT FILING DATE: 2002-06-18
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 451
;; LENGTH: 1743
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-174-575A-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCGKTC 6
DB      1187 CCGATC 1192

RESULT 15
US-10-187-755-451
;; Sequence 451, Application US/10187755
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
```

APPLICANT: Pan,James
APPLICANT: Smith,Victoria
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/187,755
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
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PRIOR APPLICATION NUMBER: 60/063121
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PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 451
LENGTH: 1743
TYPE: PRT
ORGANISM: Homo Sapien
US-10-187-755-451

Query Match 86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5,7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
||| ||
Db 1187 CCGKTC 1192

Search completed: May 6, 2003, 10:36:15
Job time : 87 secs

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TYPE: PRT
ORGANISM: Homo sapiens
US-60-485-450-1271

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Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNGKVTG 9
DB 4071 KDNPVKATG 4079

RESULT 3

US-10-425-114A-54451
Sequence 54451, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54451
LENGTH: 273
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3242-662-B11_FLI.pep
US-10-425-114A-54451

Query Match 70.2%; Score 33; DB 6; Length 273;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNGKVTG 9
DB 27 KDGLGKVG 35

RESULT 4

US-10-425-114A-38414
Sequence 38414, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38414
LENGTH: 275
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700157894_FLI.pep
US-10-425-114A-38414

Query Match 70.2%; Score 33; DB 6; Length 275;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNNGKVTG 9
DB 163 DNIGSLTG 170

RESULT 5

US-10-425-114A-66720
Sequence 66720, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66720
LENGTH: 546
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4745-008-H7_FLI.pep
US-10-425-114A-66720

Query Match 70.2%; Score 33; DB 6; Length 546;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNNGKVTG 9
DB 434 DNIGSLTG 441

RESULT 6

US-10-668-767-146
Sequence 146, Application US/10668767
GENERAL INFORMATION:
APPLICANT: Caspar, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Guttridge, Steven
APPLICANT: Raub, James
APPLICANT: Smith, Rejane
APPLICANT: Tao, Yong
APPLICANT: Wu, Lihong
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
FILE REFERENCE: BB1533 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
CURRENT FILING DATE: 2003-09-23
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 146
LENGTH: 5100
TYPE: PRT
ORGANISM: Heliothis virescens
FEATURE:
OTHER INFORMATION: PXL-HV6
US-10-668-767-146

Query Match 70.2%; Score 33; DB 6; Length 5100;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:58:28 ; Search time 4.04192 Seconds
(without alignments)
68.206 Million cell updates/sec

Title: US-09-555-115a-1_COPY_98_106
Perfect score: 47
Sequence: 1 KDNVGVKVTG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148013 seqs, 30631251 residues

Total number of hits satisfying chosen parameters: 148013

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_US03_20841-4
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	35	74.5	2463	1 PCT-US03-20841-4	Sequence 4, Appl1
2	35	74.5	4563	7 US-60-485-450-1271	Sequence 1271, Ap
3	33	70.2	273	6 US-10-425-114A-54451	Sequence 54451, A
4	33	70.2	275	6 US-10-425-114A-38414	Sequence 38414, A
5	33	70.2	546	6 US-10-425-114A-66720	Sequence 66720, A
6	33	70.2	5100	6 US-10-668-767-146	Sequence 146, App
7	33	70.2	5142	6 US-10-668-767-2	Sequence 2, Appl1
8	33	70.2	5142	6 US-10-668-767-144	Sequence 144, App
9	33	70.2	6669	1 PCT-US03-21379-80	Sequence 80, Appl
10	32	68.1	399	6 US-09-897-516A-4963	Sequence 4963, Ap
11	32	68.1	399	6 US-10-425-114A-42993	Sequence 42993, A
12	32	68.1	483	6 US-10-374-983A-13	Sequence 13, Appl
13	32	68.1	490	7 US-60-478-196-3183	Sequence 3183, Ap
14	32	68.1	594	5 US-09-897-516A-7143	Sequence 7143, Ap
15	32	68.1	594	6 US-10-425-114A-71443	Sequence 71443, A
16	32	68.1	640	6 US-10-425-114A-43992	Sequence 43992, A
17	32	68.1	1166	5 US-09-200-650E-7	Sequence 7, Appl1
18	32	68.1	1979	7 US-60-490-890-1637	Sequence 1637, Ap
19	31	66.0	142	5 US-09-897-516A-4877	Sequence 4877, Ap
20	31	66.0	314	7 US-60-489-712-2	Sequence 2, Appl1
21	31	66.0	315	7 US-60-487-610-1637	Sequence 1637, Ap
22	31	66.0	424	5 US-09-688-286D-2	Sequence 2, Appl1
23	31	66.0	424	5 US-09-051-843D-2	Sequence 2, Appl1
24	31	66.0	426	5 US-09-688-286D-4	Sequence 4, Appl1
25	31	66.0	426	5 US-09-051-843D-4	Sequence 4, Appl1
26	31	66.0	427	6 US-10-671-697-9	Sequence 9, Appl1

27	31	66.0	491	6 US-10-425-114A-47215	Sequence 47215, A
28	31	66.0	604	1 PCT-US02-38348-57	Sequence 57, Appl
29	31	66.0	943	7 US-60-490-890-331	Sequence 331, App
30	31	66.0	974	6 US-10-425-114A-62433	Sequence 62433, A
31	31	66.0	1000	6 US-10-425-114A-57734	Sequence 57734, A
32	30	63.8	75	5 US-09-897-516A-5456	Sequence 5456, Ap
33	30	63.8	136	6 US-10-425-114A-68537	Sequence 68537, A
34	30	63.8	202	1 PCT-US02-24459-92	Sequence 92, Appl
35	30	63.8	208	6 US-10-425-114A-68381	Sequence 68381, A
36	30	63.8	231	6 US-10-425-114A-63712	Sequence 63712, A
37	30	63.8	265	5 US-09-850-726-26	Sequence 26, Appl
38	30	63.8	312	6 US-10-457-009-2	Sequence 2, Appl1
39	30	63.8	351	6 US-10-425-114A-60014	Sequence 60014, A
40	30	63.8	419	6 US-10-425-114A-45372	Sequence 45372, A
41	30	63.8	440	1 PCT-US02-24459-90	Sequence 90, Appl
42	30	63.8	465	6 US-10-425-114A-71378	Sequence 71378, A
43	30	63.8	510	7 PCT-US03-05338A-25	Sequence 25, Appl
44	30	63.8	530	7 US-60-485-114-1236	Sequence 1236, Ap
45	30	63.8	533	6 US-10-425-114A-44453	Sequence 44453, A

ALIGNMENTS

RESULT 1
PCT-US03-20841-4
Sequence 4, Application PC/TUS0320841
GENERAL INFORMATION:
APPLICANT: Illumigen BioSciences Inc.
APPLICANT: Smith, Maria W.
APPLICANT: Rosenberg, Gary
APPLICANT: Bumagener, Roger E.
APPLICANT: Katzev, Michael G.
TITLE OF INVENTION: PROTEIN USEFUL IN THE DIAGNOSIS OF HEPATOCELLULAR CARCINOMA
FILE REFERENCE: 55382-10
CURRENT APPLICATION NUMBER: PCT/US03/20841
CURRENT FILING DATE: 2003-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/393,982
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2463
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-20841-4

Query Match 74.5%; Score 35; DB 1; Length 2463;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
DB 1971 KDNVGVKVTG 1979

RESULT 2
US-60-485-450-1271
Sequence 1271, Application US/60485450
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1271
LENGTH: 4563

RA Ullrich V., Tanabe T.;
RT "Isolation and molecular cloning of prostacyclin synthase from bovine
RT endothelial cells";
RL J. Biol. Chem. 269:19897-19903(1994).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Aorta;
RC MEDLINE=94354863; PubMed=8074709;
RA Pereira B., Wu K.K., Wang L.H.;
RT "Molecular cloning and characterization of bovine prostacyclin
RT synthase";
RL Biochem. Biophys. Res. Commun. 203:59-66(1994).
RN [3]
RP SEQUENCE OF 9-30 FROM N.A.
RX TISSUE=Aorta;
RC MEDLINE=94107296; PubMed=8280118;
RA Pereira B., Wu K.K., Wang L.H.;
RT "Bovine prostacyclin synthase: purification and isolation of partial
RT cDNA";
RL Biochem. Biophys. Res. Commun. 197:1041-1048(1993).
CC -!- FUNCTION: CATALYZES THE ISOMERIZATION OF PROSTAGLANDIN H2 TO
CC PROSTACYCLIN (= PROSTAGLANDIN I2).
CC -!- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9-alpha,11-alpha-epidioxy-15-
CC hydroxyprosta-5,13-dienoate -> (5Z,13E)-(15S)-6,9-alpha-epoxy-11-
CC alpha,15-dihydroxyprosta-5,13-dienoate.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE. MAY BE
CC ANCHORED TO THE MEMBRANE VIA A SINGLE TRANSMEMBRANE DOMAIN.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; D30718; BAA06383.1; -;
DR EMBL; L34208; AAA53674.1; -;
DR EMBL; S67757; AAB29680.1; -;
DR PIR; A53658; A53658. Cytochrome_P450.
DR InterPro; IPR001128; Cytochrome_P450.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; FALSE NEG.
KW Isomerase; prostaglandin biosynthesis; Heme; Transmembrane;
KW Endoplasmic reticulum.
FT TRANSMEM 1 20 POTENTIAL.
FT METAL 441 441 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 192 192 S -> N (IN REF. 2).
FT CONFLICT 353 353 A -> P (IN REF. 2).
FT CONFLICT 407 407 N -> T (IN REF. 2).
SQ SEQUENCE 500 AA; 56629 MW; 3728EEFEAE852403 CRC64;
Query Match 74.5%; Score 35; DB 1; Length 500;
Best Local Similarity 77.8%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KDNVGVKVTG 9
DB 227 KDRVGVKVG 235
RESULT 8
FXR2_MOUSE
ID FXR2_MOUSE STANDARD; PRT; 673 AA.
AC Q9WVR4; Q9WVR5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fragile x mental retardation syndrome related protein 2 homolog.
GN FXR2 OR FXR2H.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=99453761; PubMed=10524236;
RA Miyashita A., Shimizu N., Endo N., Hanyuu T., Ishii N., Ito K.,
RA Itoh Y., Shirai M., Nakajima T., Odani S., Kuwano R.;
RT "Five different genes, Eif4a1, Cd68, Supl15h, Sox15 and Fxr2h, are
RT clustered in a 40 kb region of mouse chromosome 11.";
RL Gene 237:53-60(1999).
CC -!- FUNCTION: RNA-binding protein (By similarity).
CC -!- SUBUNIT: Interacts with Fmr1 and Fxr2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 2 KH domains.
CC -!- SIMILARITY: BELONGS TO THE FMR1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AB025311; BAA82249.1; -;
DR EMBL; AB025263; BAA82249.1; JOINED.
DR EMBL; AB025264; BAA82249.1; JOINED.
DR EMBL; AB025265; BAA82249.1; JOINED.
DR EMBL; AB025266; BAA82249.1; JOINED.
DR EMBL; AB025267; BAA82249.1; JOINED.
DR EMBL; AB025268; BAA82249.1; JOINED.
DR EMBL; AB025269; BAA82147.1; -;
DR HSP; Q06787; 2FMR.
DR MGD; MGI:1346074; Fxr2h.
DR InterPro; IPR004087; KH_dom.
DR InterPro; IPR004088; KH_type_1.
DR Pfam; PF00013; KH; 2.
DR SMART; SM00322; KH; 2.
DR PROSITE; PS50084; KH_TYPE_1; 2.
KW RNA-binding; Repeat.
FT DOMAIN 228 276 KH 1.
FT DOMAIN 291 340 KH 2.
FT DOMAIN 416 420 POLY-SER.
FT DOMAIN 483 486 POLY-ARG.
FT DOMAIN 545 553 POLY-ARG.
FT DOMAIN 585 595 POLY-ARG.
SQ SEQUENCE 673 AA; 73742 MW; 01F6814D4C3B5654 CRC64;
Query Match 74.5%; Score 35; DB 1; Length 673;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KDNVGVKVTG 9
DB 300 RDLVGVKVTG 308
RESULT 9
APB_HUMAN
ID APB_HUMAN STANDARD; PRT; 4563 AA.
AC P04114; O00502; Q13787;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
DE B-48 (Apo B-48)].
GN APOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9605;

RN SEQUENCE FROM N.A.
 RP MEDLINE=87016385; PubMed=3763409;
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
 RT "Complete cDNA and derived protein sequence of human apolipoprotein
 RT B-100.";
 RL Nucleic Acids Res. 14:7501-7503(1986).
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=88003974; PubMed=3652907;
 RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
 RT "DNA sequence of the human apolipoprotein B gene.";
 RL DNA 6:363-372(1987).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87008488; PubMed=3759943;
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
 RA Gotto A.M. Jr., Chan L.;
 RT "The complete cDNA and amino acid sequence of human apolipoprotein
 RT B-100.";
 RL J. Biol. Chem. 261:12918-12921(1986).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87041416; PubMed=3464946;
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
 RA Lee N., Brewer H.B. Jr.;
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
 RT derived amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87161759; PubMed=3030729;
 RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
 RA Zannis V.I.;
 RT "The complete sequence and structural analysis of human
 RT apolipoprotein B-100: relationship between apoB-100 and apoB-48
 RT forms.";
 RL EMBO J. 5:3495-3507(1986).
 RN [5]
 RN SEQUENCE OF 709-906 FROM N.A.
 RP MEDLINE=85270450; PubMed=3860836;
 RA Deeb S.S., Motulsky A.G., Albers J.J.;
 RT "A partial cDNA clone for human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
 RN [6]
 RN SEQUENCE OF 3056-3159 FROM N.A.
 RP MEDLINE=86041888; PubMed=3903660;
 RA Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
 RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
 RT "Human apolipoprotein B: identification of cDNA clones and
 RT characterization of mRNA.";
 RL Nucleic Acids Res. 13:6937-6953(1985).
 RN [7]
 RN SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
 RP MEDLINE=86033680; PubMed=3841204;
 RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
 RA Bjurvell G.;
 RT "Molecular cloning of human apolipoprotein B cDNA.";
 RL Nucleic Acids Res. 13:8813-8826(1985).
 RN [8]
 RN SEQUENCE OF 3109-4563 FROM N.A.
 RP MEDLINE=85300528; PubMed=2994225;
 RA Knott T.J., Innerarity T.L., Jacobson S.F.,
 RA Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,
 RA Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B.,
 RA Betsholtz C., Shows T.B., Mahley R.W., Scott J.;
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
 RT sites of gene expression, and chromosomal localization.";
 RL Science 230:37-43(1985).
 RN [9]
 RN SEQUENCE OF 1-291 FROM N.A.
 RP

RX MEDLINE=86149325; PubMed=3513177;
 RA Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
 RA Chen G.C., Kirsner S.W., McEntroe G., Kane J.P.;
 RT "Isolation of a cDNA clone encoding the amino-terminal region of
 RT human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
 RN [10]
 RN SEQUENCE OF 1-1670 FROM N.A.
 RP MEDLINE=86287319; PubMed=3461454;
 RA Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Kane J.P.;
 RA Yamanaka M., Hori Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
 RT "Analysis of cDNA clones encoding the entire B-26 region of human
 RT apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
 RN [11]
 RN PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
 RP MEDLINE=88018019; PubMed=3659919;
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
 RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
 RA Gotto A.M. Jr., Li W.-H., Chan L.;
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
 RT specific in-frame stop codon.";
 RL Science 238:363-366(1987).
 RN [12]
 RN DOMAINS.
 RP MEDLINE=87039351; PubMed=3773997;
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
 RA Levy-Wilson B., Scott J.;
 RT "Complete protein sequence and identification of structural domains
 RT of human apolipoprotein B.";
 RL Nature 323:734-738(1986).
 RN [13]
 RN DOMAINS.
 RP MEDLINE=86242245; PubMed=3087360;
 RA Tangimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,
 RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;
 RT "Sequence, structure, receptor-binding domains and internal repeats
 RT of human apolipoprotein B-100.";
 RL Nature 323:738-742(1986).
 RN [14]
 RN CALCITRIUM-BINDING DATA.
 RP MEDLINE=86242245; PubMed=3087360;
 RA Dasthi N., Lee D.M., Mok T.;
 RT "Apolipoprotein B is a calcium binding protein.";
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
 RN [15]
 RN PALMITOYLATION OF CYS-1112.
 RP MEDLINE=20143590; PubMed=10679026;
 RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;
 RT "Palmitoylation of apolipoprotein B is required for proper
 RT intracellular sorting and transport of cholesterol esters and
 RT triglycerides.";
 RL Mol. Biol. Cell 11:721-734(2000).
 RN [16]
 RN VARIANT SER-4328.
 RP MEDLINE=91071750; PubMed=1979313;
 RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
 RA Cuny G., Cambien F., Roizes G.;
 RT "Detection by denaturing gradient gel electrophoresis of a new
 RT polymorphism in the apolipoprotein B gene.";
 RL Hum. Genet. 86:91-93(1990).
 RN [17]
 RN VARIANT FDB GLN-3527.
 RP MEDLINE=89098975; PubMed=2563166;
 RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
 RA McCarthy B.J.;
 RT "Association between a specific apolipoprotein B mutation and
 RT familial defective apolipoprotein B-100.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
 RN [18]
 RN VARIANT LEU-2739.

RX MEDLINE=91016974; PubMed=2216805;
 RA Huang L.-S., Gavish D., Breslow J.L.;
 RT "Sequence polymorphism in the human apoB gene at position 8344.";
 RL Nucleic Acids Res. 18:5922-5922(1990).
 RN [20]
 RP VARIANT FDB CYS-3558.
 RX MEDLINE=95190020; PubMed=7883971;
 RA Pullinger C.R., Hennessey L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
 RT "Familial ligand-defective apolipoprotein B. Identification of a new
 RT mutation that decreases LDL receptor binding affinity.";
 RL J. Clin. Invest. 95:1225-1234(1995).
 RN [21]
 RP VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
 RP AND THR-4481.
 RX MEDLINE=97044521; PubMed=8889592;
 RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
 RT PCR-SSCP.";
 RL Hum. Mutat. 8:282-285(1996).
 RN [22]
 RP VARIANTS FDB GLN-3527 AND CYS-3558.
 RX MEDLINE=97403938; PubMed=9259199;
 RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
 RA Krempf M., Giraudet P., Junien C., Boileau C.;
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous
 RT detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a
 RT French population.";
 RL Hum. Mutat. 10:160-163(1997).
 RN [23]
 RP VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
 RP AND ILE-3921.
 RX MEDLINE=98141125; PubMed=9490296;
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
 RT "Screening for mutations of the apolipoprotein B gene causing
 RT hypocholesterolemia.";
 RL Hum. Genet. 102:44-49(1998).
 CC -1- FUNCTION: APOLIPOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
 CC CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
 CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
 CC THE APOB/E RECEPTOR.
 Query Match 74.5%; Score 35; DB 1; Length 4563;
 Best Local Similarity 77.8%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KDNVGVKVTG 9
 DB 4071 KDNVPRATG 4079
 RESULT 10
 Y533 LISMO STANDARD; PRT; 89 AA.
 AC Q8Y9J4;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein lmo0533.
 GN LMO0533.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duseurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 CC -1- SIMILARITY: Belongs to the UPF0237 family.
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RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 CC -1- SIMILARITY: Belongs to the UPF0237 family.
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CC EMBL; AL596165; CAC95769.1; -.
CC PIR; A11499; A11499.
CC LIPID18; LIPID18; -.
CC HAMAP; MF 01054; -. 1.
CC InterPro; IPR002912; ACT.
CC Pfam; PF01842; ACT; 1.
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 89 AA; 10017 MW; 36CDED47F316140 CRC64;
SQ
Query Match 72.3%; Score 34; DB 1; Length 89;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KDNVGVKVTG 9
Db 10 KDNVGVIVAG 18
|||||
RESULT 12
ID MURG_CLOPE STANDARD; PRT; 357 AA.
AC Q8X1Q1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide)
DE Pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
DE (SC 2.4.1.227) Undecaprenyl-PP-MurNac-pentapeptide-UDP-GlcNAc
DE transferase.
DE MURG OR CPE2063.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohkani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: Cell wall formation. Catalyzes the transfer of a GlcNAc
CC subunit on undecaprenyl-pyrophosphoryl-MurNac-pentapeptide (lipid
CC intermediate I) to form undecaprenyl-pyrophosphoryl-MurNac-
CC (pentapeptide)GlcNAc (lipid intermediate II) (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oyl-L-Ala-
CC gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP +
CC GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-
CC diphosphoundecaprenol.
CC -!- PATHWAY: Peptidoglycan biosynthesis; last step.
CC -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 28. MurG
CC subfamily.
CC
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CC
CC EMBL; AP003192; BAB81769.1; -.
CC HAMAP; MF 00033; -. 1.
CC InterPro; IPR004276; Glyco_trans_28.
CC InterPro; IPR006009; MurG.
CC Pfam; PF04101; Glyco_tran_28_C; 1.
CC Pfam; PF03033; Glyco_transf_28; 1.
CC TIGRFAMs; TIGR01133; murG; 1.
KW Transferase; Glycosyltransferase; Cell division; Cell wall; Membrane;
KW Peptidoglycan synthesis; Complete proteome.
SQ SEQUENCE 357 AA; 39785 MW; 98715339150B5ECA CRC64;
Query Match 72.3%; Score 34; DB 1; Length 357;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KDNVGVKVTG 9
Db 154 KDNKGELTG 162
|||||
RESULT 13
ID CAF1_DICDI STANDARD; PRT; 169 AA.
AC P54670;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calumirin-1.
GN CAFA OR CAF-1.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RA Abe F., Maeda Y.;
RT "Specific expression of a gene encoding a novel calcium-binding
RT protein, CAF-1, during transition of Dictyostelium cells from growth
RT to differentiation."
RL Dev. Growth Differ. 37:39-48(1995).
CC -!- FUNCTION: MAY BE INVOLVED IN THE PHASE-SHIFT OF CELLS FROM GROWTH
CC TO DIFFERENTIATION.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN CELLS STARVED JUST
CC BEFORE THE PUTATIVE SHIFT POINT.
CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC
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CC
CC EMBL; D29986; BAA06266.1; -.
CC DictyDB; D200006; cafa.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; efhand; 4.
CC SMART; SM00054; EFh; 2.
CC PROSITE; PS00018; EF_HAND; 2.
CC Calcium-binding; Repeat.
CC CA_BIND 19 30 EF-HAND 1 (POTENTIAL).
CC CA_BIND 55 66 EF-HAND 2 (POTENTIAL).
CC CA_BIND 106 117 EF-HAND 3 (POTENTIAL).
CC CA_BIND 142 153 EF-HAND 4 (POTENTIAL).
CC SEQUENCE 169 AA; 19487 MW; 34D7D3278A569187 CRC64;
SQ
Query Match 70.2%; Score 33; DB 1; Length 169;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KDNVGVKVT 8
Db 56 KDNKGKIT 63
|||||
RESULT 14
MSPI_PLAFD STANDARD; PRT; 233 AA.
ID MSPI_PLAFD
AC P13827;
```

DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (PMMSA) (Glycoprotein 185) (GP185) (Fragment).
GN MSP-1.
OS Plasmodium falciparum (isolate CDC / Honduras).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5836;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106855; PubMed=3542719;
RA Howard R.F., Ardeshir F., Reese R.T.;
RT "Conservation and antigenicity of N-terminal sequences of GP185 from
RT different Plasmodium falciparum isolates.";
RL Gene 46:197-205(1986).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42
CC kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
CC -----
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CC -----
DR EMBL; M14632; AAB59227.1; -.
DR PIR; A25814; A25814.
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
KW Transmembrane; GPI-anchor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >233 MEROZOITE SURFACE PROTEIN 1.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 233 233
SQ SEQUENCE 233 AA; 26050 MW; 1DE4D31ACAE965 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 233;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVK 7
Db 220 KDNVGM 226
|||||:

RESULT 15
MSPI PLAFN STANDARD; PRT; 281 AA.
AC P13820;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (PMMSA) (Fragment).
GN MSP-1.
OS Plasmodium falciparum (isolate NF7 / Ghana).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5842;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88142999; PubMed=2449612;
RA Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G.,
RA Brown G.V., Anders R.F., Kemp D.J.;
RT "Variation in the precursor to the major merozoite surface antigens
RT of Plasmodium falciparum."
RL Mol. Biochem. Parasitol. 27:291-302(1988).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- MISCELLANEOUS: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF

CC 83K, 42K & 19K ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
CC -----
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CC -----
DR EMBL; M19144; AAA29654.1; -.
DR PIR; B54498; B54498.
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
KW Transmembrane; GPI-anchor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >281 MEROZOITE SURFACE PROTEIN 1.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 281 AA; 31226 MW; 6150B76E0F21B299 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 281;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVK 7
Db 235 KDNVGM 241
|||||:

Search completed: October 15, 2003, 16:58:09
Job time : 5.76467 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 18.4311 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-1_COPY_98_106

Perfect score: 47

Sequence: 1 KDNVGVKVTG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	47	100.0	234	2 Q9R5X4	Q9r5x4 staphylococ
2	47	100.0	239	2 Q05157	Q05157 staphylococ
3	47	100.0	239	2 Q53678	Q53678 staphylococ
4	47	100.0	239	2 Q06532	Q06532 staphylococ
5	47	100.0	239	2 Q06531	Q06531 staphylococ
6	47	100.0	239	2 Q06533	Q06533 staphylococ
7	47	100.0	239	2 Q06534	Q06534 staphylococ
8	47	100.0	266	16 Q8N3J6	Q8n3j6 staphylococ
9	47	100.0	271	2 Q9F0L6	Q9f0l6 staphylococ
10	47	87.2	239	2 Q06535	Q06535 staphylococ
11	37	78.7	128	2 Q87332	Q87332 corynebacte
12	37	78.7	185	16 Q8NQ03	Q8nq03 corynebacte
13	37	78.7	274	10 Q9STR7	Q9str7 arabidopsis
14	37	78.7	299	10 Q8LAK6	Q8lak6 arabidopsis
15	37	78.7	315	10 Q93VK9	Q93vk9 arabidopsis
16	37	78.7	855	16 Q8G853	Q8g853 bifidobacte

17	37	78.7	1272	10	022731	022731 arabidopsis
18	37	78.7	1826	16	Q8E7Z7	Q8e7z7 rhizobium l
19	35	74.5	65	16	Q8E531	Q8e531 streptococ
20	35	74.5	65	16	Q8DZG5	Q8dzg5 streptococ
21	35	74.5	142	16	Q8CK85	Q8ck85 pasteurella
22	35	74.5	142	16	Q8ZAP1	Q8zap1 yersinia pe
23	35	74.5	242	14	Q8BF72	Q8bf72 uncultured
24	35	74.5	248	14	Q8BFA6	Q8bfa6 uncultured
25	35	74.5	499	16	Q8YDY5	Q8ydy5 brucella me
26	35	74.5	709	16	Q8ABZ4	Q8abz4 caulobacter
27	35	74.5	738	16	Q8YCN1	Q8ycn1 brucella me
28	35	74.5	738	16	Q8FVNE	Q8fvne brucella su
29	35	74.5	808	16	Q97E37	Q97e37 clostridium
30	35	74.5	836	4	Q13785	Q13785 homo sapien
31	35	74.5	1002	16	Q8P822	Q8p822 xanthomonas
32	35	74.5	1540	6	Q29433	Q29433 sus scrofa
33	35	74.5	2829	6	Q29021	Q29021 sus scrofa
34	35	74.5	3262	4	Q13788	Q13788 homo sapien
35	34	72.3	89	16	Q92EC3	Q92ec3 listeria in
36	34	72.3	89	16	Q8Y9J4	Q8y9j4 listeria mo
37	34	72.3	109	3	Q9P8B0	Q9p8b0 agaricus bi
38	34	72.3	260	5	Q9VSY0	Q9vsv0 drosophila
39	34	72.3	313	5	Q8MVV8	Q8mvv8 plasmodium
40	34	72.3	432	16	Q8YY40	Q8yy40 anabaena sp
41	34	72.3	459	3	Q8J2R5	Q8j2r5 gibberella
42	34	72.3	487	16	Q97GM8	Q97gm8 clostridium
43	34	72.3	514	10	Q8L6A9	Q8l6a9 theobroma c
44	34	72.3	577	2	Q98FR9	Q98fr9 escherichia
45	34	72.3	591	16	Q8XM18	Q8xm18 clostridium

ALIGNMENTS

RESULT 1

Q9R5X4	PRELIMINARY;	PRT;	234 AA.
ID	Q9R5X4		
AC	Q9R5X4;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	ENTEROTOXIN-PYROGENIC toxin (Fragment).		
OS	Staphylococcus.		
OC	Bacteria; Firmicutes; Bacillales.		
OX	NCBI_TaxID=1279;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94325995; PubMed=8049778;		
RA	Van den Buesche R.A., Lyon J.D., Bohach G.A.;		
RL	Mol. Phylogenet. Evol. 2:281-292 (1993).		
DR	HSSP: P34071; ISE2.		
DR	InterPro; IPR006177; Bctrl tox.		
DR	InterPro; IPR006123; Staph/Strep toxin.		
DR	InterPro; IPR006126; Staph/Strep tox.		
DR	Pfam; PF01123; Staph Strep toxin; 1.		
DR	Pfam; PF02876; Staph Strep toxin C; 1.		
DR	PRINTS; PR00279; BACTLTOXIN		
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
FT	NON_TER 1		
FT	NON_TER 234		
SQ	SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;		

Query Match 100.0%; Score 47; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDNVGVKVTG 9

Db 93 KDNVGVKVTG 101

```
RESULT 2
O05157 ID Q05157 PRELIMINARY; PRT; 239 AA.
AC Q05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; 1JCK
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 98 KDNVKGKVTG 106
|||||

RESULT 3
Q53678 ID Q53678 PRELIMINARY; PRT; 239 AA.
AC Q53678;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 98 KDNVKGKVTG 106
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RESULT 4
Q06532 ID Q06532 PRELIMINARY; PRT; 239 AA.
AC Q06532;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 98 KDNVKGKVTG 106
|||||

RESULT 5
Q06531 ID Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; 1SE2.
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Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 98 KDNVKGKVTG 106
|||||

RESULT 4
Q06532 ID Q06532 PRELIMINARY; PRT; 239 AA.
AC Q06532;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVKGKVTG 9
DB 98 KDNVKGKVTG 106
|||||

RESULT 5
Q06531 ID Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; 1SE2.
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DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
DB 98 KDNVGVKVTG 106

RESULT 6
Q06533 PRELIMINARY; PRT; 239 AA.
ID Q06533;
AC Q06533;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RC STRAIN=MNCopeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13378; AAA26622.1; -.
DR HSSP; P34071; ISTE.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
DB 98 KDNVGVKVTG 106

RESULT 7
Q06534 PRELIMINARY; PRT; 239 AA.
ID Q06534;
AC Q06534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RC STRAIN=MNCopeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13378; AAA26622.1; -.
DR HSSP; P34071; ISTE.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
DB 98 KDNVGVKVTG 106

RESULT 8
Q8NKG6 PRELIMINARY; PRT; 266 AA.
ID Q8NKG6;
AC Q8NKG6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RC STRAIN=MNCopeland;
RX MEDLINE=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 100.0%; Score 47; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
DB 125 KDNVGVKVTG 133

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RESULT 9
Q9F0L6 PRELIMINARY; PRT; 271 AA.
ID Q9F0L6
AC Q9F0L6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2056668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 193:63-70 (2001).
DR EMBL; AF217235; AAC29599.1; -.
DR HSP; P34071; ISE2.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
Db 130 KDNVGVKVTG 138

RESULT 10
Q06535 PRELIMINARY; PRT; 239 AA.
ID Q06535
AC Q06535;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FRI 909.
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13377; AAA26621.1; -.
DR HSP; P23313; IJCK.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

Query Match 100.0%; Score 47; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDNVGVKVTG 9
Db 130 KDNVGVKVTG 138

RESULT 11
Q87332 PRELIMINARY; PRT; 128 AA.
ID Q87332
AC Q87332;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 13.5 kDa protein (Fragment).
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC13032;
RA Wehmeier L., Schafer A., Burkowski A., Kramer R., Mechold U.,
RA Walke H., Puhler A., Kalinowski J.;
RT "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp
RT metabolism.";
RL Microbiology 144:1853-1862 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC13032;
RA Berens S., Kalinowski J., Puhler A.;
RT "The role of Corynebacterium glutamicum secretion genes secD, secE and
RT secG in transporting the Streptomyces griseus alpha-amylase.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038651; AAC35495.1; -.
DR KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 128 AA; 13491 MW; 2099EE56F9F70941 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVGVKVTG 9
Db 43 DNTGKITG 50

RESULT 12
Q8NQ03 PRELIMINARY; PRT; 185 AA.
ID Q8NQ03
AC Q8NQ03;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Cgl1651.
GN CGL1651.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AP005279; BAB99044.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 185 AA; 19093 MW; 4A8819674658EA26 CRC64;

Query Match      78.7%; Score 37; DB 16; Length 185;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVGKVTG 9
Db 100 DNTGKITG 107

RESULT 13
Q9STR7 PRELIMINARY; PRT; 274 AA.
AC Q9STR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 30.6 kDa protein.
GN T24C20.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choise N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096856; CAB51068.1; -.
KW Hypothetical protein.
SQ SEQUENCE 274 AA; 30617 MW; 0E474D714F900A6D CRC64;

Query Match      78.7%; Score 37; DB 10; Length 274;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDNVGKVT 8
Db 138 KDNAGKVT 145

RESULT 14
Q8LAK6 PRELIMINARY; PRT; 299 AA.
AC Q8LAK6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,

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RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087754; RAM65290.1; -.
KW Hypothetical protein.
SQ SEQUENCE 299 AA; 33821 MW; CED6107F70C3D76F CRC64;

Query Match      78.7%; Score 37; DB 10; Length 299;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDNVGKVT 8
Db 122 KDNAGKVT 129

RESULT 15
Q93VK9 PRELIMINARY; PRT; 315 AA.
AC Q93VK9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 35.6 kDa protein.
GN T24C20.90/AT3G48210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Ecker J.R., Theologis A.;
RL "Full Length cDNA of gene T24C20.90/AT3G48210 (GI:5541727).";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RL "Full Length cDNA of gene T24C20.90/AT3G48210 (GI:5541727).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059099; AAL15205.1; -.
DR EMBL; AF370157; AAK43972.1; -.
KW Hypothetical protein.
SQ SEQUENCE 315 AA; 35578 MW; A3552C4D1CACB84E CRC64;

Query Match      78.7%; Score 37; DB 10; Length 315;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDNVGKVT 8
Db 138 KDNAGKVT 145
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 30.1018 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-9
Perfect score: 66
Sequence: 1 CAGGTGPKTKAC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	66	100.0	11	20	AA06247 Staphylococcal gro
2	66	100.0	11	24	ABG71375 Staphylococcal ent
3	66	100.0	230	12	AAR13204 Staphylococcal ent
4	66	100.0	230	14	AAR45012 Staphylococcal ent
5	66	100.0	230	22	AAB67339 Staphylococcus aur
6	66	100.0	230	23	ABE76235 Staphylococcus aur
7	66	100.0	233	12	AAR13203 Staphylococcal ent
8	66	100.0	233	14	AAR45011 Staphylococcal ent
9	66	100.0	233	18	AAW35373 Staphylococcus ent

10	66	100.0	233	18	AAW06738 Staphylococcus ent
11	66	100.0	233	21	AAV70103 Mutant Staphylococ
12	66	100.0	233	21	AAV54463 Amino acid sequenc
13	66	100.0	233	22	AAB67338 Staphylococcus aur
14	66	100.0	233	23	ABE79502 Staphylococcal ent
15	66	100.0	233	23	ABE76234 Staphylococcus aur
16	66	100.0	233	24	ABP58456 Engineered superan
17	66	100.0	233	24	ABP58456 Staphylococcal ent
18	66	100.0	233	24	ABP58457 Engineered superan
19	66	100.0	233	24	ABP58458 Staphylococcal ent
20	66	100.0	245	18	AAW35374 Staphylococcus ent
21	66	100.0	245	18	AAW35375 Staphylococcus ent
22	66	100.0	257	22	AAU14103 Peptide sequence f
23	66	100.0	257	22	AAU14104 Peptide sequence f
24	66	100.0	257	23	ABE79501 Staphylococcal ent
25	66	100.0	672	24	ABP58454 Engineered superan
26	59	89.4	28	21	ABE28216 Chimeric peptide c
27	55	83.3	257	21	AAV70102 Staphylococcal ent
28	53	80.3	22	17	AAW04491 Staphylococcal ent
29	53	80.3	22	20	AAW73914 Staphylococcal ent
30	46	69.7	4440	24	ABU07907 Novel human secret
31	45	68.2	162	20	AAV28642 Human secreted pro
32	45	68.2	184	21	AAE211301 Human KLK-L5 prote
33	45	68.2	248	21	AAE211304 Human KLK-L5 prote
34	45	68.2	248	21	AAE24032 Human PRO1303 prot
35	45	68.2	248	21	AAE24428 Human PRO1303 (UNQ
36	45	68.2	248	21	AAV99393 Human EST encoded
37	45	68.2	248	22	AAE23994 Protein of the inv
38	45	68.2	248	22	AAE66142 Human KLK-L5 prote
39	45	68.2	254	21	AAE211303 Human novel polype
40	45	68.2	254	23	ABG66676 Drosophila melanog
41	45	68.2	464	22	ABE67022 Drosophila melanog
42	44	66.7	322	22	ABE60976 Drosophila melanog
43	44	66.7	444	22	ABE59231 Drosophila melanog
44	43	65.2	415	14	AAR32922 AAMP-1. Homo sapi
45	43	65.2	415	16	AAE66773 N-terminally trunc

ALIGNMENTS

RESULT 1
AA06247
ID AA06247 standard; Peptide; 11 AA.
XX
AC AA06247;
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group A enterotoxin disulfide loop.
XX
DE Enterotoxin; SEA; toxin; disulfide loop; protein engineering.
XX
OS Staphylococcus aureus.
XX
PN WO9927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25107.
XX
PR 02-DEC-1997; 97US-0067357.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Bohach GI;
XX
DR WPI; 1999-358008/30.
XX
PT Non-toxic modified staphylococcal enterotoxins
XX
PS Disclosure; Page 3; 25pp; English.
XX

CC This peptide corresponds to the disulfide loop, i.e. amino acids
 CC 96-106, of Staphylococcus aureus group A enterotoxin (SEA). The
 CC invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically,
 CC the modification involves deletions within the disulfide loop
 CC region (see AY06261). The modified toxins retain useful biological
 CC properties, such as the ability to induce cytokine production, but
 CC have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and
 CC fever inducing activity are typically decreased by at least about
 CC 100-fold, while LD50 (in Dutch Belted rabbits) is at least
 CC 100-fold higher than the native toxin.

XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 66; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00063;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTENKTAC 11
 Db |||||

RESULT 2
 ID ABG71375 standard; Peptide; 11 AA.
 XX
 AC ABG71375;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEA disulfide loop region.
 XX
 KW Modified pyrogenic toxin; disulfide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEA.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US11619.
 XX
 PR 13-APR-2001; 2001US-283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX WPI; 2003-058608/05.
 XX
 PT New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
 PT an immune function and as a vaccine against toxic shock syndrome or
 PT food poisoning -
 XX
 PS Disclosure; Fig 15; 67pp; English.
 XX
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulfide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulfide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic
 CC response-inducing activity decreased by about 100-fold in comparison to a
 CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents a staphylococcal enterotoxin
 CC disulfide loop region.

SQ Sequence 11 AA;
 Query Match 100.0%; Score 66; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00063;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY P CAGGTENKTAC 11
 Db |||||

RESULT 3
 AAR13204
 ID AAR13204 standard; Protein; 230 AA.
 XX
 AC AAR13204;
 XX
 DT 15-OCT-1991 (first entry)
 XX
 DE Staphylococcal enterotoxin E.
 XX
 KW SEE; cancer treatment; pyrogen; tumouricide.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9110680-A.
 XX
 PD 25-JUL-1991.
 XX
 PF 17-JAN-1991; 91WO-US00342.
 XX
 PR 17-JAN-1990; 90US-0466577.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 1991-237984/32.
 XX
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC SEE was isolated and purified from S.aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEE. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophathy profiles.
 XX
 PS See AAR13203-R13211.
 XX
 SQ Sequence 230 AA;
 Query Match 100.0%; Score 66; DB 12; Length 230;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTENKTAC 11
 Db |||||

RESULT 4
 AAR45012
 ID AAR45012 standard; protein; 230 AA.
 XX
 AC AAR45012;
 XX

DT 25-MAR-2003 (updated)
 DT 08-JUN-1994 (first entry)
 XX
 DE Staphylococcal enterotoxin SEE.
 XX
 KW Staphylococcal enterotoxin; SE: cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX
 OS Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 120 /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 121 /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 123 /note= "Given in the specification as O, no further
 FT details given"
 FT Misc-difference 124 /note= "Given in the specification as U, no further
 FT details given"
 XX
 PN WO93241136-A1.
 XX
 XX 09-DEC-1993.
 XX
 XX 01-JUN-1993; 93WO-US05213.
 XX
 PR 01-JUN-1992; 92US-0891718.
 XX
 XX (STON/) STONE J L.
 PA (TERM/) Terman D S.
 XX
 XX Stone JL, Terman DS;
 XX WPI; 1993-405418/50.
 DR
 XX Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PT
 XX Disclosure; Fig 1; 90pp; English.
 PS
 XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 XX Query Match 100.0%; Score 66; DB 14; Length 230;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGTPNKTAC 11
 DB 93 CAGGTPNKTAC 103
 XX
 RESULT 5
 AAB67339
 ID AAB67339 standard; peptide; 230 AA.
 XX
 AC AAB67339;
 XX
 XX 23-APR-2001 (first entry)
 DT
 XX

DE Staphylococcus aureus enterotoxin E protein.
 XX
 KW Tumour; cancer; immune; enterotoxin.
 XX
 OS Staphylococcus aureus.
 XX
 PN US6180097-B1.
 XX
 PD 30-JAN-2001.
 XX
 XX 30-OCT-1998; 98US-0183437.
 PF
 XX 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 XX (TERM/) Terman D S.
 PA
 XX Terman DS;
 PI
 XX WPI; 2001-158657/16.
 DR
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro
 PT or in vivo comprises exogenous nucleic acids encoding a superantigen
 PT and a costimulatory molecule -
 PT
 XX Disclosure; Fig 2; 16pp; English.
 PS
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule
 CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 CC
 XX Sequence 230 AA;
 SQ
 Query Match 100.0%; Score 66; DB 22; Length 230;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGTPNKTAC 11
 DB 93 CAGGTPNKTAC 103
 XX
 RESULT 6
 ABB76235
 ID ABB76235 standard; Protein; 230 AA.
 XX
 AC ABB76235;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin E.
 XX
 KW Enterotoxin E; SEE; superantigen; antigen; tumour; cancer;
 KW antitumour; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 120 /note= "given as 'J' in the specification"
 FT Misc-difference 121 /note= "given as 'J' in the specification"
 FT Misc-difference 123 /note= "given as 'J' in the specification"
 FT

FT Misc-difference 124 /note= "given as 'O' in the specification"

FT Misc-difference 125 /note= "given as 'U' in the specification"

FT Misc-difference 125 /note= "given as 'V' in the specification"

XX US2002051765-A1.

XX 02-MAY-2002.

XX 19-DEC-2000; 2000US-0741503.

XX 31-JAN-1994; 94US-0189424.

XX 19-JUN-1995; 95US-0491746.

XX 03-OCT-1989; 89US-0416530.

XX 17-JAN-1990; 90US-0466577.

XX 17-JAN-1991; 91WO-US00342.

XX 01-JUN-1992; 92US-0891718.

XX 02-MAR-1993; 93US-0025144.

XX (TERM/) Terman D S.

XX Terman DS;

XX WPI; 2002-415198/44.

XX Reagent for treating cancer without the need for e.g. radiotherapy, comprises a specific V beta subset of T cells sensitized to a growing tumor and stimulated with superantigens -

XX Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of enterotoxin E (SEE) of Staphylococcus aureus. Similarity is shown, in several stretches of sequence, between staphylococcal enterotoxins, streptococcal pyrogenic exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the present invention, synthetic polypeptides useful in tumour therapy and in blocking or destroying autoreactive T and B lymphocyte populations are characterised by substantial structural homology to staphylococcal enterotoxin A and enterotoxin B, and to streptococcal pyrogenic exotoxins, with statistically significant sequence homology and similarity (Z value of Lipman and Pearson algorithm in Monte Carlo analysis exceeding 6) to include alignment of cysteine residues and similar hydropathy profiles. These superantigens are used to treat solid tumours, including their metastases, without radiation, surgery or standard chemotherapeutic agents. A claimed method of human cancer treatment involves contacting haematopoietic cells from a patient with one or more superantigens ex vivo to generate stimulated cells, selecting a specific V beta subset of cells, and reintroducing these cells into the patient to induce an in vivo therapeutic, tumouricidal reaction.

XX SQ Sequence 230 AA;

Query Match 100.0%; Score 66; DB 23; Length 230;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11

Db 93 CAGGTPNKTAC 103

RESULT 7

ID AAR13203

AC AAR13203 standard; protein; 233 AA.

XX AAR13203;

XX 15-OCT-1991 (first entry)

XX Staphylococcal enterotoxin A.

XX SEA; cancer treatment; pyrogen; tumouricide.

XX Staphylococcus aureus.

XX WO9110680-A.

XX 25-JUL-1991.

XX 17-JAN-1991; 91WO-US00342.

XX 17-JAN-1990; 90US-0466577.

XX (TERM/) Terman D S.

XX Terman DS;

XX WPI; 1991-237984/32.

XX Treating cancer with enterotoxin from Staphylococcus aureus - administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions

XX Disclosure; Fig 1; 74pp; English.

XX SEA was isolated and purified from S.aureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEA. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles.

XX See also AAR13204-R13211.

XX SQ Sequence 233 AA;

Query Match 100.0%; Score 66; DB 12; Length 233;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11

Db 96 CAGGTPNKTAC 106

RESULT 8

ID AAR45011

AC AAR45011P standard; protein; 233 AA.

XX AAR45011;

XX 25-MAR-2003 (updated)

XX 08-JUN-1994 (first entry)

XX Staphylococcal enterotoxin SEA.

XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; perfusion system.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 49

FT /note= "Given in the specification as O, no further details given"

XX WO9324136-A1.

XX 09-DEC-1993.

XX 01-JUN-1993; 93WO-US05213.

CC cancer, infectious diseases and immunological disorders. The
 CC nucleic acid, optionally in combination with cytokine or chemokine
 CC nucleic acids, is delivered to an animal using e.g. liposomes. It
 CC acts by controlling the activity of effector cells, such as T-cells,
 CC macrophages, monocytes and/or natural killer cells. Localised
 CC prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal.
 XX
 SQ Sequence 233 AA;
 Query Match 100.0%; Score 66; DB 18; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGTPNKTAC 11
 |||||
 Db 96 CAGGTPNKTAC 106
 RESULT 11
 AAY70103
 ID AAY70103 standard; Protein; 233 AA.
 XX
 AC AAY70103;
 DT 05-JUN-2000 (first entry)
 XX
 DE Mutant Staphylococcal enterotoxin A for vaccine A489270P.
 XX
 KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
 KW treatment; superantigen-associated bacterial infection; A489270P.
 XX
 OS Staphylococcus sp.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..233
 FT /label= Mature Staphylococcal enterotoxin A
 FT /note= "Mutant sequence without the leader peptide"
 FT Misc-difference 2 /note= "Encoded by AG"
 FT Misc-difference 18 /note= "Encoded by TTG"
 FT Misc-difference 48 /note= "Wild type Leu substituted with Arg"
 FT Misc-difference 70 /note= "Wild type Asp substituted with Arg"
 FT Misc-difference 92 /note= "Wild type Tyr substituted with Ala"
 FT Misc-difference 157 /note= "Encoded by CTT"
 FT Misc-difference 180 /note= "Encoded by CAG"
 FT
 FT
 XX WO200009154-A1.
 XX
 PD 24-FEB-2000.
 XX
 XX 13-AUG-1998; 98WO-US16766.
 XX
 PR 13-AUG-1998; 98WO-US16766.
 XX
 PA (REED-) REED ARMY INST RES WALTER.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2000-224177/19.
 DR N-PSDB; AA251106.
 XX
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 FT diagnosis of superantigen-associated bacterial infections -
 XX

PS Claim 8; Page 74-76; 118pp; English.
 XX
 CC The present amino acid sequence is the mutant Staphylococcal enterotoxin
 CC A (SEA), a bacterial superantigen toxin (SAG), used for the
 CC formulation of SEA vaccine A489270P. The coding region of this SAG toxin
 CC is altered by site directed mutagenesis, that results in disruption of
 CC binding of the toxin to both the MHC class II or T-cell antigen
 CC receptor. This altered SAG toxin has the leader peptide cleaved by native
 CC bacterial enzymatic mechanism and the first residue of the mature protein
 CC is encoded by the transcriptional start site (ATG). SEA has
 CC antibacterial and cytostatic activity. This sequence is useful for the
 CC production of SEA vaccines and specific antibodies. This vaccine
 CC overcomes the disadvantages of the chemically inactivated toxoids and is
 CC designed to protect individuals against one or several related
 CC staphylococcal and streptococcal toxins. It is used for the diagnosis and
 CC treatment or amelioration of superantigen-associated bacterial
 CC infections.
 XX
 SQ Sequence 233 AA;
 Query Match 100.0%; Score 66; DB 21; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGTPNKTAC 11
 |||||
 Db 96 CAGGTPNKTAC 106
 RESULT 12
 AAY54463
 ID AAY54463 standard; Protein; 233 AA.
 XX
 AC AAY54463;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Amino acid sequence of a mutant Staphylococcal enterotoxin A.
 XX
 KW Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;
 KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;
 KW Staphylococcal intoxication; Staphylococcus exotoxin.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "Glu encoded by AGAA"
 FT Misc-difference 4 /note= "Ser encoded by C"
 FT 0
 XX WO200002523-A2.
 PN
 XX 20-JAN-2000.
 PD
 XX 09-JUL-1999; 99WO-US15569.
 PF
 XX 10-JUL-1998; 98US-0092416.
 PR
 XX (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.
 PA
 XX Lee JS, Pushko P, Smith JF, Ulrich RG;
 PI WPI; 2000-160826/14.
 DR N-PSDB; AA245833.
 XX
 XX New DNA construct useful as vaccines against enterotoxins of
 PT Staphylococcus aureus which causes gastrointestinal distress, or toxic
 PT shock syndrome -
 XX
 PS Disclosure; Page 28; 30pp; English.
 XX The present sequence is represents a mutant Staphylococcal enterotoxin A.

CC It is encoded by a mutant SEA gene. The mutant gene product is unable to
 CC bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB
 CC genes were inserted into a Venezuelan equine encephalitis (VEE) replicon
 CC vector, to produce vaccine vectors. The mutant gene product is
 CC unable to bind to the MHC on T-cells, and so is non-toxic.
 CC Self-replicating RNA derived from the recombinant VEE vectors can be
 CC used as a nucleic acid vaccine, or to transfect cells along with RNA
 CC from helper plasmids. The recombinant proteins produced are used as
 CC vaccines for providing immunity against Staphylococcal enterotoxin A
 CC as a diagnostic tool for detection of Staphylococcus enterotoxin. The
 CC transformed host cells are used to analyse the effectiveness of drugs
 CC and agents which inhibit S. aureus exotoxins or release of exotoxins.
 CC Infectious alpha-virus particles comprising the mutant SEA or SEB genes
 CC are used for providing immunity against Staphylococcal enterotoxins by
 CC generating a protective immune reaction in humans or animals. The
 CC vaccines are used to reduce disease symptoms or reduce severity of
 CC disease caused by enterotoxins of S. aureus.

XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 66; DB 21; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTENKTKAC 11
 Db 96 CAGGTENKTKAC 106
 |||||

RESULT 13
 AAB67338
 ID AAB67338 standard; peptide; 233 AA.
 XX
 AC AAB67338;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin A protein.
 XX
 DE Tumour; cancer; immune; enterotoxin.
 KW
 XX Staphylococcus aureus.
 OS
 XX US6180097-B1.
 PN
 XX 30-JAN-2001.
 PD
 XX 30-OCT-1998; 98US-0183437.
 PF
 XX 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91US-0500342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) Terman D S.
 XX
 XX Terman DS;
 PI
 XX WPI; 2001-158657/16.
 DR
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro
 PT or in vivo comprises exogenous nucleic acids encoding a superantigen
 PT and a costimulatory molecule -
 XX
 XX Disclosure; Fig 2; 16pp; English.
 PS
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule

CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.

XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 66; DB 22; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTENKTKAC 11
 Db 96 CAGGTENKTKAC 106
 |||||

RESULT 14
 ABB79502
 ID ABB79502 standard; Protein; 233 AA.
 XX
 AC ABB79502;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Staphylococcal enterotoxin A vaccine, cytoplasmic (A489270C).
 XX
 DE Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;
 KW attenuation; mutant; mutein.
 XX
 OS Staphylococcus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "encoded by AT, apparent frameshift"
 FT Misc-difference 48 /note= "wild-type Leu substituted by Arg"
 FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"
 FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"
 XX
 PN US6399332-B1.
 XX
 XX 04-JUN-2002.
 XX
 PF 01-SEP-1998; 98US-0144776.
 XX
 PR 25-JUN-1997; 97US-0882431.
 XX
 XX (USSA) US SEC OF ARMY.
 XX
 XX Ulrich QG, Olson MA, Bavari S;
 XX WPI; 2002-546281/58.
 DR N-PSDB; ABB84223.
 XX
 PT Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases -
 XX
 PS Claim 5; Column 37-39; 46pp; English.
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, cytoplasmic (A489270C). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA
 CC sequence: L48R, Y89A and D70R. These mutations reduce the binding
 CC of the toxin to major histocompatibility complex (MHC) Class II
 CC and/or T cell receptors. The protein is expressed as a nonsecreted
 CC product within host Escherichia coli cells. The vaccine is used to
 CC protect against superantigen toxin infections. Superantigen
 CC attributes are absent, but the superantigen is effectively
 CC recognised by the immune system and an appropriate antibody

CC response is produced. In examples from the invention, attenuated
 CC superantigen toxins were shown to protect animals against challenge
 CC with wild-type toxin. Methods of producing and using the altered
 CC superantigen toxins as vaccines, and in diagnosis and therapy, are
 CC provided. A multivalent vaccine consisting of altered superantigen
 CC toxins from SEA, SEB, SEC-1, TSE-1 and streptococcal SPEa is
 CC predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins.
 XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 66; DB 23; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTENKTAC 11
 |||||
 Db 96 CAGGTENKTAC 106

RESULT 15
 ABB76234
 ID ABB76234 standard; Protein; 233 AA.
 XX AC ABB76234;
 XX DT 09-AUG-2002 (first entry)
 XX DE Staphylococcus aureus enterotoxin A.
 XX KW Enterotoxin A; SEA; superantigen; antigen; tumour; cancer;
 XX KW antitumour; therapy.
 XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers
 FT FT Misc-difference 49
 FT FT /note= "amino acid residue given as 'O' in the
 FT FT specification"

XX PN US2002051765-A1.
 XX PD 02-MAY-2002.
 XX PF 19-DEC-2000; 2000US-0741503.
 XX PR 31-JAN-1994; 94US-0189424.
 XX PR 19-JUN-1995; 95US-0491746.
 XX PR 03-OCT-1989; 89US-0416530.
 XX PR 17-JAN-1990; 90US-0466577.
 XX PR 17-JAN-1991; 91WO-US00342.
 XX PR 01-JUN-1992; 92US-0891718.
 XX PR 02-MAR-1993; 93US-0025144.

XX (TERM/) Terman D S.
 XX Terman DS;
 XX PI
 XX WPI; 2002-415198/44.
 XX DR

XX Reagent for treating cancer without the need for e.g. radiotherapy,
 XX comprises a specific V beta subset of T cells sensitized to a growing
 XX tumor and stimulated with superantigens -
 XX Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of enterotoxin A
 XX (SEA) of Staphylococcus aureus. Similarity is shown, in several
 XX stretches of sequence, between staphylococcal enterotoxins,
 XX streptococcal pyrogenic exotoxins and staphylococcal exfoliative
 XX toxins (see ABB76234-44). In the present invention, synthetic
 XX polypeptides useful in tumour therapy and in blocking or destroying
 XX autoreactive T and B lymphocyte populations are characterised by

CC substantial structural homology to staphylococcal enterotoxin A and
 CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
 CC statistically significant sequence homology and similarity (Z value
 CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
 CC 6) to include alignment of cysteine residues and similar hydrophathy
 CC profiles. These superantigens are used to treat solid tumours,
 CC including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient
 CC with one or more superantigens ex vivo to generate stimulated cells,
 CC selecting a specific V beta subset of cells, and reintroducing
 CC these cells into the patient to induce an in vivo therapeutic,
 CC tumouricidal reaction.
 XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 66; DB 23; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTENKTAC 11
 |||||
 Db 96 CAGGTENKTAC 106

Search completed: October 15, 2003, 16:56:53
 Job time : 32.2018 secs

Thu Oct 16 09:57:40 2003

GenCore version 5.1.6
Copyright (c) 1993 - 2003
time 8.43114 Seconds
16 million cell updates/sec

OM protein - protein search, using sw mode2 Million cell updates/sec

October 15, 2003, 16:55

Run on:

us-09-555-115a-9

328717

Title: score: 66 CAGG chosen parameters: 328717

Perfect score: BUC

Scoring table: 00000

Match 0%

Match 100%

Searched: 5 first 45 summaries

Total Read Patents AA:*

- /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/68 COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	66	100.0	82	4	US-09-144-776B-17
2	66	100.0	82	4	US-09-144-776B-19
3	66	100.0	226	3	US-08-896-933-24
4	66	100.0	226	4	US-09-314-235-24
5	66	100.0	232	3	US-08-896-933-23
6	66	100.0	232	4	US-09-314-235-23
7	66	100.0	233	1	US-08-446-918A-4
8	66	100.0	233	2	US-08-580-806-4
9	66	100.0	233	4	US-09-144-776B-4
10	66	100.0	233	4	US-08-695-692B-7
11	66	100.0	233	4	US-08-695-692B-8
12	66	100.0	237	3	US-08-486-099-112
13	66	100.0	257	3	US-08-486-099-113
14	66	100.0	257	3	US-08-360-107A-122
15	66	100.0	257	3	US-08-360-107A-123
16	66	100.0	257	3	US-08-484-223B-112
17	66	100.0	257	3	US-08-484-223B-113
18	66	100.0	257	3	US-08-919-597-112
19	66	100.0	257	3	US-08-919-597-113
20	66	100.0	257	3	US-08-475-668A-112
21	66	100.0	257	3	US-08-475-668A-113
22	66	100.0	257	3	US-08-485-551A-112
23	66	100.0	257	3	US-08-485-551A-113
24	66	100.0	257	3	US-08-471-913A-112
25	66	100.0	257	3	US-08-471-913A-113
26	66	100.0	257	3	US-08-485-264A-112
27	66	100.0	257	3	US-08-485-264A-113

28	66	100.0	257	4	US-08-474-349A-112	Sequence 112, App
29	66	100.0	257	4	US-08-474-349A-113	Sequence 113, App
30	66	100.0	257	4	US-09-144-776B-2	Sequence 2, Appli
31	66	100.0	257	4	US-08-470-896-112	Sequence 112, App
32	66	100.0	257	4	US-08-470-896-113	Sequence 113, App
33	66	100.0	257	4	US-08-485-546A-112	Sequence 112, App
34	66	100.0	257	4	US-08-485-546A-113	Sequence 113, App
35	59	89.4	28	3	US-08-896-933-22	Sequence 22, Appl
36	59	89.4	28	4	US-09-314-235-22	Sequence 22, Appl
37	53	80.3	22	1	US-08-220-378-4	Sequence 4, Appli
38	53	80.3	22	2	US-08-696-012-4	Sequence 4, Appli
39	45	68.2	162	4	US-09-244-111-6	Sequence 6, Appli
40	43	65.2	415	5	PCT-US93-00601-2	Sequence 2, Appli
41	43	65.2	415	5	PCT-US94-07107A-7	Sequence 7, Appli
42	43	65.2	426	5	PCT-US94-07107A-7	Sequence 7, Appli
43	42	63.6	119	4	US-09-252-991A-22545	Sequence 22545, A
44	90	60.6	1400	4	US-08-630-915A-37	Sequence 37, Appl
45	39	59.1	72	1	US-08-439-818A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 639332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Attv)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17

Query Match 100.0%; Score 66; DB 4; Length 82;

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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
Db 54 CAGGTPNKTAC 64

RESULT 2
US-09-144-776B-19
; Sequence 19, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; COMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; FAX: (301) 619-7714
; SEQ ID NO: 19;
; US-09-144-776B-19
; CHARACTERISTICS:
; Query Match
; Best Local Similarity
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
Db 54 CAGGTPNKTAC 64

RESULT 3
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-24
; Query Match
; Best Local Similarity 100.0%; Score 66; DB 4; Length 82;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
Db 93 CAGGTPNKTAC 103

RESULT 4
US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-314-235-24
; Query Match
; Best Local Similarity 100.0%; Score 66; DB 4; Length 226;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
Db 93 CAGGTPNKTAC 103

RESULT 5
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER US/08/896,933
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; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match      100.0%; Score 66; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTENKTAC 11
Db      95 CAGGTENKTAC 105

RESULT 6
US-09-314-235-23
; Sequence 23, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-23

Query Match      100.0%; Score 66; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTENKTAC 11
Db      95 CAGGTENKTAC 105

RESULT 7
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver

; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-4

Query Match      100.0%; Score 66; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTENKTAC 11
Db      96 CAGGTENKTAC 106

RESULT 8
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match      100.0%; Score 66; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAGGTNKTAC 11
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Db      96 CAGGTNKTAC 106

RESULT 9
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MCMC -504 Scott Street
; MCMC-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match      100.0%; Score 66; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAGGTNKTAC 11
      |||||
Db      96 CAGGTNKTAC 106

RESULT 10
US-08-695-692B-7
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; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match      100.0%; Score 66; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAGGTNKTAC 11
      |||||
Db      96 CAGGTNKTAC 106

RESULT 11
US-08-695-692B-8
; Sequence 8, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-695-692B-8

Query Match 100.0%; Score 66; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGPNKTAC 11
Db 96 CAGGTGPNKTAC 106

RESULT 12
US-08-486-099-112
; Sequence 112, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match 100.0%; Score 66; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGPNKTAC 11
Db 120 CAGGTGPNKTAC 130

RESULT 13
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match 100.0%; Score 66; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGPNKTAC 11
Db 120 CAGGTGPNKTAC 130
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Db      120 CAGGTENKTAC 130

RESULT 14
US-08-360-107A-122
; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-122

Query Match      100.0%; Score 66; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTENKTAC 11
      |||||
Db      120 CAGGTENKTAC 130

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Job time : 9.43114 secs

us-09-555-115a-9.ra1
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-123

Query Match      100.0%; Score 66; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGGTENKTAC 11
      |||||
Db      120 CAGGTENKTAC 130

Search completed: October 15, 2003, 17:08:29
Job time : 9.43114 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 16.6647 Seconds
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Title: US-09-555-115A-9
Perfect score: 66
Sequence: 1 CAGGTNKTAC 11

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Searched: 600653 seqs, 161128416 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	82	15	US-10-002-784A-32
2	66	100.0	82	15	US-10-002-784A-34
3	66	100.0	233	8	US-08-882-431-4
4	66	100.0	233	11	US-09-900-766-2
5	66	100.0	233	11	US-09-900-766-3
6	66	100.0	233	11	US-09-900-766-4
7	66	100.0	233	11	US-09-900-766-7
8	66	100.0	233	15	US-10-002-784A-4
9	66	100.0	233	15	US-10-283-838-7
10	66	100.0	233	15	US-10-283-838-8
11	66	100.0	248	10	US-09-870-759-16
12	66	100.0	248	12	US-09-751-708A-16
13	66	100.0	257	10	US-09-870-759-8
14	66	100.0	257	12	US-09-751-708A-8
15	66	100.0	257	15	US-10-002-784A-2

16	66	100.0	672	11	US-09-900-766-1	Sequence 1, Appli
17	55	83.3	257	8	US-08-882-431-2	Sequence 2, Appli
18	46	69.7	4440	12	US-10-199-672-525	Sequence 525, App
19	46	69.7	4440	12	US-10-187-749-525	Sequence 525, App
20	46	69.7	4440	12	US-10-194-457-525	Sequence 525, App
21	46	69.7	4440	12	US-10-184-642-525	Sequence 525, App
22	46	69.7	4440	12	US-10-196-747-525	Sequence 525, App
23	46	69.7	4440	12	US-10-173-689-525	Sequence 525, App
24	46	69.7	4440	12	US-10-173-690-525	Sequence 525, App
25	46	69.7	4440	12	US-10-173-691-525	Sequence 525, App
26	46	69.7	4440	12	US-10-173-692-525	Sequence 525, App
27	46	69.7	4440	12	US-10-173-694-525	Sequence 525, App
28	46	69.7	4440	12	US-10-173-695-525	Sequence 525, App
29	46	69.7	4440	12	US-10-173-699-525	Sequence 525, App
30	46	69.7	4440	12	US-10-173-707-525	Sequence 525, App
31	46	69.7	4440	12	US-10-174-569-525	Sequence 525, App
32	46	69.7	4440	12	US-10-174-583-525	Sequence 525, App
33	46	69.7	4440	12	US-10-174-587-525	Sequence 525, App
34	46	69.7	4440	12	US-10-174-589-525	Sequence 525, App
35	46	69.7	4440	12	US-10-174-591-525	Sequence 525, App
36	46	69.7	4440	12	US-10-175-736-525	Sequence 525, App
37	46	69.7	4440	12	US-10-175-742-525	Sequence 525, App
38	46	69.7	4440	12	US-10-175-744-525	Sequence 525, App
39	46	69.7	4440	12	US-10-175-745-525	Sequence 525, App
40	46	69.7	4440	12	US-10-175-748-525	Sequence 525, App
41	46	69.7	4440	12	US-10-175-751-525	Sequence 525, App
42	46	69.7	4440	12	US-10-175-754-525	Sequence 525, App
43	46	69.7	4440	12	US-10-176-480-525	Sequence 525, App
44	46	69.7	4440	12	US-10-176-489-525	Sequence 525, App
45	46	69.7	4440	12	US-10-176-754-525	Sequence 525, App

ALIGNMENTS

RESULT 1
US-10-002-784A-32
; Sequence 32, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin A
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match 100.0%; Score 66; DB 15; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTNKTAC 11
|||||
Db 54 CAGGTNKTAC 64

RESULT 2
US-10-002-784A-34
; Sequence 34, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33

; APPLICANT: Ulrich, Robert G.
 ; TITLE OF INVENTION: Bacterial Superantigen Vaccines
 ; FILE REFERENCE: 003/233/SAP
 ; CURRENT APPLICATION NUMBER: US/10/002,784A
 ; CURRENT FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
 ; PRIOR FILING DATE: 97-06-25; 98-09-01
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Apple Macintosh Microsoft Word 6.0
 ; SEQ ID NO 34
 ; LENGTH: 82
 ; TYPE: PRT
 ; ORGANISM: staphylococcal enterotoxin E
 ; FEATURE:
 ; OTHER INFORMATION: partial sequence as shown in Figure 3
 US-10-002-784A-34

Query Match 100.0%; Score 66; DB 15; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.00074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
 Db 54 CAGGTPNKTAC 64
 |||||

RESULT 3
 US-08-882-431-4
 ; Sequence 4, Application US/08882431
 ; Publication No. US2003009015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; APPLICANT: Mark A. Olson
 ; APPLICANT: Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; TITLE OF INVENTION: Vaccines
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John Moran
 ; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/882,431
 ; FILING DATE: June 25, 1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Moran, John
 ; REGISTRATION NUMBER: 26,313
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 US-08-882-431-4

Query Match 100.0%; Score 66; DB 8; Length 233;

Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
 Db 96 CAGGTPNKTAC 106
 |||||

RESULT 4
 US-09-900-766-2
 ; Sequence 2, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN
 ; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P02188US0;10104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: (1)..(233)
 ; OTHER INFORMATION: Chimeric Protein
 US-09-900-766-2

Query Match 100.0%; Score 66; DB 11; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
 Db 96 CAGGTPNKTAC 106
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RESULT 5
 US-09-900-766-3
 ; Sequence 3, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN
 ; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P02188US0;10104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: (1)..(233)
 ; OTHER INFORMATION: Chimeric Protein
 US-09-900-766-3

Query Match 100.0%; Score 66; DB 11; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
 |||||

Db 96 CAGGTPNKTAC 106

RESULT 6

US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BUORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 100.0%; Score 66; DB 11; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTPNKTAC 11

Db 96 CAGGTPNKTAC 106

RESULT 7

US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BUORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 100.0%; Score 66; DB 11; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTPNKTAC 11

Db 96 CAGGTPNKTAC 106

RESULT 8

US-10-002-784A-4
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: ULRICH, ROBERT G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
/33

; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match 100.0%; Score 66; DB 15; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTPNKTAC 11

Db 96 CAGGTPNKTAC 106

RESULT 9

US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-283-838-7

Query Match 100.0%; Score 66; DB 15; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 96 CAGGTPNKTAC 106

RESULT 10

US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US2003092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match 100.0%; Score 66; DB 15; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGTPNKTAC 11
|||||
Db 96 CAGGTPNKTAC 106

RESULT 11

US-09-870-759-16
; Sequence 16, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PR8
; ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match 100.0%; Score 66; DB 10; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 120 CAGGTPNKTAC 130

RESULT 12

US-09-751-708A-16
; Sequence 16, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 100.0%; Score 66; DB 12; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 120 CAGGTPNKTAC 130

RESULT 13

US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 100.0%; Score 66; DB 10; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11

Db 120 CAGGTENKTAC 130

RESULT 14
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match 100.0%; Score 66; DB 12; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTENKTAC 11
Db 120 CAGGTENKTAC 130

RESULT 15
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match 100.0%; Score 66; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTENKTAC 11
Db 120 CAGGTENKTAC 130

Search completed: October 15, 2003, 17:46:58
Job time : 17.6647 secs

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RESULT 2

A281179 enterotoxin E precursor - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C/Accession: A28179
J.R. Couch, J.L. Soltis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A/Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin A
A/Reference number: A28179; MUID:86257005; PMID:3384800
A/Accession: A28179
A/Molecule type: DNA
A/Residues: 1-257 <COU>
A/Cross-references: GB:M21319; NID:G153001; PID:AAA26617.1; PID:G153002
C/Superfamily: enterotoxin B

Query Match 100.0%; Score 66; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 120 CAGGTPNKTAC 130

RESULT 3
C89984
enterotoxin P [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89984
R;Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701743; PIDN:BA43036.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
C;Superfamily: enterotoxin B

Query Match 80.3%; Score 53; DB 2; Length 260;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 123 CTGGTPFKTAC 133

RESULT 4
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89942
R;Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701400; PIDN:BA42694.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1430

Query Match 63.6%; Score 42; DB 2; Length 157;
Best Local Similarity 63.6%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 135 CHGATNKTQC 145

RESULT 5
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16840
R;Geisel, C.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T10E10.
A;Reference number: Z18588
A;Accession: T16840
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1101 <GEI>
A;Cross-references: EMBL:U39644; NID:gl049339; PID:gl049343; PIDN:AAA80360.1; CESP:T10E10
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 60.6%; Score 40; DB 2; Length 1101;
Best Local Similarity 54.5%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 513 CPDGTPTTSC 523

RESULT 6 0 4
F75357
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75357
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75357
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <WHI>
A;Cross-references: GB:AE0002017; GB:AE000513; NID:G6459527; PIDN:AAF11318.1; PID:G6459536
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRI757
A;Map position: 1

Query Match 59.1%; Score 39; DB 2; Length 328;
Best Local Similarity 54.5%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||||
Db 285 CGGNTPKVSC 295

RESULT 7
A30527
major surface antigen precursor - Toxoplasma gondii
N;Alternate names: p30 protein precursor
C;Species: Toxoplasma gondii
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1998
C;Accession: A30527
R;Burg, J.L.; Perelman, D.; Kasper, L.H.; Ware, P.L.; Boothroyd, J.C. J. Immunol. 141, 3584-3591, 1988
A;Title: Molecular analysis of the gene encoding the major surface antigen of Toxoplasma gondii.
A;Reference number: A30527; MUID:89035485; PMID:3183382
A;Accession: A30527
A;Molecule type: mRNA
A;Residues: 1-336 <BUR>
A;Cross-references: GB:X14080; GB:M23658; NID:gl0722; PID:gl0723
A;Note: it is uncertain whether Met-1 or Met-18 is the initiator

C:Keywords: glycoprotein; surface antigen
F:1-47/Domain: signal sequence #status predicted <SIG>
F:48-336/Product: major surface antigen #status predicted <MAT>
F:258/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.1%; Score 39; DB 2; Length 336;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||:|
Db 285 CTGGSPEKHC 295

RESULT 8

A46478
major surface antigen p30 - Toxoplasma gondii
N:Alternate names: membrane antigen p30
C:Species: Toxoplasma gondii
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C:Accession: A46478; A46457
R:Kasper, L.H.; Khan, I.A.; Ely, K.H.; Buelow, R.; Boothroyd, J.C.
J. Immunol. 148, 1493-1498, 1992
A:Title: Antigen-specific (p30) mouse CD8+ T cells are cytotoxic against Toxoplasma gondii
A:Reference number: A46478; MUID:92166389; PMID:1538132
A:Accession: A46478
A:Molecule type: DNA
A:Residues: 1-336 <RAS>
A:Cross-references: GB:S85174; NID:g246016; PID:g246017
A:Experimental source: strain P
A:Note: sequence extracted from NCBI backbone (NCBIN:85174, NCBIP:85176)
R:Bulow, R.; Boothroyd, J.C.
J. Immunol. 147, 3496-3500, 1991
A:Title: Protection of mice from fatal Toxoplasma gondii infection by immunization with
A:Reference number: A46457; MUID:92043720; PMID:1940349
A:Accession: A46457
A:Molecule type: DNA
A:Residues: 1-336 <BL>
A:Cross-references: GB:S63900; NID:g238694; PID:g238695
A:Experimental source: strain C
A:Note: sequence extracted from NCBI backbone (NCBIN:63900, NCBIP:63901)
C:Keywords: surface antigen

Query Match 59.1%; Score 39; DB 2; Length 336;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||:|
Db 285 CTGGSPEKHC 295

RESULT 9

I38488
trophinin - human
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C:Accession: I38488
R:Fukuda, M.N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami, M.; Aoki, D.; Nozawa, S.
Genes Dev. 9, 1199-1210, 1995
A:Title: Trophinin and tasin, a novel cell adhesion molecule complex with potential inv
A:Reference number: I38487; MUID:95278733; PMID:7758945
A:Accession: I38488
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-749 <RES>
A:Cross-references: EMBL:U04811; NID:g905357; PIDN:AAA79334.1; PID:g836820
C:Superfamily: elastin

Query Match 59.1%; Score 39; DB 2; Length 749;
Best Local Similarity 54.5%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||:|
Db 486 CRGGPSTGAC 496

RESULT 10

S44754
C1489.8 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Sep-1997
C:Accession: S44754
R:Favell, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C14B9.
A:Reference number: S44617
A:Accession: S44754
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1257 <FAV>
A:Cross-references: EMBL:L15188; NID:g289640; PID:g289641
C:Genetics:
A:Introns: 102/1; 143/2; 241/3; 315/3; 368/3; 460/2; 549/2; 641/3; 676/2; 727/1; 873/2;

Query Match 59.1%; Score 39; DB 2; Length 1257;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGGTPNKTAC 11
|||:|
Db 1213 CASSNPNTTC 1223

RESULT 11

A87619
hypothetical protein CC2987 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A87619
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87619
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <STO>
A:Cross-references: GB:AE005673; NID:gl3424621; PIDN:AAK24949.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2987

Query Match 57.6%; Score 38; DB 2; Length 255;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTPNKTAC 11
|||:|
Db 232 GDNRTAC 239

RESULT 12

H70247
hypothetical protein BBJ23 - Lyme disease spirochete plasmid J/1p38
C:Species: Borrelia burgdorferi (lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: H70247
R:Fraser, C.M.; Castjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70247
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-274 <KLE>
A;Cross-references: GB:AE000787; NID:g2690175; PIDN:AAC66119.1; PID:g2690211; TIGR:BBJ23
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match 57.6%; Score 38; DB 2; Length 274;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGGTPNKT 9
| | | | |
DB 193 AGGDPNKT 200

RESULT 13

T42565

capsid protein 22 - equine herpesvirus 4 (strain NS80567)

C;Species: equine herpesvirus 4

A;Variety: strain NS80567

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C;Accession: T42565

R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998

A;Title: The DNA sequence of equine herpesvirus-4.

A;Reference number: 222173; MUID:98264497; PMID:9603335

A;Accession: T42565

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-462 <TEL>

A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59537.1; PID:g2605965

A;Experimental source: strain NS80567

C;Genetics:

A;Gene: 22

C;Superfamily: varicella-zoster virus gene 20 protein

Query Match 57.6%; Score 38; DB 2; Length 462;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTPNKTAC 11
| | | | |
DB 405 GRPNKTSC 412

RESULT 14

A53219

singed protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 13-Sep-1998

C;Accession: A53219

R;Paterson, J.; O'Hare, K.
Genetics 129, 1073-1084, 1991

A;Title: Structure and transcription of the singed locus of Drosophila melanogaster.

A;Reference number: A53219; MUID:92146932; PMID:1723709

A;Accession: A53219

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-512 <PAT>

A;Cross-references: GB:X17548

A;Note: authors translated the codon CAC for residue 283 as Leu

C;Genetics:

A;Gene: FlyBase:sn

A;Cross-references: FlyBase:FBgn0003447

C;Superfamily: actin bundling protein

Query Match 57.6%; Score 38; DB 2; Length 512;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 4.47904 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-9
Perfect score: 66
Sequence: 1 CAGGTPNKTAC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	66	100.0	257	1	ETXA STAAW
2	66	100.0	257	1	ETXE STAAU
3	45	68.2	248	1	KLKC HUMAN
4	39	59.1	336	1	P30 TOXGO
5	39	59.1	1188	1	KPBA CAEEL
6	39	59.1	1387	1	TROP HUMAN
7	38	57.6	512	1	SING DROME
8	38	57.6	1337	1	PTPO HUMAN
9	37	56.1	239	1	CLDE HUMAN
10	37	56.1	239	1	CLDE MOUSE
11	37	56.1	456	1	GUNA MICBI
12	37	56.1	515	1	APX1 CAEEL
13	37	56.1	518	1	BAR2 SCHCO
14	37	56.1	708	1	TRFL CAMDR
15	36	54.5	29	1	CYOC VIOOD
16	36	54.5	29	1	KABS OLDAP
17	36	54.5	29	1	VARA VIOAR
18	36	54.5	29	1	VARC VIOAR
19	36	54.5	107	1	RLA2 TRYCR
20	36	54.5	109	1	YKGJ ECOLI
21	36	54.5	124	1	KAB1 OLDAP
22	36	54.5	258	1	ETXD STAAU
23	36	54.5	261	1	YH86 SYN3
24	35	53.0	263	1	YQDI CAEEL
25	35	53.0	264	1	MOBB BPT4
26	35	53.0	465	1	VP19 HSVEB
27	35	53.0	480	1	KLFA HUMAN
28	35	53.0	603	1	V162 FOWPV
29	35	53.0	630	1	TNPB STAAU
30	35	53.0	630	1	TNPE STAAU
31	35	53.0	719	1	RM62 DROME
32	35	53.0	754	1	LOL3 MOUSE
33	35	53.0	766	1	Y713 METJA

RESULT 1
ETXA STAAW STANDARD; PRT; 257 AA.
AC PI3163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN ENTA OR MW1889.
OS Staphylococcus aureus (strain MW2), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-acquired MRSA.";
RT Lancet 359:1819-1827(2002).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=ERI337;
RC MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T., Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin type A.";
RL EMBO J. 14:3292-3301(1995).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RP MEDLINE=97113025; PubMed=8943278;
RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M., Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;

P21804 gallus gall
P32540 mengo encep
P58447 viola arven
P58452 viola arven
P58453 viola arven
O42152 ambystoma m
O9u620 callinectes
P18077 homo sapien
O90Y3 ictalurus p
O55142 mus musculu
P04646 rattus norv
P58455 oldenlandia

ALIGNMENTS


```
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin: 1.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal;
KW Alternative splicing.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 248 KALLIKREIN 12.
FT ACT_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 28 161 BY SIMILARITY.
FT DISULFID 47 63 BY SIMILARITY.
FT DISULFID 133 235 BY SIMILARITY.
FT DISULFID 140 206 BY SIMILARITY.
FT DISULFID 172 186 BY SIMILARITY.
FT DISULFID 196 222 BY SIMILARITY.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 236 248 KYDWMIRMIMRNN -> NSTLVGLGTSWNFNSQPF (in isoform 2).
FT FTID=VSP 005403.
FT SEQUENCE 248 AA; 26733 MW; BB473E98F8BAF703 CRC64;

Query Match 68.2%; Score 45; DB 1; Length 248;
Best Local Similarity 63.6%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTPTNKTAC 11
DB 186 CAGGVGQDQAC 196
|||||:|:|:|

RESULT 4
P30_TOXGO
ID P30_TOXGO STANDARD; PRT; 336 AA.
AC P13564;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Major surface antigen p30 precursor.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89035485; PubMed=3183382;
RA Burg J.L., Perelman D., Kasper L.H., Ware P.L., Boothroyd J.C.;
RT "Molecular analysis of the gene encoding the major surface antigen of Toxoplasma gondii.";
RL J. Immunol. 141:3584-3591(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95161920; PubMed=7858408;
RA Moleon I., Beuchamp P., Cesbron M.F., Tourvieille B.;
RT "Cloning of the gene encoding the p30 antigen of Toxoplasma gondii by PCR to insert it in transgenic mice.";
RL Arch. Med. Res. 25:463-466(1994).
CC -1- SUBCELLULAR LOCATION: SURFACE OF EXTRA- AND INTRACELLULAR TACHYZOITES AND ALSO COMPONENT OF THE VESICULAR NETWORK WITHIN THE PARASITOPHOUS VACUOLE.
CC -1- DEVELOPMENTAL STAGE: DETECTED ONLY IN RAPIDLY DIVIDING AND INVASIVE TACHYZOITES.
CC -1- DISEASE: TOXOPLASMOSIS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-18 IS THE INITIATOR.
-----
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-----
CC EMBL: X14080; CAA32244.1; -
CC EMBL: X14080; CAA32245.1; ALT_INIT.
CC EMBL: S76248; AAB33440.1; -
CC PIR: A30527; A30527
CC PDB: 1KZQ; 31-JUL-02.
CC Pfam: PF04092; SAG; 1.
KW Antigen; Signal; 3D-structure.
FT SIGNAL 1 47 POTENTIAL.
FT CHAIN 48 336 MAJOR SURFACE ANTIGEN P30.
FT SEQUENCE 336 AA; 34829 MW; 96C7BCEB2EB97FFE CRC64;

Query Match 59.1%; Score 39; DB 1; Length 336;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPTNKTAC 11
DB 285 CTGSGPERGHC 295
|||||:|:|:|

RESULT 5
KPBA_CABEL
ID KPBA_CABEL STANDARD; PRT; 1188 AA.
AC P34335; 0
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase B kinase alpha subunit).
DE GN C14B9.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Showkneen R., Sime M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RN Nature 368:32-38(1994).
RP REVISIONS.
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PHOSPHORYLASE B KINASE CATALYZES THE PHOSPHORYLATION OF SERINE IN CERTAIN SUBSTRATES, INCLUDING TROPONIN I. THE ALPHA CHAIN MAY BIND CALMODULIN (BY SIMILARITY).
CC -1- PATHWAY: Glycogen metabolism.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHORYLASE B KINASE REGULATORY CHAINS FAMILY.
-----
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CC -----
 DR EMBL; L15188; AAA27954.2; --
 DR WormPep; C1489.8; CE26870.
 KW Hypothetical protein; Glycogen metabolism; Calmodulin-binding.
 SQ SEQUENCE 1188 AA; 135558 MW; DE9BB875F3603863 CRC64;

Query Match 59.1%; Score 39; DB 1; Length 1188;
 Best Local Similarity 54.5%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGGTPNKATC 11
 ||| |||
 DB 1144 CASSNPNTTC 1154

RESULT 6

ID TROP HUMAN STANDARD; PRT; 1387 AA.
 AC Q12816; Q9NU89; Q9UPN8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trophinin.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

1)
 RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC MEDLINE=99397452; PubMed=10470851;

RA Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,

Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XIV.

RT The complete sequences of 100 new cDNA clones from brain which code

for large proteins in vitro.";

RL DNA Res. 6:197-205(1995).

2)
 RN SEQUENCE FROM N.A.

RP Ambrose K.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

3)
 RN SEQUENCE OF 639-1387 FROM N.A.

RP MEDLINE=95278733; PubMed=7758945;

RA Fukuda M.N., Sato T., Nakayama J., Klier G., Mikami M., Aoki D.,

Nozawa S.;

RT "Trophinin and tactivin, a novel cell adhesion molecule complex with

potential involvement in embryo implantation.";

RL Genes Dev. 9:1199-1210(1995).

CC -1- FUNCTION: COULD BE INVOLVED WITH BYSTIN AND TASTIN IN A CELL

ADHESION MOLECULE COMPLEX THAT MEDIATES AN INITIAL ATTACHMENT OF

THE BLASTOCYST TO UTERINE EPITHELIAL CELLS AT THE TIME OF THE

EMBRYO IMPLANTATION. DIRECTLY RESPONSIBLE FOR HOMOPHILIC CELL

ADHESION.

CC -1- SUBUNIT: DIRECTLY BINDS BYSTIN, AND INDIRECTLY TASTIN.

CC -1- TISSUE SPECIFICITY: STRONG EXPRESSION AT IMPLANTATION SITES. FOUND

IN THE PLACENTA FROM THE SIXTH WEEK OF PREGNANCY. WAS LOCALIZED IN

THE CYTOPLASM OF THE SYNCYTOTROPHOBLAST IN THE CHORIONIC VILLI

AND IN ENDOMETRIAL DECIDUAL CELLS AT THE UTEROPLACENTAL INTERFACE.

CC AFTER WEEK 10, THE LEVEL DECREASED AND THEN DISAPPEARED FROM

PLACENTAL VILLI. ALSO FOUND IN MACROPHAGES.

CC -1- SIMILARITY: Contains 1 MAGE domain.

CC

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CC -----
 DR EMBL; AB029037; BAA83066.1; --
 DR EMBL; AL049732; CAB86651.1; --
 DR EMBL; U04811; AAA79334.1; --
 DR PIR; I38488; I38488
 DR Genew; HGNC:12326; TRO.
 DR MIM; 300132; --
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0007566; P:embryo implantation; TAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; TAS.
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS00838; MAGE; 1.
 DR KW Cell adhesion; Antigen; Repeat.
 FT DOMAIN 400 598
 FT DOMAIN 707 1381
 FT CONFLICT 653 653
 FT CONFLICT 692 692
 FT CONFLICT 694 694
 FT CONFLICT 724 724
 FT CONFLICT 768 768
 FT CONFLICT 780 780
 FT CONFLICT 982 982
 FT CONFLICT 1012 1012
 FT CONFLICT 1387 AA; 138804 MW; 412D1E5754B5A416 CRC64;
 SQ SEQUENCE 1387 AA; 138804 MW; 412D1E5754B5A416 CRC64;
 Query Match 59.1%; Score 39; DB 1; Length 1387;
 Best Local Similarity 54.5%; Pred. No. 62;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAGGTPNKATC 11
 ||| |||
 DB 1124 CFGGPPSTGAC 1134

RESULT 7
 SING DROME
 ID SING DROME STANDARD; PRT; 512 AA.
 AC Q24524; Q9W3L8;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Singed protein.
 GN SN OR CGI536.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=92146932; PubMed=1723709;
 RA Paterson J., O'Hare K.;

"Structure and transcription of the singed locus of Drosophila melanogaster.";
 RL Genetics 129:1073-1084(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: PROBABLY ACTS AS AN ACTIN BUNDLING PROTEIN. MAY HAVE A
CC ROLE IN THE ASYMMETRIC ORGANIZATION AND/OR MOVEMENT OF CYTOPLASMIC
CC COMPONENTS. IT HAS A ROLE IN SOMATIC CELLS DURING THE FORMATION OF
CC ADULT BRISTLES AND HAIRS, AND IN THE FEMALE GERMLINE DURING
CC OOGENESIS.
CC
CC -!- SIMILARITY: BELONGS TO THE FASCIN FAMILY.
CC
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CC
CC EMBL; X17549; CAA35585.1; -.
CC EMBL; X17550; CAA35585.1; JOINED.
CC EMBL; AE003442; AAP46307.1; -.
CC FlyBase; FBgn0003447; sn.
CC Actin-binding.
KW Actin-binding.
SQ SEQUENCE 512 AA; 57279 MW; A021886A9C7B6C48 CRC64;

Query Match 57.6%; Score 38; DB 1; Length 512;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTPTNKTAC 11
| | | | |
Db 126 GGTPTDKLVC 134

RESULT 8
PTPU HUMAN
AC Q12913; Q15255; PRT; 1337 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP eta) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).
GN PTPRJ OR DEP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=95024024; PubMed=7937872;
RA Oestman A., Yang Q., Tonks N.K.;
RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
RT is enhanced with increasing cell density.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95086212; PubMed=7994032;
RA Honda H., Inakawa J., Nishida J., Yazaki Y., Hirai H.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT a novel protein-tyrosine phosphatase, HPTP eta.";
RL Blood 84:4186-4194(1994).
CC -!- FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTACT INHIBITION OF
CC CELL GROWTH.
CC
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -!- PTM: N- AND O-GLYCOSYLATED.
CC
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd148.htm".
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U10886; AAB36687.1; -.
CC EMBL; D37781; BAA07035.1; -.
CC FIR; I38670; I38670.
CC HSP; P18052; LYFO.
CC Genew; HGNC:9673; PTPRJ.
CC MIM; 600925; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . . ; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; TAS.
CC InterPro; IPR0003961; FN III.
CC InterPro; IPR000387; TYR phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 6.
CC PRINTS; PR00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00060; FN3; 8.
CC SMART; SM00194; PTPc; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase.
KW SIGNAL
FT SIGNAL 1 35
FT CHAIN 36 1337 PROTEIN-TYROSINE PHOSPHATASE ETA.
FT DOMAIN 36 975 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 976 996 POTENTIAL.
FT DOMAIN 997 1337 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 199 FIBRONECTIN TYPE-III 1.
FT DOMAIN 366 446 FIBRONECTIN TYPE-III 2.
FT DOMAIN 454 532 FIBRONECTIN TYPE-III 3.
FT DOMAIN 548 615 FIBRONECTIN TYPE-III 4.
FT DOMAIN 626 710 FIBRONECTIN TYPE-III 5.
FT DOMAIN 1065 1337 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1239 1239 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 525 525 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 784 784 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 790 790 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 824 824 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 910 910 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CONFLICT 261 261 D -> G (IN REF. 2)
FT CONFLICT 918 929 YNKLPLGSGYR -> LQHEAGTSGLLP (IN REF. 2).
SQ SEQUENCE 1337 AA; 145985 MW; E686DE6D1F64236E CRC64;

Query Match 57.6%; Score 38; DB 1; Length 1337;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGN 7
Db 35 CAGGTGS 41

RESULT 9
CLDE_HUMAN STANDARD; PRT; 239 AA.
ID CLDE_HUMAN
AC O95500;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Claudin-14.
GN CLDN14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT DFNB29 ASP-85.
RC TISSUE=Liver;
RX MEDLINE=21097730; PubMed=11163249;
RA Wilcox E.R., Burton O.L., Naz S., Riazuddin S., Smith T.N.,
RA Ploplis B., Belyantseva I., Ben-Yosef T., Liburd N.A., Morell R.J.,
RA Kachar B., Wu D.K., Griffith A.J., Riazuddin S., Friedman T.B.;
RT "Mutations in the gene encoding tight junction claudin-14 cause
RL autosomal recessive deafness DFNB29."
RN Cell 104:165-172(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,

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RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388557; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: LIVER, KIDNEY. ALSO FOUND IN EAR.
CC -!- DISEASE: Defects in CLDN14 are the cause of an autosomal recessive
form of nonsyndromic sensorineural deafness (DFNB29) [MIM:605608].
CC -!- SIMILARITY: Belongs to the claudin family.

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EMBL: AJ132445; CAA10669.1; -
DR EMBL: AF3114090; AAG60052.1; -
DR EMBL: AF001726; BAA95509.1; -
DR EMBL: BC012126; AAH12126.1; -
DR Genew; HGNC:2035; CLDN14.
DR MIM; 605608; -
DR GO; GO:006461; P:protein complex assembly; TAS.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin sup.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane; Disease mutation; Deafness.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT VARIANT 85 85 V -> D (in DFNB29).
FT /FTID=VAR_010738.
SQ SEQUENCE 239 AA; 25699 MW; DD41652F7FD0E09A CRC64;

Query Match 56.1%; Score 37; DB 1; Length 239;

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Best Local Similarity 77.8%; Pred. No. 25;		Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 CAGGTPNKT 9		
Db	107 CAGGTPAKT 115		
RESULT 10			
CLDB_MOUSE	STANDARD;	PRT;	239 AA.
AC	Q92053; Q9D284;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Claudin-14.		
GN	CLDN14.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RA	Morita K., Furuse M., Tsukita S.;		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.		
RC	TISSUE=Brain;		
RX	MEDLINE=21097730; PubMed=1163249;		
RA	Wilcox E.R., Burton Q.L., Naz S., Riazuddin S., Smith T.N.,		
RA	Ploplis B., Belyantseva I., Ben-Yosef T., Liburd N.A., Morell R.J.,		
RA	Kachar B., Wu D.K., Griffith A.J., Riazuddin S., Friedman T.B.;		
RT	"Mutations in the gene encoding tight junction claudin-14 cause		
RT	autosomal recessive deafness DFNB29.";		
RL	Cell 104:165-172 (2001).		
RN	[3]		
RP	REVISIONS TO 115; 129; 166 AND 187.		
RA	Wilcox E.R., Burton Q.L., Naz S., Riazuddin S., Smith T.N.,		
RA	Ploplis B., Belyantseva I., Ben-Yosef T., Liburd N.A., Morell R.J.,		
RA	Kachar B., Wu D.K., Griffith A.J., Riazuddin S., Friedman T.B.;		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Colon;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690 (2001).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: AT POSTNATAL DAY 4, EXPRESSION IS APICALLY		
CC	LOCATED IN THE INNER AND OUTER HAIR CELL REGION OF THE ENTIRE		
CC	ORGAN OF CORTI. BY POSTNATAL DAY 8, EXPRESSION IS HIGHEST IN THE		
CC	SUPPORTING CELLS OF THE ORGAN OF CORTI AND PRESENT IN ALL OTHER		
CC	SENSORY EPITHELIA OF THE INNER EAR VESTIBULAR ORGANS. ALSO		
EXPRESSED IN LIVER AND KIDNEY.			
-1- SIMILARITY: Belongs to the claudin family.			
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entities requires a license agreement (see http://www.isb-sib.ch/announce/			
or send an email to license@isb-sib.ch).			
CC	EMBL; AF124429; AAD17323.1; -		
DR	EMBL; AF1314089; AAG60051.2; -		
DR	EMBL; AK020255; BAB32041.1; -		
DR	MGD; MGI:1860425; Cldn14.		
DR	InterPro; IPR006187; Claudin.		
DR	InterPro; IPR006188; Claudin sup.		
DR	InterPro; IPR004031; PMP22 Claudin.		
DR	Pfam; PF00822; PMP22 Claudin; 1.		
DR	PRINTS; PR01077; CLAUDIN.		
DR	PROSITE; PS01346; CLAUDIN; 1.		
KW	Tight junction; Transmembrane.		
FT	TRANSMEM 8 28		
FT	POTENTIAL.		
FT	TRANSMEM 82 102		
FT	POTENTIAL.		
FT	TRANSMEM 116 136		
FT	POTENTIAL.		
FT	TRANSMEM 163 183		
FT	POTENTIAL.		
FT	CONFLICT 115 115		
FT	T -> N (IN REF. 1).		
FT	CONFLICT 119 119		
FT	V -> M (IN REF. 4).		
FT	CONFLICT 129 129		
FT	G -> A (IN REF. 1).		
FT	CONFLICT 166 166		
FT	L -> M (IN REF. 1).		
FT	CONFLICT 187 187		
FT	D -> E (IN REF. 1).		
SQ	SEQUENCE 239 AA; 25614 MW; 24DE6AEADA56BB61 CRC64;		
Query Match 56.1%; Score 37; DB 1; Length 239;			
Best Local Similarity 77.8%; Pred. No. 25;			
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1 CAGGTPNKT 9		
Db	107 CAGGTPAKT 115		
RESULT 11			
ID	GUNA MICBI	STANDARD;	PRT; 456 AA.
AC	P26414;		
DT	01-AUG-1992 (Rel. 23, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Endoglucanase A precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)		
DE	(Cellulase).		
GN	CELA.		
OS	Microbispora bispora.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Pseudonocardineae; Pseudonocardaceae; Thermobispora.		
OX	NCBI_TaxID=2006;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Yablonsky M.D., Elliston K.O., Eveleigh D.E.;		
RL	(in) Coughlan M.P. (eds.);		
RL	Production, characterization and application of cellulose,		
RL	hemicellulose and lignin enzyme degrading systems, pp.77-83, Elsevier,		
RL	London (1989).		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic		
CC	linkages in cellulose, lichenin and cereal beta-D-glucans.		
CC	-1- SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)		
CC	domain.		
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY B (FAMILY 6 OF GLYCOSYL		
CC	HYDROLASES).		
CC	HSP; P26222; LTML.		
DR	InterPro; IPR001919; Bac_celose-bind.		
DR	InterPro; IPR001524; Glyco_hydro_6.		
DR	Pfam; PR00553; CBM_2; 1.		

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DR Pfam; PF01341; Glyco_hydro_6; 1.
DR PRINTS; PR00733; GLYDRLASE6.
DR ProDom; PD003733; Glyco_hydro_6; 1.
DR SMART; SM00637; CBD_I1; 1.
DR PROSITE; PS00561; CBD_BACTERIAL; 1.
DR PROSITE; PS00655; GLYCOSYL_HYDROL_F6_1; 1.
DR PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 456 ENDOGLUCANASE A.
FT DOMAIN 31 322 CATALYTIC.
FT DOMAIN 323 355 LINKER ("HINGE") (PRO-SER BOX).
FT DOMAIN 356 456 CELLULOSE-BINDING.
FT ACT_SITE 113 113 BY SIMILARITY.
FT ACT_SITE 151 151 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 300 300 NUCLEOPHILE (BY SIMILARITY).
FT DISULFID 114 159 BY SIMILARITY.
FT DISULFID 267 302 BY SIMILARITY.
FT DISULFID 360 453 BY SIMILARITY.
SQ SEQUENCE 456 AA; 47011 MW; B06D8595E322848F CRC64;

Query Match 56.1%; Score 37; DB 1; Length 456;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AGTTPNKTA 10
Db 119 AGGAPNHTA 127

RESULT 12
APX1 CAEEL
ID APX1 CAEEL STANDARD; PRT; 515 AA.
AC P41950; Q9TXN4;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anterior pharynx in excess protein 1 precursor.
GN APX-1 OR K08D9.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A., AND FUNCTION.
RX STRAIN=Bristol N2;
RX MEDLINE=94208066; PubMed=8156602;
RA Mello C.C., Draper B.W., Priess J.R.;
RT "The maternal genes apx-1 and gip-1 and establishment of
dorsal-ventral polarity in the early C. elegans embryo.";
RL Cell 77:95-106(1994).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Clarke K., Wohldmann P., Drone K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RC REVISIONS.
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the specification of the blastomere cell
CC ABP fate. Contributes to the establishment of the dorsal-ventral
CC axis in the early embryo.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 5 EGF-like domains.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
-----
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DR EMBL; U07628; AAA17738.1; -.
DR EMBL; AF101319; AAC69353.4; -.
DR HSSP; P00740; 1EDM.
DR WormPep; K08D9.3; CE30819.
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0030154; P: cell differentiation; NAS.
DR GO; GO:0008595; P: determination of anterior/posterior axis, e. . .; NAS.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01414; DSL; 1.
DR PRINTS; PR00008; EGF; 4.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 4.
DR PROSITE; PS00022; EGF_1; 4.
DR PROSITE; PS01186; EGF_2; 3.
KW Differentiation; Repeat; Transmembrane; EGF-like domain;
KW Glycoprotein; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 515 ANTERIOR PHARYNX IN EXCESS PROTEIN 1.
FT DOMAIN 27 392 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 393 413 POTENTIAL.
FT DOMAIN 414 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 108 172 DSL.
FT DOMAIN 173 205 EGF-LIKE 1.
FT DOMAIN 203 238 EGF-LIKE 2.
FT DOMAIN 240 280 EGF-LIKE 3.
FT DOMAIN 284 322 EGF-LIKE 4.
FT DOMAIN 325 349 EGF-LIKE 5 (INCOMPLETE).
FT DISULFID 177 187 BY SIMILARITY.
FT DISULFID 181 193 BY SIMILARITY.
FT DISULFID 195 204 BY SIMILARITY.
FT DISULFID 207 218 BY SIMILARITY.
FT DISULFID 213 226 BY SIMILARITY.
FT DISULFID 228 237 BY SIMILARITY.
FT DISULFID 244 256 BY SIMILARITY.
FT DISULFID 250 268 BY SIMILARITY.
FT DISULFID 270 279 BY SIMILARITY.
FT DISULFID 288 300 BY SIMILARITY.
FT DISULFID 294 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 515 AA; 55818 MW; F41192A5268C24D9 CRC64;

Query Match 56.1%; Score 37; DB 1; Length 515;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CAGTTPNKTKAC 11
Db 177 CAGGCSNRGRC 187

RESULT 13
BAR2 SCHCO
ID BAR2 SCHCO STANDARD; PRT; 518 AA.
AC Q05659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Pheromone B alpha 2 receptor (Fragment).
GN BAR2.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;

```

RN SEQUENCE FROM N.A.
 RP STRAIN=12-43;
 RX MEDLINE=96080162; PubMed=7489176;
 RA Wendland J., Vaillancourt L.J., Hegner J., Lengeler K.B.,
 RA Laddison K.J., Specht C.A., Raper C.A., Kothe E.;
 RT "The mating-type locus B alpha 1 of Schizosaccharomyces pombe contains a
 RT pheromone receptor gene and putative pheromone genes.";
 RL EMBO J. 14:5271-5278(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE BAP2 PHEROMONE, A PRENYLATED MATING
 CC FACTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 4 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; X91168; CAA62595.1; -;
 DR PIR; S61920; S61920.
 DR InterPro; IPR001499; STE3_GPCR.
 DR Pfam; PF02076; STE3; 1.
 DR PRINTS; PR00899; GPCRSTE3.
 KW Transmembrane; G-protein coupled receptor; Pheromone response.
 FT TRANSMEM 8 28
 FT TRANSMEM 36 56
 FT TRANSMEM 70 90
 FT TRANSMEM 110 130
 FT NON TER 518 518
 SQ SEQUENCE 518 AA; 57999 MW; AA635E46A1BF7C44 CRC64;
 Query Match 56.1%; Score 37; DB 1; Length 518;
 Best Local Similarity 54.5%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CAGGTGPNKTAC 11
 DB 288 CAGGAPOLRRRC 298
 RESULT 14
 TRFL CAMDR
 ID _TRFL CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Puhani Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SUBUNIT: Monomer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ131674; CAB53387.1; -;
 DR EMBL; AF165879; AAF82241.1; -;
 DR PDB; 1DTZ; 20-JUN-01.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TF_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal; 3D-structure.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.
 FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0869D430 CRC64;
 Query Match 56.1%; Score 37; DB 1; Length 708;
 Best Local Similarity 63.6%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CAGGTGPNKTAC 11
 DB 192 CAGTGENKAC 202

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RESULT 15
CYOC_VIOOD
ID CYOC_VIOOD STANDARD; PRT; 29 AA.
AC P58474; P58450;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cycloviolacin O12 (Varv peptide E).
OS Viola odorata (Sweet violet), and
OS Viola arvensis (European field pansy) (Field violet). Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Violaceae; Viola.
OX NCBI_TaxID=97441, 97415;
RN [1]
RP SEQUENCE.
RC SPECIES=V.odorata;
RX MEDLINE=20069951; PubMed=10600388;
RA Craik D.J.; Daly N.L.; Bond T.; Wayne C.;
RT "Plant cyclotides: a unique family of cyclic and knotted proteins that
RT defines the cyclic cysteine knot structural motif.";
RL J. Mol. Biol. 294:1327-1336(1999).
RN [2]
RP SEQUENCE.
RC SPECIES=V.arvensis;
RX MEDLINE=99177275; PubMed=10075760;
RA Goeransson U., Luijendijk T., Johansson S., Bohlin L., Claesson P.;
RT "Seven novel macrocyclic polypeptides from Viola arvensis.";
RL J. Nat. Prod. 62:283-286(1999).
CC -!- FUNCTION: Probably participates in a plant defense mechanism.
CC -!- PTM: This is a cyclic peptide.
CC -!- CAUTION: This peptide is cyclic, its sequence was chosen to start
CC at the position shown below by similarity to Oak1 (kalata B1)
CC whose DNA sequence is known.
DR Pfam; PF03784; Cyclotide; 1.
KW Multigene family.
FT DISULFID 5 19
FT DISULFID 9 21
FT DISULFID 14 26
SQ SEQUENCE 29 AA; 2916 MW; 323641013F82FA18 CRC64;
Query Match 54.5%; Score 36; DB 1; Length 29;
Best Local Similarity 54.5%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CAGGTPNKYAC 11
Db 9 CVGGTCNTPGC 19

```

Search completed: October 15, 2003, 16:58:12
Job time : 7.57904 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 22:5269 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-9
Perfect score: 66
Sequence: 1 CAGGTPNKYAC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	66	100.0	260	Q931M4	Q931m4 staphylococ
2	57	86.4	288	O85217	O85217 staphylococ
3	53	80.3	260	Q99SU3	Q99su3 staphylococ
4	48	72.7	250	O8GFM6	O8gfm6 staphylococ
5	46	69.7	978	P91777	P91777 pacifastacu
6	45	68.2	399	O8IP39	O8ip39 drosophila
7	45	68.2	420	O819N4	O819n4 bombyx mori
8	45	68.2	464	Q9NKB2	Q9nkb2 drosophila
9	44	66.7	379	Q9I7M7	Q9i7m7 drosophila
10	44	66.7	400	Q9GRG2	Q9grg2 tenebrio mo
11	44	66.7	444	Q9V4W6	Q9v4w6 drosophila
12	44	66.7	781	Q9NKK72	Q9nkk72 drosophila
13	44	66.7	1022	Q8IP30	Q8ip30 drosophila
14	42	63.6	157	Q99TP7	Q99tp7 staphylococ
15	42	63.6	229	O8NW97	O8nw97 staphylococ
16	42	63.6	241	O8E8F1	O8e8f1 shewanella

17	42	63.6	257	16	Q8EGC4	Q8egc4 shewanella
18	42	63.6	265	16	Q8D6N7	Q8d6n7 vibrio vuln
19	41	62.1	289	10	Q945T9	Q945t9 phytophthor
20	41	62.1	538	13	Q9DFU0	Q9dfu0 sparus aura
21	40.5	61.4	123	5	Q95VV9	Q95vv9 plasmodium
22	40	60.6	114	5	Q8T351	Q8t351 plasmodium
23	40	60.6	131	5	Q8T4X9	Q8t4x9 plasmodium
24	40	60.6	234	11	Q9CV76	Q9cv76 mus musculu
25	40	60.6	259	5	O45048	O45048 anopheles g
26	40	60.6	269	16	O8DJN5	O8djn5 synecococc
27	40	60.6	405	5	Q8SZ60	Q8sz60 drosophila
28	40	60.6	412	5	Q8MUM0	Q8mum0 manduca sex
29	40	60.6	891	5	Q9VV38	Q9vv38 drosophila
30	40	60.6	966	5	Q22378	Q22378 caenorhabdi
31	39.5	59.8	123	5	Q8T4V5	Q8t4v5 plasmodium
32	39.5	59.8	126	5	Q9XZ99	Q9xz99 plasmodium
33	39.5	59.8	2120	5	O8IAK1	O8iak1 plasmodium
34	39	59.1	126	4	Q9UHE2	Q9uhe2 homo sapien
35	39	59.1	145	16	Q8XNL3	Q8xnl3 clostridium
36	39	59.1	146	12	Q8JMB4	Q8jmb4 manestra co
37	39	59.1	226	4	Q9V5T7	Q9v5t7 homo sapien
38	39	59.1	265	5	Q9VAX6	Q9vax6 drosophila
39	39	59.1	328	16	Q9RTK3	Q9rtk3 deinococcus
40	39	59.1	336	5	Q27000	Q27000 toxoplasma
41	39	59.1	336	5	Q27298	Q27298 toxoplasma
42	39	59.1	356	3	Q9UUN6	Q9uun6 nectria hae
43	39	59.1	713	11	Q9EPE8	Q9ep8 mus musculu
44	39	59.1	970	2	Q8GQ14	Q8gq14 pseudomonas
45	39	59.1	1253	11	Q61810	Q61810 mus musculu

ALIGNMENTS

RESULT 1

Q931M4	PRELIMINARY;	PRT;	260 AA.
ID	Q931M4		
AC	Q931M4;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Enterotoxin P.		
GN	SEP OR SAV1948.		
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699).		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=158878;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21311952; PubMed=11418146;		
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C., Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;		
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus aureus";		
RL	Lancet 357:1225-1240(2001).		
DR	EMBL; AF003364; BAB58110.1; -.		
DR	InterPro; IPR006177; Bctr1 tox.		
DR	InterPro; IPR006123; Staph/Strep toxin.		
DR	InterPro; IPR006126; Staph/Strep tox.		
DR	InterPro; IPR006173; Staph_tox_OB.		
DR	Pfam; PF01123; Staph_strep_toxin; 1.		
DR	PRINTS; PR00279; BACTRLTOXIN.		
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;		

Query Match 100.0%; Score 66; DB 16; Length 260;

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Best Local Similarity 100.0%; Pred. No. 0.001; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 1 CAGGTPNKTAC 11
Db 123 CAGGTPNKTAC 133

RESULT 2
O85217 ID O85217 PRELIMINARY; PRT; 268 AA.
AC O85217;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin J.
GN SEJ.
OS Staphylococcus aureus.
OG Plasmid pIB485.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KS11410;
RX MEDLINE=99052098; PubMed=9835033;
RA Zhang S., Iandolo J.J., Stewart G.C.;
RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
RL PEMS Microbiol. Lett. 168:227-233(1998).
DR EMBL; AF053140; AAC78590.1; -.
DR HSSP; P13163; IESF.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 268 AA; 31230 MW; AC5F346060ACE22 CRC64;

Query Match 86.4%; Score 57; DB 2; Length 268;
Best Local Similarity 81.8%; Pred. No. 0.041; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 CAGGTPNKTAC 11
Db 120 CSGGKPNKTAC 130

RESULT 3
Q99SU3 ID Q99SU3 PRELIMINARY; PRT; 260 AA.
AC Q99SU3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin P.
GN SEP OR SA1761.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Negai Y., Lian J., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
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RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus";
DR Lancet 357:1225-1240(2001).
DR EMBL; AF003135; BAB43036.1; -.
DR HSSP; P13163; ISXT.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 80.3%; Score 53; DB 16; Length 260;
Best Local Similarity 81.8%; Pred. No. 0.2; 2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 2;

QY 1 CAGGTPNKTAC 11
Db 123 CTGGTPFKTAC 133

RESULT 4
Q8GFM6 ID Q8GFM6 PRELIMINARY; PRT; 250 AA.
AC Q8GFM6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE E-1, EDINA plasmid DNA, complete sequence.
OS Staphylococcus aureus.
OG Plasmid EDINA plasmid.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-1;
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
RL plasmid";
DR Submitted (JAN-2001) to the EMBL/GenBank/DBDJ databases.
KW Plasmid.
SQ SEQUENCE 250 AA; 28955 MW; 047728506D12DF76 CRC64;

Query Match 72.7%; Score 48; DB 2; Length 250;
Best Local Similarity 72.7%; Pred. No. 1.5; 3; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 3;

QY 1 CAGGTPNKTAC 11
Db 113 CNGGEENKTC 123

RESULT 5
P91777 ID P91777 PRELIMINARY; PRT; 978 AA.
AC P91777;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Masquerade-like protein precursor.
OS Pacifastacus leniusculus (Signal crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Astacidae; Pacifastacus.
OX NCBI_TaxID=6720;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=20209362; PubMed=10744675;
RA Huang T.S., Wang H., Lee S.Y., Johansson M.W., Soderhall K.,
RA Cerenius L.;
RT "A cell adhesion protein from the crayfish *Pacifastacus leniusculus*, a
RT serine proteinase homologue similar to *Drosophila* masquerade.";
RL J. Biol. Chem. 275:19996-10001 (2000).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; Y11145; CAAY2032.2; -;
DR HSP; P00734; I87X.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser-protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP SPC; 1.
DR PROSITE; PS00240; TRYP SIN DOM; 1.
DR PROSITE; PS00134; TRYP SIN_HIS; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 17 POTENTIAL.
SQ SEQUENCE 978 AA; 98857 MW; 6F682F77C585B7C6 CRC64;
Query Match 69.7%; Score 46; DB 5; Length 978;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAGGTPTKATC 11
DB 897 CAGGEENKDAC 907
||||| |||||
RESULT 6
Q8IP39
ID Q8IP39 PRELIMINARY; PRT; 399 AA.
AC Q8IP39;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG31780-PA.
GN CG31780.
OS *Drosophila melanogaster* (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196066; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.P., Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Dew Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle B. J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez C., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacle B. J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
RA Phouanehong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Kearle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003648; AAN10904.1; -;
SQ SEQUENCE 399 AA; 44018 MW; 575C1FD99B9C7FCD CRC64;
Query Match 68.2%; Score 45; DB 5; Length 399;
Best Local Similarity 63.6%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAGGTPTKATC 11
DB 239 CAGGEPKDC 249
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RESULT 7
Q819N4
ID Q819N4 PRELIMINARY; PRT; 420 AA.
AC Q819N4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Masquerade-like serine proteinase homolog.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;


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Query Match      68.2%; Score 45; DB 5; Length 464;
Best Local Similarity 63.6%; Pred. No. 9.1;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGGTPTKATC 11
Db 284 CAGGEPKDC 294
|||||

RESULT 9
Q917M7 PRELIMINARY; PRT; 379 AA.
AC Q917M7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CAG4793 protein.
GN BG:DS07486.3 OR CG4793.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,

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Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hrabecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS003649; BAG2436.2; -.
DR HSSP; P00742; IHCG.
DR FlyBase; FBgn0028514; BG:DS07486.3.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser protease_Try.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
SQ SEQUENCE 379 AA; 42057 MW; 5C814D5C55A70C02 CRC64;

Query Match      66.7%; Score 44; DB 5; Length 379;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTPTKATC 11
Db 276 CAGGEPKDC 286
|||||

RESULT 10
Q9GRG2 PRELIMINARY; PRT; 400 AA.
AC Q9GRG2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phenoloxidase activating factor.
GN PPAP.
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larva;
RX MEDLINE=20467200; PubMed=11012672;
RA Kwon T.H., Kim M.S., Choi H.W., Joo C.H., Cho M.Y., Lee B.L.;
RT "A masquerade-like serine proteinase homologue is necessary for
RT phenoloxidase activity in the coleopteran insect, Holotrichia
RT diomphalia larvae."
RL Eur. J. Biochem. 267:6188-6196(2000).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; A400904; CAC12696.1; -.
DR HSSP; P00763; LDPO.
DR InterPro; IPR001314; Chymotrypsin.

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DR InterPro: IPR001254; Ser. protease_Try.
DR Pfam: PF00089; trypsin: 1
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
DR PROSITE; PSS0134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 400 AA; 43754 MW; DEB882CB715D7D97 CRC64;

Query Match 66.7%; Score 44; DB 5; Length 400;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKATC 11
Db 324 CAGGEPKQKTC 334

RESULT 11
Q9V4W6 PRELIMINARY; PRT; 444 AA.
AC Q9V4W6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG8586 protein.
GN CG8586.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh A.T., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
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```
RL Science 287:2185-2195 (2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AE003836; AAF59059.1; -.
DR HSSP; P00763; IDPO.
DR FlyBase; FBgn0033320; CG8586.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00089; trypsin: 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 444 AA; 49632 MW; 7F386DB4793B63A7 CRC64;

Query Match 66.7%; Score 44; DB 5; Length 444;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKATC 11
Db 370 CAGGEPKQKTC 380

RESULT 12
Q9NK72 PRELIMINARY; PRT; 781 AA.
AC Q9NK72;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE BG:DS07486.3 protein.
GN BG:DS07486.3 OR CG4793.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RA "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Chavez M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomoton M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Swirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AS003414; AAF44976.1; -.
DR HSSP; P00763; IDPO.
DR FlyBase; FBgn0028514; BG:DS07486.3.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001547; Glyco hydro 5.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00089; trypsin: 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
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KW Hydrolase; Protease; Serine protease.
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Query Match 66.7%; Score 44; DB 5; Length 781;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKTCAC 11
Db 276 CAGGEGKDTCTC 286

RESULT 13
Q8IP30 PRELIMINARY; PRT; 1022 AA.
AC Q8IP30;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE CG4793-PC.
GN BG:DS07486.3.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgett W.R., K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

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RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase.
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
SQ EMBL; AB003649; AA010922.1; -.
DE SEQUENCE 1022 AA; 110303 MW; 1C60EA835609BE9D CRC64;

Query Match 66.7%; Score 44; DB 5; Length 1022;
Best Local Similarity 63.6%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTPNKTCAC 11
Db 276 CAGGEGKDTCTC 286

RESULT 14
Q99TP7 PRELIMINARY; PRT; 157 AA.
AC Q99TP7;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE Hypothetical protein SAV1602.
GN SAV1602 OR SA1430.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003362; BAB57764.1; -.
DR EMBL; AF003134; BAB42694.1; -.
DR HSSP; P13163; 1SXT.
DR InterPro; IPR006126; Staph/Strept_tox.

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DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph Strp toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 157 AA; 17824 MW; D9AD68BECB1B1702 CRC64;
Query Match 63.6%; Score 42; DB 16; Length 157;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTPNKTAC 11
Db 135 CHGGATNKTQC 145
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ID Q8NW97 PRELIMINARY; PRT; 229 AA.
AC Q8NW97;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MW1552 protein.
GN MW1552.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004827; BAB95417.1; -.
DR InterPro; IPR006177; Bcrl toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 229 AA; 26728 MW; AD3DAF9EA1AE3677 CRC64;
Query Match 63.6%; Score 42; DB 16; Length 229;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTPNKTAC 11
Db 95 CHGGATNKTQC 105

Search completed: October 15, 2003, 17:04:06
Job time : 26.5269 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 57.4671 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-10

Perfect score: 121

Sequence: 1 CYFSKKTNDINSHQTPKRKTC 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	121	100.0	21	20	Staphylococcal gro
2	121	100.0	21	24	Staphylococcal ent
3	113	93.4	239	12	Staphylococcal ent
4	113	93.4	239	14	Staphylococcal ent
5	113	93.4	239	22	Staphylococcus aur
6	113	93.4	239	23	Staphylococcus aur
7	113	93.4	255	18	Staphylococcus ent
8	113	93.4	265	21	Staphylococcal ent
9	113	93.4	266	21	Plant-optimized mu

10	113	93.4	266	23	ABB79503	Staphylococcal ent
11	110	90.9	239	19	AAW64647	Synthetic SEB prot
12	104	86.0	239	21	AAW70106	Mutant Staphylococ
13	104	86.0	239	23	ABB79505	Staphylococcal ent
14	104	86.0	240	21	AAW54465	Mutant Staphylococ
15	104	86.0	265	21	AAW70105	Mutant Staphylococ
16	104	86.0	266	21	AAW54464	Amino acid sequenc
17	104	86.0	266	23	ABB79504	Staphylococcal ent
18	49.5	40.9	477	22	ABB71778	Drosophila melanog
19	49	40.5	299	24	ABU02349	S. pneumoniae type
20	49	40.5	300	21	AAW81582	Streptococcus pneu
21	48	39.7	85	23	ABP31919	Human ORF892 prote
22	48	39.7	87	23	ABP31501	Human structural p
23	46	38.0	670	23	ABP38095	Staphylococcus epi
24	45.5	37.6	164	22	AAW81858	S. epidermidis ope
25	45.5	37.6	164	22	AAW82518	S. epidermidis ope
26	45.5	37.6	337	22	AAU36972	Staphylococcus aur
27	45.5	37.6	360	22	AAU33795	Staphylococcus aur
28	45.5	37.6	366	23	ABP38834	Staphylococcus epi
29	45	37.2	82	21	AAW11545	SEN virus protein
30	45	37.2	224	23	ABP61020	Lactobacillus rham
31	45	37.2	247	21	AAW83081	F-box protein FBP-
32	45	37.2	247	23	AAO22467	Human F-box protei
33	45	37.2	408	22	AAW48304	Human ZF23 protein
34	45	37.2	414	23	ABG70045	Human prey protein
35	45	37.2	468	23	ABP43604	Clone MGC:9282. H
36	45	37.2	471	21	AAW90287	Human peptidase, H
37	45	37.2	471	22	AAW93481	Human protein sequ
38	45	37.2	471	23	AAW47764	F-casette structu
39	44	36.4	53	22	AAU29612	Novel human secret
40	44	36.4	196	22	AAW82460	S. epidermidis ope
41	44	36.4	201	23	ABP39474	Staphylococcus epi
42	44	36.4	344	18	AAW11822	Porcine CD34 from
43	44	36.4	627	24	ABB82646	Drosophila DevG22
44	44	36.4	788	22	ABB67949	Drosophila melanog
45	43.5	36.0	203	24	ABU25500	Aspergillus fumiga

ALIGNMENTS

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RESULT 1
AAW06248
ID AAW06248 standard; Peptide; 21 AA.
XX
AC
AC
XX
XX
DT 23-AUG-1999 . (first entry)
XX
DE Staphylococcal group B enterotoxin disulfide loop.
XX
KW Enterotoxin; SEB; toxin; disulfide loop; protein engineering.
XX
OS Staphylococcus aureus.
XX
PN WO927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25107.
XX
PR 02-DEC-1997; 97US-0067357.
XX
(PA IDAH-) IDAHO RES FOUND INC.
XX
PI Bohach GI;
XX
DR WPI; 1999-358008/30.
XX
PT Non-toxic modified staphylococcal enterotoxins
XX
PS Disclosure; Page 3; 25pp; English.
XX

```

CC This peptide corresponds to the disulfide loop, i.e. amino acids
 CC 93-114, of Staphylococcus aureus group B enterotoxin (SEB). The
 CC invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically,
 CC the modification involves deletions within the disulfide loop
 CC region (see AA06261). The modified toxins retain useful biological
 CC properties, such as the ability to induce cytokine production, but
 CC have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and
 CC fever inducing activity are typically decreased by at least about
 CC 100-fold, while LD50 (in Dutch Belted rabbits) is at least about
 CC 100-fold higher than the native toxin.

SQ Sequence 21 AA;
 Query Match 100.0%; Score 121; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTK 21
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 Db 1 CYFSKKTNDINSHQTPKRTK 21

RESULT 2
 ABG71376
 ID ABG71376 standard; Peptide; 21 AA.
 XX
 AC ABG71376;
 XX
 XX 29-JAN-2003 (first entry)
 DT
 XX Staphylococcal enterotoxin SEB disulphide loop region.
 DE
 XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEB.

XX Staphylococcus aureus.
 OS
 XX WO200283169-A1.
 PN
 XX 24-OCT-2002.
 PD
 XX 11-APR-2002; 2002WO-US11619.
 PF
 XX 13-APR-2001; 2001US-283720P.
 PR
 XX (IDAH-) IDAHO RES FOUND INC.
 PA
 XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 PI WPI; 2003-058608/05.
 XX
 DR New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
 PT an immune function and as a vaccine against toxic shock syndrome or
 PT food poisoning -
 PT Disclosure; Fig 15; 67pp; English.

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic
 CC response-inducing activity decreased by about 100-fold in comparison to a
 CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents a staphylococcal enterotoxin
 CC disulphide loop region.

SQ Sequence 21 AA;
 Query Match 100.0%; Score 121; DB 24; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTK 21
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 Db 1 CYFSKKTNDINSHQTPKRTK 21

RESULT 3
 AAR13206
 ID AAR13206 standard; Protein; 239 AA.
 XX
 AC AAR13206;
 XX
 DT 15-OCT-1991 (first entry)
 DT
 XX Staphylococcal enterotoxin B.
 DE
 XX SEB; cancer treatment; pyrogen; tumouricide.

XX Staphylococcus aureus.
 OS
 XX WO9110680-A.
 PN
 XX 25-JUL-1991.
 PD
 XX 17-JAN-1991; 91WO-US00342.
 PF
 XX 17-JAN-1990; 90US-0466577.
 PR
 XX (TERM/) TERMAN D S.
 PA
 XX Terman DS;
 PI WPI; 1991-237984/32.
 XX
 DR Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC SEB was isolated and purified from S.aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEB. Synthetic
 CC polypeptides having structural homology to staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophathy profiles.
 CC See AAR13203-R13211.

SQ Sequence 239 AA;
 Query Match 93.4%; Score 113; DB 12; Length 239;
 Best Local Similarity 95.2%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTK 21
 |||||
 Db 93 CYFSKKTNDINSHQTPKRTK 113

RESULT 4
 AAR45014
 ID AAR45014 standard; protein; 239 AA.

XX
 AC AAR45014;
 XX

DT 25-MAR-2003 (updated)
 DT 08-JUN-1994 (first entry)
 XX
 DE Staphylococcal enterotoxin SEB.
 XX
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9324136-A1.
 XX
 PD 09-DEC-1993.
 XX
 PF 01-JUN-1993; 93WO-US05213.
 XX
 PR 01-JUN-1992; 92US-0891718.
 XX
 PA (STON/) STONE J L.
 PA (TERM/) Terman D S.
 XX
 PI Stone JL, Terman DS;
 XX
 DR WPI; 1993-405418/50.
 XX
 PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 XX
 PS Disclosure; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 239 AA;
 Query Match 93.4%; Score 113; DB 14; Length 239;
 Best Local Similarity 95.2%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYFSKKTNDINSHQTPKRTKTC 21
 DB ||||| ||||| ||||| ||||| |||||
 93 CYFSKKTNDINSHQTPKRTKTC 113
 RESULT 5
 AAB67341
 ID AAB67341 standard; peptide; 239 AA.
 XX
 AC AAB67341;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin B protein.
 XX
 KW Tumour; cancer; immune; enterotoxin.
 XX
 OS Staphylococcus aureus.
 XX
 PN US6180097-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 30-OCT-1998; 98US-0183437.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 XX

PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) Terman D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2001-158657/16.
 XX
 PT Tumor cell capable of stimulating antitumor immune reactivity in vitro
 PT or in vivo comprises exogenous nucleic acids encoding a superantigen
 PT and a costimulatory molecule -
 XX
 PS Disclosure; Fig 2; 16pp; English.
 XX
 CC The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule
 CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 XX
 SQ Sequence 239 AA;
 Query Match 93.4%; Score 113; DB 22; Length 239;
 Best Local Similarity 95.2%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYFSKKTNDINSHQTPKRTKTC 21
 DB ||||| ||||| ||||| ||||| |||||
 93 CYFSKKTNDINSHQTPKRTKTC 113
 RESULT 6
 ABB76237
 ID ABB76237 standard; Protein; 239 AA.
 XX
 AC ABB76237;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin B.
 XX
 KW Enterotoxin B; SEB; superantigen; antigen; tumour; cancer;
 KW antitumour; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 227
 XX /note= "given as 'O' in the specification"
 PN US2002051765-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 19-DEC-2000; 2000US-0741503.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) Terman D S.
 XX

PI Terman DS;
 XX WPI; 2002-415198/44.
 XX
 PT Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens -
 XX
 XX Disclosure; Fig 2; 17pp; English.
 XX
 CC The present sequence is the protein sequence of enterotoxin B
 CC (SEB) of *Staphylococcus aureus*. Similarity is shown, in several
 CC stretches of sequence, between staphylococcal enterotoxins,
 CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative
 CC toxins (see AB576234-44). In the present invention, synthetic
 CC polypeptides useful in tumour therapy and in blocking or destroying
 CC autoreactive T and B lymphocyte populations are characterised by
 CC substantial structural homology to staphylococcal enterotoxin A and
 CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
 CC statistically significant sequence homology and similarity (Z value
 CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
 CC 6) to include alignment of cysteine residues and similar hydrophathy
 CC profiles. These superantigens are used to treat solid tumours,
 CC including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient
 CC with one or more superantigens ex vivo to generate stimulated cells,
 CC selecting a specific V beta subset of cells, and reintroducing
 CC these cells into the patient to induce an in vivo therapeutic,
 CC tumouricidal reaction.
 XX
 XX Sequence 239 AA;

Query Match 93.4%; Score 113; DB 23; Length 239;
 Best Local Similarity 95.2%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPRKRTC 21
 |||||
 DB 93 CYFSKKTNDINSHQTPRKRTC 113

RESULT 7
 AA06737
 ID AA06737 standard; Protein; 255 AA.

AC AA06737;

DT 08-MAR-1997 (first entry)

DE *Staphylococcus enterotoxin B*.

XX Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
 KW vaccine; adjuvant.

OS *Staphylococcus* sp.

FH Key Location/Qualifiers
 FT Peptide 1..15
 FT /label= Sig_peptide

XX WO9636366-A1.

XX 21-NOV-1996.

XX 20-MAY-1996; 96WO-US07432.

XX 29-DEC-1995; 95US-0580806.

XX 18-MAY-1995; 95US-0446918.

XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.

PI Dow SW, Elmslie RE, Potter TA;
 XX WPI; 1997-011857/01.
 DR N-PSDB; AAT45698.
 XX
 PT Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer
 XX
 XX Example 1; Page 96-97; 131pp; English.

XX A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B
 CC (AA06737) superantigen. Nucleic acids encoding superantigens (see
 CC also AA06738-39), esp. truncated forms of the superantigen lacking
 CC the leader peptide, can be utilised in the gene therapy of cancer,
 CC infectious diseases and immunological disorders. The nucleic acid,
 CC optionally in combination with cytokine or chemokine nucleic acids,
 CC is delivered to an animal using e.g. liposomes. It acts by
 CC controlling the activity of effector cells, such as T-cells,
 CC macrophages, monocytes and/or natural killer cells. Localised
 CC prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal.

XX Sequence 255 AA;

Query Match 93.4%; Score 113; DB 18; Length 255;
 Best Local Similarity 95.2%; Pred. No. 3.4e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPRKRTC 21
 |||||
 DB 109 CYFSKKTNDINSHQTPRKRTC 129

RESULT 8

AA070104

ID AAY70104 standard; Protein; 265 AA.

AC AAY70104;

DT 05-JUN-2000 (first entry)

DE *Staphylococcal enterotoxin B*.

XX Superantigen toxin; SAG; *Staphylococcal enterotoxin B*; SEB; cytostatic;
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis;
 KW treatment; superantigen-associated bacterial infection.

OS *Staphylococcus* sp.

FH Key Location/Qualifiers
 FT Peptide 2..28
 FT /label= Leader_peptide
 FT Protein 29..265
 FT /label= Mature Staphylococcal enterotoxin B
 FT /note= "Includes transcription start site residue, Met"

FT Misc-difference 177 /note= "Encoded by ACT"

FT Misc-difference 220 /note= "Encoded by GAG"

FT Misc-difference 221 /note= "Encoded by AATAGC"

FT Misc-difference 236 /note= "Encoded by ATT"

XX WO200009154-A1.

XX 24-FEB-2000.

XX 13-AUG-1998; 98WO-US16766.

XX 13-AUG-1998; 98WO-US16766.

XX (REED-) REED ARMY INST RES WALTER.
 XX Ulrich RG, Olson MA, Bavari S;
 PI WPI; 2000-224177/19.
 DR N-PSDB; AA251107.
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 PT diagnosis of superantigen-associated bacterial infections -
 PS Claim 9; Page 78-79; 118pp; English.
 XX The present amino acid sequence is the Staphylococcal enterotoxin B
 CC (SEB), a bacterial superantigen toxin (SAG). The coding region
 CC of the SAG toxin when altered by site directed mutagenesis, results
 CC in disruption of binding of the toxin to both the MHC class II or T-cell
 CC antigen receptor. SEB has antibacterial and cytostatic activity. This
 CC sequence is useful for the production of SEB vaccines and specific
 CC antibodies. This vaccine overcomes the disadvantages of the chemically
 CC inactivated toxoids and is designed to protect individuals against one
 CC or several related staphylococcal and streptococcal toxins. It is used
 CC for the diagnosis and treatment or amelioration of superantigen-
 CC associated bacterial infections.
 XX SQ Sequence 265 AA;
 Query Match 93.4%; Score 113; DB 21; Length 265;
 Best Local Similarity 95.2%; Pred. No. 3.6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYFSKKTNDINSHQTPKRKTC 21
 DB 120 CYFSKKTNDINSHQTPKRKTC 140
 |||||
 RESULT 9
 AAAY92319
 ID AAAY92319 standard; Protein; 266 AA.
 XX AC AAAY92319;
 XX DT 10-AUG-2000 (first entry)
 XX DE Plant-optimized mutant staphylococcal enterotoxin B.
 XX Rep; replicase; rescue; replication; vector; gene expression;
 KW recombinant protein production; plant; intronless; enterotoxin B.
 XX Staphylococcus sp.
 OS Synthetic.
 XX WO200020557-A2.
 PN 13-APR-2000.
 XX 07-OCT-1999; 99WO-US23520.
 PF 07-OCT-1998; 98US-0103352.
 PR (UYCO-) UNIV CORNELL BOYCE INST PLANT RES.
 XX PA Mason HS, Palmer KE, Mor TS, Hefferson KL, Arntzen C;
 PI WPI; 2000-303756/26.
 DR N-PSDB; AAA09240.
 XX Nucleic acids comprising a portion of a long intergenic region of a
 PT geminivirus genome and a sequence comprising a geminiviral replicase
 PT gene, useful for amplifying a gene of interest and overproducing a
 PT protein of interest in plants
 XX Example 17; Fig 36; 121pp; English.

XX A pair of nucleic acids comprising a portion of a long intergenic region
 CC (LIR) of a geminivirus genome lacking a sequence encoding a geminiviral
 CC coat protein, and a nucleic acid comprising a geminiviral replicase gene
 CC linked to a fruit ripening-dependent promoter, are new. Strains of
 CC Escherichia coli and Agrobacterium tumefaciens transfected with an
 CC expression vector containing the nucleic acids and a gene of interest are
 CC useful for the production of transgenic plants (or cells). The sequences
 CC and methods are useful for amplifying a gene of interest and
 CC overproducing a protein of interest in recombinant plants.
 XX SQ Sequence 266 AA;
 Query Match 93.4%; Score 113; DB 21; Length 266;
 Best Local Similarity 95.2%; Pred. No. 3.6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYFSKKTNDINSHQTPKRKTC 21
 DB 120 CYFSKKTNDINSHQTPKRKTC 140
 |||||
 RESULT 10
 ABB79503
 ID ABB79503 standard; Protein; 266 AA.
 XX AC ABB79503;
 XX DT 23-SEP-2002 (first entry)
 XX DE Staphylococcal enterotoxin B vaccine (B42360210).
 XX Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;
 KW attenuation.
 XX Staphylococcus sp.
 OS US6399332-B1.
 PN 04-JUN-2002.
 XX 01-SEP-1998; 98US-0144776.
 PF 25-JUN-1997; 97US-0882431.
 PR (USSA) US SEC OF ARMY.
 XX Ulrich RG, Olson MA, Bavari S;
 PI WPI; 2002-546281/58.
 DR N-PSDB; ABN84224.
 XX Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases -
 PS Disclosure; Column 41-43; 46pp; English.
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin B (SEB) vaccine B42360210. The invention relates to a
 CC vaccine against superantigen toxin-associated bacterial diseases.
 CC Superantigen vaccines were developed by engineering changes in the
 CC receptor-binding portions of superantigen toxins such as SEB to
 CC reduce receptor-binding affinities and toxicity while maintaining
 CC antigenicity. In examples from the invention, attenuated
 CC superantigen toxins were shown to protect animals against challenge
 CC with wild-type toxin. Methods of producing and using the altered
 CC superantigen toxins as vaccines, and in diagnosis and therapy, are
 CC provided. A multivalent vaccine consisting of altered superantigen
 CC toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEa is
 CC predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins.
 XX

```

SQ Sequence 266 AA;
Query Match 93.4%; Score 113; DB 23; Length 266;
Best Local Similarity 95.2%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRKTC 21
    |||||
Db 120 CYFSKKTNDINSHQTPKRKTC 140

RESULT 11
AAW64647
ID AAW64647 standard; peptide; 239 AA.
XX
AC AAW64647;
XX
DT 23-OCT-1998 (first entry)
XX
DE Synthetic SEB protein fragment.
XX
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
XX
OS Synthetic.
XX Staphylococcus aureus.
XX
PN W09829444-AL.
XX
PD 09-JUL-1998.
XX
PF 30-DEC-1997; 97WO-IL00438.
XX
PR 30-DEC-1996; 96IL-0119938.
XX
PA (YISS ) YISSUS RES & DEV CO.
XX
PI Arad G, Kaempfer R;
XX
WPI; 1998-388042/33.
XX
New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
XX
Example 8; Page 41; 68pp; English.
XX
AAW64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by
CC PET.
XX
SQ Sequence 239 AA;
Query Match 90.9%; Score 110; DB 19; Length 239;
Best Local Similarity 90.5%; Pred. No. 9.2e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRKTC 21
    |||||
Db 93 CYFSKKTNDINSHQTPKRKTC 113

us-09-555-115a-10.rag
RESULT 12
AAV70106
ID AAY70106 standard; Protein; 239 AA.
XX
AC AAY70106;
XX
DT 05-JUN-2000 (first entry)
XX
DE Mutant Staphylococcal enterotoxin B for vaccine B899445C.
XX
KW Superantigen toxin; SAG; Staphylococcal enterotoxin B; SEB; cytostatic;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
KW treatment; superantigen-associated bacterial infection; B899445C.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..239
FT /label= Mature Staphylococcal enterotoxin B
FT /note= "Mutant" sequence without leader peptide"
FT Misc-difference 20 /note= "Encoded by TTG"
FT Misc-difference 45 /note= "Wild type Leu substituted with Arg"
FT Misc-difference 89 /note= "Wild type Tyr substituted with Ala"
FT Misc-difference 94 /note= "Wild type Tyr substituted with Ala"
FT Misc-difference 171 /note= "Encoded by AAT"
XX
PN W0200009154-AL.
XX
PD 24-FEB-2000.
XX
PF 13-AUG-1998; 98WO-US16766.
XX
PR 13-AUG-1998; 98WO-US16766.
XX
PA (REED-) REED ARMY INST RES WALTER.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
WPI; 2000-224177/19.
XX
N-PSDB; AAZ51109.
XX
Nucleic acid encoding superantigen toxin useful as a vaccine and for
PT diagnosis of superantigen-associated bacterial infections -
XX
Claim 11; Page 85-86; 118pp; English.
XX
The present amino acid sequence is the mutant Staphylococcal
CC enterotoxin B (SEB), a bacterial superantigen toxin (SAG), used for the
CC formulation of SEB vaccine B899445C. The coding region of this SAG toxin
CC is altered by site directed mutagenesis, that results in disruption of
CC binding of the toxin to both the MHC class II or T-cell antigen
CC receptor. This altered SAG toxin has the leader peptide cleaved by native
CC bacterial enzymatic mechanism and the first residue of the mature protein
CC is encoded by the transcriptional start site (ATG). SEB has
CC antibacterial and cytostatic activity. This sequence is useful for the
CC production of SEB vaccines and specific antibodies. This vaccine
CC overcomes the disadvantages of the chemically inactivated toxoids and is
CC designed to protect individuals against one or several related
CC staphylococcal and streptococcal toxins. It is used for the diagnosis and
CC treatment or amelioration of superantigen-associated bacterial
CC infections.
XX
SQ Sequence 239 AA;
Query Match 86.0%; Score 104; DB 21; Length 239;
Best Local Similarity 90.5%; Pred. No. 7.6e-08;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```


Db 94 CAFSKKTNDINSHQTDKRTK 114

RESULT 15

AA70105

ID AA70105 standard; Protein; 265 AA.

XX AC AA70105;

XX 05-JUN-2000 (first entry)

XX Mutant Staphylococcal enterotoxin B for SEB vaccine B2360210P.

DE Superantigen toxin; SAG; Staphylococcal enterotoxin B; SEB; cytostatic;

XX antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;

KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;

KW treatment; superantigen-associated bacterial infection; B2360210P.

XX

OS Staphylococcus sp.

XX

PH Key Location/Qualifiers

FT Peptide 2..28

FT /label= Leader_peptide

FT Protein 29..265

FT /label= Mature Staphylococcal enterotoxin B

FT /note= "Mutant sequence includes transcription start

FT site residue, Met"

FT Misc-difference 72

FT /note= "Wild type Leu substituted with Arg"

FT Misc-difference 87

FT /note= "Encoded by AAT"

FT Misc-difference 116

FT /note= "Wild type Tyr substituted with Ala"

FT Misc-difference 121

FT /note= "Wild type Tyr substituted with Ala"

FT Misc-difference 177

FT /note= "Encoded by ACT"

FT Misc-difference 220

FT /note= "Encoded by GAG"

FT Misc-difference 221

FT /note= "Encoded by AATAGC"

FT Misc-difference 256

FT /note= "Encoded by ATT"

XX

PN W0200009154-A1.

XX

PD 24-FEB-2000.

XX

XX 13-AUG-1998; 98WO-US16766.

XX

XX 13-AUG-1998; 98WO-US16766.

XX (REED-) REED ARMY INST RES WALTER.

XX

XX Ulrich RG, Olson MA, Bavari S;

PI WPI: 2000-224177/19.

XX DR N-PSDB; AA251108.

XX

XX Nucleic acid encoding superantigen toxin useful as a vaccine and for

PT diagnosis of superantigen-associated bacterial infections -

XX

XX Claim 10; Page 81-83; 118pp; English.

XX

XX The present amino acid sequence is the mutant Staphylococcal enterotoxin

CC B (SEB), a bacterial superantigen toxin (SAG), used for the formulation

CC of SEB vaccine B2360210P. The coding region of this SAG toxin is altered

CC by site directed mutagenesis, that results in disruption of binding of

CC the toxin to both the MHC class II or T-cell antigen receptor. SEB has

CC antibacterial and cytostatic activity. This sequence is useful for the

CC production of SEB vaccines and specific antibodies. This vaccine

CC overcomes the disadvantages of the chemically inactivated toxoids and is

CC designed to protect individuals against one or several related

0 .

CC staphylococcal and streptococcal toxins. It is used for the diagnosis

CC and treatment or amelioration of superantigen-associated bacterial

CC infections.

XX

SQ Sequence 265 AA;

Query Match 86.0%; Score 104; DB 21; Length 265;

Best Local Similarity 90.5%; Pred. No. 8.5e-08;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CYFSKKTNDINSHQTPKRTK 21

DB 120 CAFSKKTNDINSHQTDKRTK 140

Search completed: October 15, 2003, 16:56:54

Job time : 58.5671 secs

0 .

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:51:46 ; Search time 16.0958 Seconds
(without alignments)
55.202 Million cell updates/sec

Title: US-09-555-115A-10

Perfect score: 121

Sequence: 1 CYFSKKTNDINSHQTPKRTK 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	93.4	89	4	US-09-144-776B-20
2	113	93.4	239	3	US-08-896-933-26
3	113	93.4	239	4	US-09-314-235-26
4	113	93.4	255	1	US-08-446-918A-2
5	113	93.4	255	2	US-08-580-806-2
6	113	93.4	266	4	US-09-414-276-8
7	113	93.4	286	4	US-09-144-776B-6
8	104	86.0	239	4	US-09-144-776B-10
9	104	86.0	266	4	US-09-144-776B-8
10	95	78.5	239	3	US-08-896-933-21
11	95	78.5	239	4	US-09-314-235-21
12	50	41.3	91	4	US-09-732-210-453
13	46	38.0	670	4	US-09-134-001C-2940
14	45.5	37.6	366	4	US-09-134-001C-3679
15	45	37.2	224	4	US-09-724-623-63
16	44	36.4	201	4	US-09-134-001C-4319
17	44	36.4	344	2	US-08-475-634D-19
18	42.5	35.1	382	2	US-08-455-968E-5
19	42.5	35.1	382	2	US-08-823-516-139
20	42	34.7	79	4	US-09-149-476-399
21	42	34.7	1723	4	US-09-194-612A-31
22	41	33.9	89	3	US-08-784-582-53
23	41	33.9	135	2	US-08-647-960-5
24	41	33.9	274	3	US-08-784-582-71
25	40	33.1	621	4	US-09-331-568A-2
26	40	33.1	621	4	US-09-331-568A-26
27	40	33.1	1088	4	US-09-233-857-4

28	39.5	32.6	647	4	US-09-134-001C-5458	Sequence 5458, Ap
29	39	32.2	100	4	US-09-732-210-1171	Sequence 1171, Ap
30	39	32.2	124	4	US-09-690-454-181	Sequence 181, App
31	39	32.2	152	4	US-08-504-617-5	Sequence 5, Appli
32	39	32.2	200	4	US-09-282-146-2	Sequence 2, Appli
33	39	32.2	335	4	US-09-107-532A-4702	Sequence 4702, Ap
34	39	32.2	351	2	US-08-929-417-2	Sequence 2, Appli
35	39	32.2	445	4	US-09-996-243-177	Sequence 177, App
36	39	32.2	456	4	US-09-134-001C-3772	Sequence 3772, Ap
37	39	32.2	828	4	US-09-107-532A-4191	Sequence 4191, Ap
38	39	32.2	1024	4	US-09-562-737-86	Sequence 86, Appli
39	38.5	31.8	510	4	US-09-852-067-2	Sequence 2, Appli
40	38	31.4	38	3	US-09-172-841-9	Sequence 9, Appli
41	38	31.4	38	4	US-08-951-621-9	Sequence 9, Appli
42	38	31.4	40	1	US-08-735-963-3	Sequence 3, Appli
43	38	31.4	40	2	US-09-105-057-3	Sequence 3, Appli
44	38	31.4	40	3	US-09-304-214-3	Sequence 3, Appli
45	38	31.4	192	1	US-08-735-963-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-144-776B-20
; Sequence 20, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Attv)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-144-776B-20

Query Match 93.4%; Score 113; DB 4; Length 89;

Best Local Similarity 95.2%; Pred. No. 1.6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 53 CYFSKKTNDINSHQTDKRTKTC 73

RESULT 2
US-08-896-933-26
; Sequence 26, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-26

Query Match 93.4%; Score 113; DB 3; Length 239;
Best Local Similarity 95.2%; Pred. No. 4.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 93 CYFSKKTNDINSHQTDKRTKTC 113

RESULT 3
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-26

Query Match 93.4%; Score 113; DB 4; Length 239;
Best Local Similarity 95.2%; Pred. No. 4.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 93 CYFSKKTNDINSHQTDKRTKTC 113

RESULT 4
US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/446,918A
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 93.4%; Score 113; DB 1; Length 255;
Best Local Similarity 95.2%; Pred. No. 5.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 109 CYFSKKTNDINSHQTDKRTKTC 129

RESULT 5
US-08-580-806-2
; Sequence 2, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/580,806

FILING DATE: US/08/580,806
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-580-806-2

Query Match 93.4%; Score 113; DB 2; Length 255;
Best Local Similarity 95.2%; Pred. No. 5.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTCT 21
|||||

DB 109 CYFSKKTNDINSHQTPKRTCT 129
|||||

RESULT 6
US-09-414-276-8

Sequence 8, Application US/09414276
Patent No. 6392121

GENERAL INFORMATION:

APPLICANT: Mason, Hugh

APPLICANT: Palmer, Kenneth

APPLICANT: Hefferon, Kathleen

APPLICANT: Mor, Tsafir

APPLICANT: Arntzen, Charles

TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants

FILE REFERENCE: 4868/84453

CURRENT APPLICATION NUMBER: US/09/414,276

CURRENT FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 8

LENGTH: 266

TYPE: PRT

ORGANISM: bean yellow dwarf virus

US-09-414-276-8

Query Match 93.4%; Score 113; DB 4; Length 266;
Best Local Similarity 95.2%; Pred. No. 5.4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTCT 21
|||||

DB 120 CYFSKKTNDINSHQTPKRTCT 140
|||||

RESULT 7
US-09-144-776B-6

Sequence 6, Application US/09144776B
Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCWR-JA (Charles H. Harris-Patent
Atty)

CITY: FORT DETRICK
STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,776B

FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER: <Unknown>

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 266

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-144-776B-6

Query Match 93.4%; Score 113; DB 4; Length 266;
Best Local Similarity 95.2%; Pred. No. 5.4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTCT 21
|||||

DB 120 CYFSKKTNDINSHQTPKRTCT 140
|||||

RESULT 8

US-09-144-776B-10

Sequence 10, Application US/09144776B
Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCWR-JA (Charles H. Harris-Patent
Atty)

CITY: FORT DETRICK
STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-144-776B-10

Query Match      86.0%; Score 104; DB 4; Length 239;
Best Local Similarity 90.5%; Pred. No. 1.2e-08;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYPFSKKTNDINSHQTPKRTKC 21
Db 93 CAPSKKTNDINSHQTDKRTKC 113

RESULT 9
US-09-144-776B-8
; Sequence 8, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Sina Bavari
; Mark A. Olson
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-144-776B-8

Query Match      86.0%; Score 104; DB 4; Length 266;
Best Local Similarity 90.5%; Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1oCYFSKKTNDINSHQTPKRTKC 21
Db 120 CAFSKKTNDINSHQTDKRTKC 140

RESULT 10
US-08-896-933-21
; Sequence 21, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-21

Query Match      78.5%; Score 95; DB 3; Length 239;
Best Local Similarity 76.2%; Pred. No. 3e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKC 21
Db 92 CYFSKKTNNIDSHENTKRTKC 112

RESULT 11
US-09-314-235-21
; Sequence 21, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21

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1 CYFSKKTNDINSHQTPKRTC 21
 105 CYNKRTNDID 115

Query Match 78.5%; Score 95; DB 4; Length 239;
 Best Local Similarity 76.2%; Pred. No. 3e-07;
 Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 CYFSKKTNDINSHQTPKRTC 21
 92 CYFSKKTNDIDSHENTKRTC 112

RESULT 12
 US-09-732-210-453
 ; Sequence 453, Application US/097322210
 ; Patent No. 6573361

GENERAL INFORMATION:
 ; APPLICANT: Bunkers, Greg J.
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Mittanck, Cindy A.
 ; APPLICANT: Seale, Jeffrey W.
 ; APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 FILE REFERENCE: 38-21(15036)B
 CURRENT APPLICATION NUMBER: US/09/732,210
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,513
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: US 60/169,340
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 1753
 SEQ ID NO 453

LENGTH: 91
 TYPE: PRT
 ORGANISM: Marchantia polymorpha
 US-09-732-210-453

Query Match 41.3%; Score 50; DB 4; Length 91;
 Best Local Similarity 44.4%; Pred. No. 1.1;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

2 YFSKKTNDINSHQTPKRC 19
 42 FFNVKVISVSHRLPKKK 59

RESULT 13
 US-09-134-001C-2940
 ; Sequence 2940, Application US/09134001C
 ; Patent No. 6380370

GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 2940

LENGTH: 670
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-2940

Query Match 38.0%; Score 46; DB 4; Length 670;
 Best Local Similarity 63.6%; Pred. No. 40;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 CYFSKKTNDIN 11
 105 CYNKRTNDID 115

RESULT 14
 US-09-134-001C-3679
 ; Sequence 3679, Application US/09134001C
 ; Patent No. 6380370

GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 3679
 LENGTH: 366

TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3679

Query Match 37.6%; Score 45.5; DB 4; Length 366;
 Best Local Similarity 47.4%; Pred. No. 24;
 Matches 9; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

1 CYFSKKTNDINSHQTPKRC 19
 277 CFFS---NDLNIRTKTEK 292

RESULT 15
 US-09-724-623-63
 ; Sequence 63, Application US/09724623
 ; Patent No. 6476209

GENERAL INFORMATION:
 ; APPLICANT: Glenn, Matthew
 ; APPLICANT: Lubbers, Mark W
 ; APPLICANT: Dekker, James
 ; TITLE OF INVENTION: Polynucleotides, materials incorporating
 ; FILE REFERENCE: 104801
 ; CURRENT APPLICATION NUMBER: US/09/724,623

CURRENT FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 63
 LENGTH: 224
 TYPE: PRT
 ORGANISM: Lactobacillus rhamnosus
 US-09-724-623-63

Query Match 37.2%; Score 45; DB 4; Length 224;
 Best Local Similarity 37.5%; Pred. No. 17;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

6 KTNDINSHQTPKRTC 21
 81 RNDFAHQSPQSNK 96

Search completed: October 15, 2003, 17:08:30
 Job time : 17.0958 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 31.8144 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115A-10

Perfect score: 121
Sequence: 1 CYFSKKTNDINSHQTPKRTK.21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 60053 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 60053

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	93.4	89	15	US-10-002-784A-35
2	113	93.4	265	8	US-08-882-431-6
3	113	93.4	266	10	US-09-870-759-10
4	113	93.4	266	12	US-09-751-708A-10
5	113	93.4	266	15	US-10-002-784A-6
6	113	93.4	266	15	US-10-151-336-8
7	110	90.9	239	9	US-09-150-947B-12
8	110	90.9	239	12	US-10-172-425B-12
9	104	86.0	239	8	US-08-882-431-10
10	104	86.0	239	15	US-10-002-784A-10
11	104	86.0	265	8	US-08-882-431-8
12	104	86.0	266	15	US-10-002-784A-8
13	49	40.5	239	11	US-09-769-787-82
14	45.5	37.6	337	9	US-09-815-242-12565
15	45.5	37.6	360	9	US-09-815-242-5291

45	37.2	224	12	US-10-288-930-63	Sequence 63, Appl
16	37.2	247	14	US-10-042-417-36	Sequence 36, Appl
17	37.2	414	15	US-10-043-487-219	Sequence 219, App
18	37.2	414	15	US-10-128-714-3158	Sequence 3158, Ap
19	36.0	203	15	US-10-101-464A-780	Sequence 780, App
20	35.5	130	15	US-09-940-244-139	Sequence 139, App
21	35.1	382	11	US-10-290-386-139	Sequence 139, App
22	35.1	382	12	US-10-033-297-139	Sequence 139, App
23	35.1	382	14	US-09-809-391-399	Sequence 399, App
24	34.7	79	11	US-09-882-171-399	Sequence 399, App
25	34.7	1723	15	US-10-141-956-31	Sequence 31, Appl
26	34.7	96	9	US-09-925-299-1436	Sequence 1436, Ap
27	34.3	96	11	US-09-925-302-615	Sequence 615, App
28	34.3	171	9	US-09-533-029-2	Sequence 2, Appl
29	34.3	294	11	US-10-295-403-92	Sequence 92, Appl
30	34.3	294	15	US-10-278-536-130	Sequence 130, App
31	34.3	294	16	US-10-149-407-1	Sequence 1, Appl
32	34.3	838	12	US-10-149-407-4	Sequence 4, Appl
33	34.3	838	12	US-09-764-887-162	Sequence 162, App
34	34.3	59	9	US-10-073-961-162	Sequence 80, Appl
35	33.9	164	9	US-09-828-644-80	Sequence 80, Appl
36	33.9	487	9	US-09-925-302-667	Sequence 667, App
37	33.9	487	9	US-09-764-847-968	Sequence 968, App
38	33.1	55	10	US-10-092-154-968	Sequence 968, App
39	33.1	55	15	US-09-867-550-2018	Sequence 2018, Ap
40	33.1	73	9	US-09-764-891-3334	Sequence 3334, Ap
41	33.1	108	11	US-10-128-714-3405	Sequence 3405, Ap
42	33.1	489	15	US-10-128-714-8405	Sequence 8405, Ap
43	33.1	496	15	US-09-864-761-46473	Sequence 46473, A
44	33.1	601	9		
45	33.1				

ALIGNMENTS

RESULT 1
US-10-002-784A-35
; Sequence 35, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 35
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin B
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-35

Query Match 93.4%; Score 113; DB 15; Length 89;
Best Local Similarity 95.2%; Pred. No. 4.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CYFSKKTNDINSHQTPKRTK 21
Db 53 CYFSKKTNDINSHQTPKRTK 73
RESULT 2
US-08-882-431-6
; Sequence 6, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,

```
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-6

Query Match 93.4%; Score 113; DB 8; Length 265;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRKTC 21
Db 120 CYFSKKTNDINSHQTPKRKTC 140

RESULT 3
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-870-759-10

Query Match 93.4%; Score 113; DB 10; Length 266;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CVFSKKTNDINSHQTPKRKTC 21
Db 120 CVFSKKTNDINSHQTPKRKTC 140

RESULT 4
US-09-751-708A-10
; Sequence 10, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-751-708A-10

Query Match 93.4%; Score 113; DB 12; Length 266;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVFSKKTNDINSHQTPKRKTC 21
Db 120 CVFSKKTNDINSHQTPKRKTC 140

RESULT 5
US-10-002-784A-6
; Sequence 6, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 6
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B
; US-10-002-784A-6

Query Match 93.4%; Score 113; DB 15; Length 266;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVFSKKTNDINSHQTPKRKTC 21
Db 120 CVFSKKTNDINSHQTPKRKTC 140

RESULT 6
US-10-151-336-8
; Sequence 8, Application US/10151336
; Publication No. US20030079248A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
```


; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafirir
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/10/151,336
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/414,276
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-10-151-336-8

Query Match 93.4%; Score 113; DB 15; Length 266;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 120 CYFSKKTNDINSHQTPKRTKTC 140

RESULT 7

US-09-150-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-12

Query Match 90.9%; Score 110; DB 9; Length 239;
Best Local Similarity 90.5%; Pred. No. 3.5e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 93 CYFSKKTNDINSHQTPKRTKTC 113

RESULT 8

US-10-172-425B-12
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 056031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12

Query Match 90.9%; Score 110; DB 12; Length 239;
Best Local Similarity 90.5%; Pred. No. 3.5e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
Db 93 CYFSKKTNDINSHQTPKRTKTC 113

RESULT 9

US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 86.0%; Score 104; DB 8; Length 239;
Best Local Similarity 90.5%; Pred. No. 2.9e-08;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTKTC 21
| | | | | | | | | | | | | | | | | | | | | |

Query Match 40.5%; Score 49; DB 11; Length 299;
 Best Local Similarity 61.5%; Pred. No. 12;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 DINSHOTPKKTC 21
 Db 277 DLETHQTHKKVC 289
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 | : : : : : |

RESULT 14
 US-09-815-242-12565
 ; Sequence 12565, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12565
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-12565

Query Match 37.6%; Score 45.5; DB 9; Length 337;
 Best Local Similarity 47.4%; Pred. No. 47;
 Matches 9; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
 QY 1 CYFSKKTNDINSHOTPKRK 19
 Db 248 CFFS---NDLNIHRTKTEK 263
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 | : | | | : | : | : | : |

RESULT 15
 US-09-815-242-5291
 ; Sequence 5291, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5291
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-5291

Query Match 37.6%; Score 45.5; DB 9; Length 360;
 Best Local Similarity 47.4%; Pred. No. 50;
 Matches 9; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
 QY 1 CYFSKKTNDINSHOTPKRK 19
 Db 271 CFFS---NDLNIHRTKTEK 286
 | : | | | : | : | : | : |
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 Job time : 32.8144 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 15.9701 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115A-10

Perfect score: 121

Sequence: 1 CVFSKKTNDINSHQTPKRTK 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	93.4	266	1 ENSAB6	enterotoxin B prec
2	54	44.6	690	2 I51298	transforming prote
3	50	41.3	91	1 R5LV23	ribosomal protein
4	49.5	40.9	321	2 T06845	hypothetical prote
5	49	40.5	299	2 F98080	hypothetical prote
6	49	40.5	299	2 H95216	cation efflux syst
7	49	40.5	715	2 T04881	hypothetical prote
8	46	38.0	415	1 TVHUSA	transforming prote
9	46	38.0	482	2 C82871	glutamyl-tRNA synt
10	46	38.0	694	1 TVHUSN	transforming prote
11	45.5	37.6	366	2 D89941	conserved hypothet
12	45	37.2	315	2 C97007	hypothetical prote
13	45	37.2	488	2 S64140	hypothetical prote
14	44.5	36.8	603	2 T39574	hypothetical dnaJ
15	44	36.4	188	1 R5XU14	ribosomal protein
16	44	36.4	629	2 S31174	hypothetical prote
17	43.5	36.0	328	2 A89867	hypothetical prote
18	43	35.5	212	2 C71623	hypothetical prote
19	43	35.5	517	2 S49795	alpha-1,2-nanoovyl
20	43	35.5	553	2 S22354	finger protein zip
21	43	35.5	738	2 S40992	hypothetical prote
22	43	35.5	1026	2 T34506	hypothetical prote
23	43	35.5	1030	2 T37868	probable helicase
24	42.5	35.1	111	2 T17582	hypothetical prote
25	42.5	35.1	382	2 S22267	hypothetical prote
26	42.5	35.1	1740	2 T43773	hypothetical prote
27	42	34.7	191	2 B99315	hypothetical prote
28	42	34.7	218	2 T31642	hypothetical prote
29	42	34.7	325	2 I65354	stem cell antigen

30	42	34.7	371	2 T04971	hypothetical prote
31	42	34.7	381	2 C90395	DNA repair protein
32	42	34.7	382	2 I52565	stem cell antigen
33	42	34.7	435	2 AD1404	similar to phage p
34	42	34.7	447	2 H81368	probable helicase
35	42	34.7	464	2 S67069	hypothetical prote
36	42	34.7	484	2 A64251	glutamate-tRNA lig
37	42	34.7	500	1 EPFF	zip protein precu
38	42	34.7	553	2 I45067	steroid hormone re
39	42	34.7	561	2 T34083	hypothetical prote
40	42	34.7	597	2 F90481	conserved hypothet
41	42	34.7	612	2 T18848	hypothetical prote
42	42	34.7	925	2 T19361	hypothetical prote
43	42	34.7	968	2 T29532	hypothetical prote
44	42	34.7	1123	2 T28139	PK4 protein kinase
45	42	34.7	1345	2 T41960	major capsid prote

ALIGNMENTS

RESULT 1

ENSAB6

enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 18-Jun-1999

C:Accession: S27360; A92065; S27240; A01815

R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986

A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

A:Reference number: S27360; MUID:86168029; PMID:3957869

A:Accession: S27360

A:Molecule type: DNA

A:Residues: 1-266 <JON>

A:Cross-references: EMBL:M1118; NID:g152999; PIDN:AAA88550.1; PID:g153000

A:Experimental source: strain S6

R:Huang, I.Y. & Bergdoll, M.S.

J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide

A:Reference number: A92065; MUID:71007902; PMID:5470821

A:Accession: A92065

A:Molecule type: protein

A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT', 133

A:Experimental source: strain S-6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3511-3517, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition

A:Reference number: A92064; MUID:71007901; PMID:5470820

A:Contents: annotation; chymotryptic peptides

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3493-3510, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition

A:Reference number: A92063; MUID:71007900; PMID:5470819

A:Contents: annotation; tryptic peptides

R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A:Title: Purification of staphylococcal enterotoxin B.

A:Reference number: A90548; MUID:66035792; PMID:4953912

A:Contents: annotation; biological source of protein

R:Alakhov, V.Y.; Klinksky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni

Eur. J. Biochem. 209, 823-828, 1992

A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B

A:Reference number: S27240; MUID:93049338; PMID:1425690

A:Accession: S27240

A:Molecule type: protein

A:Residues: 28-42; 128-148 <ALA>

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin; extracellular protein; toxin

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-266/Product: enterotoxin B #status experimental <MAT>

F:120-140/Disulfide bonds: #status experimental

Query Match

93.4%; Score 113; DB 1; Length 266;

Best Local Similarity 95.2%; Pred. No. 1.3e-09; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRTK 21
DB 120 CYFSKKTNDINSHQTPKRTK 140

RESULT 2

transforming protein sno-N - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jul-2000
C:Accession: I51298; I51191
C:Givol, I.; Boyer, P.L.; Hughes, S.H.
Gene 156, 271-276, 1995
A:Title: Isolation and characterization of the chicken c-sno gene.
A:Reference number: I51298; MUID:95278756; PMID:7758967

A:Accession: I51298
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-690 <GV>
A:Cross-references: GB:S78406; NID:G999204; PIDN:AAD14280.1; PID:G4261980
R:Boyer, P.L.; Colmenares, C.; Stavnezer, E.; Hughes, S.H.
Oncogene 8, 457-466, 1993
A:Title: Sequence and biological activity of chicken snON cDNA clones.
A:Reference number: I51191; MUID:93149607; PMID:8426750
A:Accession: I51191
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-690 <BOY>
A:Cross-references: GB:S53899; NID:G264522; PIDN:AAB25175.1; PID:G264523
C:Genetics:

A:Gene: c-sno
A:Introns: 369/3; 482/1; 562/3; 637/3
C:Superfamily: ski transforming protein

Query Match 44.6%; Score 54; DB 2; Length 690;
Best Local Similarity 43.5%; Pred. No. 2.8; Mismatches 4; Indels 2; Gaps 1;

QY 1 CY--FSKKTNDINSHQTPKRTK 21
DB 297 CYGMFSPQIFVMSHSPDKRTK 319

RESULT 3

R51V23
ribosomal protein L23 - liverwort (Marchantia polymorpha) chloroplast
C:Species: chloroplast Marchantia polymorpha
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999
C:Accession: A02816; S01554; J50243

R:Ohyama, K.
submitted to the EMBL Data Library, October 1986
A:Reference number: A00150
A:Accession: A02816
A:Molecule type: DNA
A:Residues: 1-91 <OHY>
R:Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A:Title: Chloroplast gene organization deduced from complete sequence of liverwort March
A:Reference number: A38014
A:Contents: annotation; gene organization, sites, features
R:Fukuzawa, H.; Kohchi, T.; Sano, T.; Shirai, H.; Umesono, K.; Inokuchi, H.; Ozeki, H.;
J. Mol. Biol. 203, 333-351, 1988
A:Title: Structure and organization of Marchantia polymorpha chloroplast genome. III. Ge
A:Reference number: S01529; MUID:89068687; PMID:3199436
A:Accession: S01554
A:Molecule type: DNA
A:Residues: 1-91 <FUK1>
A:Cross-references: GB:X04465; GB:Y00686; NID:g11640; PIDN:CAA28128.1; PID:g11717
R:Fukuzawa, H.; Uchida, Y.; Yamano, Y.; Ohyama, K.; Komano, T.
Agric. Biol. Chem. 49, 2725-2731, 1985

A:Title: Molecular cloning of promoters functional in Escherichia coli from chloroplast
A:Reference number: A90020
A:Accession: JS0243
A:Molecule type: DNA
A:Residues: 1-91 <FUK2>
C:Genetics:
A:Gene: rpl23
A:Genome: chloroplast
C:Superfamily: Escherichia coli ribosomal protein L23
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 41.3%; Score 50; DB 1; Length 91;
Best Local Similarity 44.4%; Pred. No. 1.8; Mismatches 5; Indels 0; Gaps 0;

QY 2⁰YFSKKTNDINSHQTPKPK 19
DB 42 FFNVKVISVNSHRLPKKK 59

RESULT 4

T06845
hypothetical protein ycf39 - Cyanophora paradoxa cyanelle
C:Species: cyanelle Cyanophora paradoxa
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C:Accession: T06845
R:Stierwalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
submitted to the EMBL Data Library, July 1995
A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A:Reference number: Z15840
A:Accession: T06845
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-321 <STI>
A:Cross-references: EMBL:U30821; NID:G1016083; PIDN:AAA81188.1; PID:g1016101
A:Experimental source: cv. strain Pringsheim LB555
C:Genetics:
A:Gene: ycf39
A:Genome: cyanelle
C:Keywords: cyanelle

Query Match 40.9%; Score 49.5; DB 2; Length 321;
Best Local Similarity 50.0%; Pred. No. 6.7; Mismatches 4; Indels 3; Gaps 1;

QY 2 YFS---KKTNDINSHQTPKRT 20
DB 295 YFSRLKRLKEINSQSQSKKKT 316

RESULT 5

F98080
hypothetical protein czcd [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 06-Jan-2003
C:Accession: F98080
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98080
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00475.1; PID:g15459345; GSPDB:GN00174
C:Genetics:
A:Gene: czcd

C:Superfamily: zinc transporter Znt-2

Query Match 40.5%; Score 49; DB 2; Length 299;

```

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
R;Accession: S06054
R;C/Nomura, N.; Saeamoto, S.; Ishii, S.; Date, T.; Matsui, M.; Ishizaki, R.
Nucleic Acids Res. 17, 5489-5500, 1989
A;Title: Isolation of human cDNA clones of ski and the ski-related gene, sno.
A;Reference number: S06052; MUID:89345144; PMID:2762147
A;Accession: S06054
A;Molecule type: mRNA
A;Residues: 1-415 <NOM>
A;Cross-references: JMBL:X15217; NID:G36508; PIDN:CAA33287.1; PID:G36509
A;Note: the sequence from clone lambda-sno3 differs from that shown in having 38-Ala
C;Comment: Transforming protein sno-A may function as a transcription factor regulating
C;Genetics:
A;Gene: GDB:SNO
A;Cross-references: GDB:204117
C;Superfamily: ski transforming protein
C;Keywords: alternative splicing; proto-oncogene; transforming protein
F;369-381/Region: hydrophobic

Query Match      38.0%; Score 46; DB 1; Length 415;
Best Local Similarity 36.8%; Pred. No. 29;
Matches      7; Conservative      8; Mismatches      4; Indels      0; Gaps      0;

Qy      3 FSKKTNDINSHTPKRKC 21
      |:|:|:|:|:|:|
Db      298 FAPQTFVMSHRSRDPKRTC 316

RESULT 9
C82871

```

K; Glass, J.R.; Derkowitz, E.O.; Gibbs, J.S.; Reimer, C.R.; Chen, E.T.; Caspell, G.N.
 submitted to GenBank, February 2000
 A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A; Reference number: A82870
 A; Accession: C82871
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-482 <GIA>
 A; Cross-references: GB:AF222894; GB:AF222894; NID:G6899599; PIDN:AAF31013.1; GSPDB:GN001
 A; Experimental source: serovar 3, biovar 1
 C; Genetics:
 A; Gene: gltX; UU599
 A; Genetic code: SGC3
 C; Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

```

Query Match          38.0%; Score 46; DB 2; Length 482;
Best Local Similarity 44.0%; Prd. No. 33;
Matches 11; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

Qy 1 CYFSKKTNDIN-----SHQTPKPK 19
   | | | | | | | | | | | | | |
Db 106 CFCSEQLDADRELAEGSHQTPKPK 130

```

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RESULT 10
TVHUSN
transforming protein sno-N - human
N;Alternate names: ski-related novel gene, non-Alu-containing
N;Contains: transforming protein sno-I
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text_change 18-Jun-1999
C;Accession: S06052; S42108; S13508

```

Nucleic Acids Res. 17, 3483-3500, 1989
 A;Title: Isolation of human cDNA clones of ski and the ski-related gene, sno.
 A;Reference number: S06052; MUID:89345144; PMID:2762147
 A;Accession: S06052
 A;Molecule type: mRNA
 A;Residues: 1-684 <NOM>

Search completed: October 15, 2003, 17:06:21
Job time : 18.9701 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 8.5509 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115a-10
Perfect score: 121
Sequence: 1 CYFSKKTNDINSHQTPKRTC 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	113	93.4	266	1 ETXB_STAAU	P01552 staphylococ
2	50	41.3	91	1 RK23_MARPO	P06390 marchantia
3	49.5	40.9	321	1 YC39_CYPAA	P48279 cyanophora
4	49	40.5	629	1 SKIL_MOUSE	O60665 mus muscula
5	46.5	38.4	556	1 FLIF_BUCAP	O8ka45 buchnera ap
6	46	38.0	482	1 SYE_URSPA	O9ppp0 ureaplasma
7	46	38.0	684	1 SKIL_HUMAN	P12757 homo sapien
8	45	37.2	471	1 FBX3_HUMAN	O9uk99 homo sapien
9	45	37.2	488	1 YGM9_YEAST	O01163 saccharomyc
10	44	36.4	92	1 RK23_MESVI	O9mut8 mesostigma
11	44	36.4	187	1 RL18_XENLA	P02412 xenopus lae
12	44	36.4	503	1 SYK_EUCAP	O8k9c5 buchnera ap
13	43	35.5	517	1 KTR7_YEAST	P40504 saccharomyc
14	43	35.5	594	1 ZF37_MOUSE	P17141 mus musculu
15	43	35.5	1030	1 YE02_SCHPO	O13799 schizosacch
16	42.5	35.1	382	1 RA27_YEAST	P26793 saccharomyc
17	42	34.7	234	1 RB20_HUMAN	O9nx57 homo sapien
18	42	34.7	382	1 CD34_MOUSE	O64314 mus musculu
19	42	34.7	484	1 SYE_MYCGE	P47700 mycoplasma
20	42	34.7	488	1 UZ1P_DROME	P10379 drosophila
21	42	34.7	569	1 PYRD_PLAFA	O08210 plasmodium
22	42	34.7	588	1 NH23_CAEEL	P41828 caenorhabdi
23	42	34.7	1345	1 VCAP_HSV7J	P52347 human herpe
24	41.5	34.3	163	1 FK27_ARATH	O38936 arabidopsis
25	41.5	34.3	294	1 WR70_ARATH	O91y00 arabidopsis
26	41.5	34.3	309	1 YJ53_YEAST	P47129 saccharomyc
27	41.5	34.3	838	1 RN19_HUMAN	O9nv58 homo sapien
28	41	33.9	89	1 IAPP_HUMAN	P10997 homo sapien
29	41	33.9	326	1 AOX3_SOYBN	O03376 glycine max
30	41	33.9	366	1 APN1_YEAST	P22936 saccharomyc
31	41	33.9	467	1 YJEA_BACSU	O34798 bacillus su
32	41	33.9	477	1 YGJ1_ECOLI	P42590 escherichia
33	41	33.9	555	1 O16G_BACCO	O45101 bacillus co

34	41	33.9	778	1 RHP9_SCHPO	P87074 schizosacch
35	41	33.9	924	1 CC13_YEAST	P32797 saccharomyc
36	41	33.9	1041	1 UNB3_CAEEL	Q23064 caenorhabdi
37	41	33.9	1343	1 RPOB_BUCBP	Q89b20 buchnera ap
38	41	33.9	3178	1 YS89_CAEEL	Q09624 caenorhabdi
39	40	33.1	89	1 IAPP_CANFA	P17716 canis famli
40	40	33.1	451	1 ARF2_PLAFA	P13824 plasmodium
41	40	33.1	490	1 CAR3_DICDI	P35352 dictyosteli
42	40	33.1	621	1 GIDA_HELPJ	Q9zm19 helicobacte
43	40	33.1	621	1 GIDA_HELPJ	P56138 helicobacte
44	40	33.1	685	1 TRFE_PAROL	O93438 paralichthy
45	40	33.1	744	1 NSF_HUMAN	P46459 homo sapien
0	0	0	0	0	0

ALIGNMENTS

RESULT 1	ETXB_STAAU	STANDARD;	PRT;	266 AA.
ID	ETXB_STAAU	STANDARD;	PRT;	266 AA.
AC	P01552;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	13-AUG-1987	(Rel. 05, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Enterotoxin type B precursor (SEB).			
GN	ENTB.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86168029; PubMed=3957869;			
RA	Jones C.L., Khan S.A.;			
RT	"Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";			
RL	J. Bacteriol. 166:29-33 (1986).			
RN	[2]			
RP	SEQUENCE OF 40-91 FROM N.A.			
RX	MEDLINE=8529855; PubMed=3898073;			
RA	Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;			
RT	"Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854 (1985).			
RN	[3]			
RP	SEQUENCE OF 28-266 (S-6).			
RX	MEDLINE=71007902; PubMed=5470821;			
RA	Huang I.-Y., Bergdoll M.S.;			
RT	"The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";			
RL	J. Biol. Chem. 245:3518-3525 (1970).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).			
RX	MEDLINE=93063291; PubMed=1436058;			
RA	Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;			
RT	"Crystal structure of staphylococcal enterotoxin B, a superantigen.";			
RL	Nature 359:801-806 (1992).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.			
RX	MEDLINE=94203282; PubMed=8152483;			
RA	Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,			
RT	Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;			
RL	"Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";			
RN	Nature 368:711-718 (1994).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.			
RX	MEDLINE=99096298; PubMed=9881971;			
RA	Li H., Ilera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,			
RT	Karjalainen K., Mariuzza R.A.;			
RL	"Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B.";			
RL	Immunity 9:807-816 (1998).			

```

RN RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; M11118; AAA88550.1; -.
DR PIR; S27360; ENSAB6.
DR PDB; 1SEB; 20-JUN-96.
DR PDB; 2SEB; 28-JAN-98.
DR PDB; 3SEB; 27-MAY-98.
DR PDB; 1SE3; 16-JUN-97.
DR PDB; 1SE4; 15-OCT-97.
DR PDB; 1SEB; 04-MAR-99.
DR PDB; 1DSM; 14-MAR-01.
DR PDB; 1DSK; 28-JUN-00.
DR PDB; 1DSZ; 28-JUN-00.
DR PDB; 1DSE; 28-JUN-00.
DR InterPro; IPR006117; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN 2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE B.
FT DISULFID 120 140
FT CONFLICT 56 58 DDN -> NND (IN REF. 3).
FT CONFLICT 69 77 DQFLYFDLI -> NEFFDLIYL (IN REF. 3).
FT CONFLICT 118 118 MISSING (IN REF. 3).
FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
FT CONFLICT 133 135 QTD -> ENT (IN REF. 3).
FT CONFLICT 149 150 NG -> GN (IN REF. 3).
FT CONFLICT 156 156 Y -> YY (IN REF. 3).
FT CONFLICT 185 186 QE -> EQ (IN REF. 3).
FT CONFLICT 233 233 D -> N (IN REF. 3).
FT CONFLICT 245 247 DN -> ND (IN REF. 3).
FT STRAND 29 29
FT HELIX 41 43
FT TURN 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT TURN 90 94
FT STRAND 98 104
FT TURN 105 106
FT TURN 108 113
FT STRAND 116 116

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FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT HELIX 184 199
FT STRAND 209 218
FT TURN 219 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;

Query Matcho 93.4%; Score 113; DB 1; Length 266;
Best Local Similarity 95.2%; Pred.No. 3.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVFSKKTNDINSHQTPKRTKTC 21
   |||||
DB 120 CVFSKKTNDINSHQTPKRTKTC 140

RESULT 2
RK23 MARPO
ID RK23 MARPO STANDARD; PRT; 91 AA.
AC P06390;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chloroplast 50S ribosomal protein L23.
GN RPL23.
OS Marchantia polymorpha (Liverwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiaceae;
OC Marchantiaceae; Marchantia.
OX NCBI_TaxID=3197;
RN [1]_TaxID=3197;
RP SEQUENCE FROM N.A.
RX MEDLINE=89068687; PubMed=3199436;
RA Fukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H.,
RA Ozeki H., Ohyama K.;
RT "Structure and organization of Marchantia polymorpha chloroplast
RT genome. III. Gene organization of the large single copy region from
RT rbcL to trnI(CAU).";
RL J. Mol. Biol. 203:333-351(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
RA Ozeki H.;
RT "Chloroplast gene organization deduced from complete sequence of
RT liverwort Marchantia polymorpha chloroplast DNA.";
RL Nature 322:572-574(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Fukuzawa H., Uchida Y., Yamano Y., Ohyama K., Komano T.;
RT "Molecular cloning of promoters functional in Escherichia coli from
RT chloroplast DNA of a liverwort, Marchantia polymorpha.";
RL Agric. Biol. Chem. 49:2725-2731(1985).
CC -!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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RX MEDLINE=97351167; PubMed=9207045;
RA Pearson-White S., Crittenden R.;
RT "Proto-oncogene Snc expression, alternative isoforms and immediate
RL early serum response.";
RN Nucleic Acids Res. 25:2930-2937(1997).
RN [3]
RP SEQUENCE OF 13-684 FROM N.A. (ISOFORM SNOI), VARIANT ALA-38, AND
RP TISSUE SPECIFICITY.
RC MEDLINE=94051573; PubMed=8233802;
RA Pearson-White S.;
RT "Snc1, a novel alternatively spliced isoform of the ski proto-oncogene
RT homolog, snc1.";
RL Nucleic Acids Res. 21:4632-4638(1993).
CC -!- FUNCTION: May have regulatory role in cell division or
CC differentiation in response to extracellular signals.
CC -!- SUBUNIT: INTERACTS WITH SMAD2 AND SMAD3.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=SNON;
CC IsoId=P12757-1; Sequences=Displayed;
CC IsoId=P12757-2; Sequence=VSP_004392, VSP_004394;
CC Name=SNON2;
CC IsoId=P12757-3; Sequences=VSP_004395, VSP_004396;
CC Name=SNOI;
CC IsoId=P12757-4; Sequences=VSP_004393;
CC -!- TISSUE SPECIFICITY: SNON and SNOA isoforms are widely expressed.
CC Highest expression is found in skeletal muscle, followed by
CC placenta and lung. Lowest expression in heart, brain and pancreas.
CC Expression of isoform SNOI is restricted to skeletal muscle.
CC -!- SIMILARITY: TO THE SKI ONCOGENE.
CC -----
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CC -----
CC EMBL; X15219; CAA33289.1; -
CC DR EMBL; X15217; CAA33287.1; -
CC DR EMBL; U70730; AAB65850.1; -
CC DR EMBL; Z19588; CAA79636.1; -
CC DR PIR; S06052; TVHUSN.
CC DR PIR; S06054; TVHUSA.
CC TRANSFAC; T04642; -
CC DR Genew; HGNC:10897; SKIL.
CC MIM; 165340; -
CC DR GO; GO:0005634; C.nucleus; ISS.
CC DR GO; GO:0030154; P.cell differentiation; ISS.
CC DR InterPro; IPR003380; Transform_Ski.
CC DR Pfam; PF02437; Ski_Sno; 1.
CC KW Proto-oncogene; Alternative splicing; Polymorphism.
CC VARSPPLIC 367 415
CC TAPASMEIQSWPVVPIKQGDHVSQTHSPHPSYLYMCDK
CC VAPNVSL -> ASFLYQFLIMVYVFEMKILCVNLCM
CC LNAIHAATTKYLVLYCSF (in isoform SNOA).
CC /FTId=VSP_004392.
CC Missing (in isoform SNOI).
CC /FTId=VSP_004393.
CC Missing (in isoform SNOA).
CC /FTId=VSP_004394.
CC SK -> NA (in isoform SNON2).
CC /FTId=VSP_004395.
CC Missing (in isoform SNON2).
CC /FTId=VSP_004396.
CC V -> A.
CC /FTId=VAR_011677.
CC G -> R (IN REF. 3).
CC FT CONFLICT 13 13
CC FT SEQUENCE 684 AA; 77004 MW; 92AB80C7EB5F7AAE CRC64;
SQ
Query Match 38.0%; Score 46; DB 1; Length 684;

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Best Local Similarity 36.8%; Pred. No. 18;
Matches 7; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 3 PSKTKNDINSHOTPKRKTC 21
   | : | : | : | : | : |
DB 298 FAPQTFVWHSHRSPDKRTC 316

RESULT 8
FBX3 HUMAN
ID FBX3 HUMAN STANDARD; PRT; 471 AA.
AC Q9UK99; Q9NUX2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE F-box only protein 3.
GN FBX03 OR FBX3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RA "NEO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 6-415 FROM N.A.
RX MEDLINE=20003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins.";
RL Curr. Biol. 9:1180-1182(1999).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 F-box domain.
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CC -----
CC EMBL; AK001943; BAA91991.1; -
CC DR EMBL; AF176702; AAF03702.1; -
CC DR Genew; HGNC:13582; FBX03.
CC DR GO; GO:0004840; F.ubiquitin conjugating enzyme activity; TAS.
CC DR GO; GO:0004842; F.ubiquitin-protein ligase activity; TAS.
CC DR GO; GO:0006508; P.proteolysis and peptidolysis; TAS.
CC InterPro; IPR001810; F-box.
CC Pfam; PF04379; DUF525; 1.
CC Pfam; PF00646; F-box; 1.
CC SMART; SM00256; FBOX; 1.
CC PROSITE; PS0181; FBOX; 1.
CC Ubl conjugation.
FT DOMAIN 10 56 F-BOX.
FT DOMAIN 419 452 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 433 456 POLY-ARG.
FT DOMAIN 463 466 POLY-ARG.
FT CONFLICT 164 164 T -> A (IN REF. 2).
FT CONFLICT 414 415 EM -> VS (IN REF. 2).
SQ SEQUENCE 471 AA; 54590 MW; F7AA88193E14E67E CRC64;

Query Match 37.2%; Score 45; DB 1; Length 471;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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QY      1 CYPESKKTNDINSHQTPKRTK 21
Db      37 CYSVRLSQSHDPLWRRHC 57

RESULT 9
YGM9 YEAST
ID YGM9 YEAST STANDARD; PRT; 488 AA.
AC Q01163;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 55.6 kDa protein in CSE1-SOHI intergenic region.
GN YGL129C OR G2856.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96287651; PubMed=8686378;
RA Rodriguez-Belmonte E., Rodriguez Torres A.M., Tizon B., Cadahia J.L.,
RA Gonzalez-Siso I., Ramil E., Becerra M., Gonzalez-Dominguez M.,
RA Cerdan E.;
RT "Sequence analysis of a 10 kb DNA fragment from yeast chromosome VII
RT reveals a novel member of the DnaJ family.";
RL Yeast 12:145-148(1996).
RN [2]
RP SEQUENCE OF 39-488 FROM N.A.
RX STRAIN=DBY939;
RX MEDLINE=92250598; PubMed=1315757;
RA Shibagaki Y., Itoh N., Yamada H., Nagata S., Mizumoto K.;
RT "mRNA capping enzyme. Isolation and characterization of the gene
RT encoding mRNA guanylyltransferase subunit from Saccharomyces
RT cerevisiae.";
RL J. Biol. Chem. 267:9521-9528(1992).
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CC -----
DR EMBL; X87252; CAA60702.1; -
DR EMBL; 272651; CAA96838.1; -
DR EMBL; D10263; BAA01104.1; -
DR PIR; S64140; S64140.
DR SGD; S0003097; RSM23.
DR GO; GO:0005763; C-mitochondrial small ribosomal subunit; IDA.
DR GO; GO:0003735; F:structural constituent of ribosome; IDA.
DR GO; GO:0006412; P:protein biosynthesis; IDA.
KW Hypothetical protein; ATP-binding.
FT NP BIND 188 195 ATP (POTENTIAL).
SQ SEQUENCE 488 AA; 55562 MW; C5988A8858BEA18 CRC64;

Query Match 37.2%; Score 45; DB 1; Length 488;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      3 FSKKKTNDINSHQTPKRTK 20
Db      73 FSKKSSVSSYSKAKRT 90

RESULT 10
RK23 MESVI
ID RK23 MESVI STANDARD; PRT; 92 AA.
AC Q9MUT8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

QY      16-OCT-2001 (Rel. 40, Last annotation update)
DE Chloroplast 50S ribosomal protein L23.
GN RPL23.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AF166114; AAF43813.1; -
DR InterPro; IPR001014; Ribosomal_L23.
DR Pfam; PF00276; Ribosomal_L23; 1.
DR ProDom; PD001141; Ribosomal_L23; 1.
DR PROSITE; PS00050; RIBOSOMAL_L23; FALSE NEG.
KW Ribosomal protein; Chloroplast; rRNA-binding.
SQ SEQUENCE 92 AA; 10714 MW; A6BBADC44DC3DA27 CRC64;

Query Match 36.4%; Score 44; DB 1; Length 92;
Best Local Similarity 33.3%; Pred. No. 4.5;
Matches 6; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      2 YFSKKTNDINSHQTPKPK 19
Db      43 PFNVKVLNVNTHRPKPK 60

RESULT 11
RL18 XENLA
ID RL18 XENLA STANDARD; PRT; 187 AA.
AC P02412;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 60S ribosomal protein L18 (L14B).
GN RPL18 OR RPL14B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Oocyte;
RX MEDLINE=87040730; PubMed=3774540;
RA Beccari E., Mazzetti P., Mileo A.M., Bozzoni I., Pierandrei-Amaldi P.,
RA Amaldi P.;
RT "Sequences coding for the ribosomal protein L14 in Xenopus laevis and
RT Xenopus tropicalis; homologies in the 5' untranslated region are
RT shared with other r-protein mRNAs.";
RL Nucleic Acids Res. 14:7633-7646(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87146501; PubMed=3822843;
RA Beccari E., Mazzetti P.;
RT "The nucleotide sequence of the ribosomal protein L14 gene of Xenopus
RT laevis.";
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CC -----
CC EMBL; Z46728; CAA86709.1; -.
CC PIR; S49795; S49795.
CC SGD; S0001347; KTR7.
CC GO; GO:0007047; P:cell wall organization and biogenesis; IMP.
CC InterPro; IPR002685; Glyco trans_15.
CC Pfam; Pf01793; Glyco trans_15; 1.
CC Transferrase; Glycosyltransferase; Transmembrane; Signal-anchor;
CC Glycoprotein.
CC DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 24 44 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC DOMAIN 45 517 LUMENAL (POTENTIAL).
CC DOMAIN 45 85 STEM REGION (BY SIMILARITY).
CC DOMAIN 86 517 CATALYTIC (BY SIMILARITY).
CC ACT SITE 367 367 NUCLEOPHILE (POTENTIAL).
CC CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 517 AA; 61437 MW; 3E02FABA5456DEF CRC64;

Query Match 35.5%; Score 43; DB 1; Length 517;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTP 16

Db 458 CVCPRKGEDIEDHSTP 473

RESULT 14

ZFP37_MOUSE
ID ZFP37_MOUSE STANDARD; PRT; 594 AA.
AC F17141; Q62514;
DT 01-AUG-1990 (Rel. 15, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 37 (zfp-37) (Male germ cell specific zinc finger protein).
GN ZFP37 OR ZFP-37.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/CA, CBA/C57BL/6; TISSUE=Brain;
RX MEDLINE=96301401; PubMed=8660973;
RA Mazarakis N., Michalovich D., Karis A., Grosveld F., Galjart N.;
RT "zfp-37 is a member of the KRAB zinc finger gene family and is
RL expressed in neurons of the developing and adult CNS.";
RL Genomics 33:247-257(1996).
RN [2]
RP SEQUENCE OF 42-594 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=92310982; PubMed=1614869;
RA Burke P.S., Wolgemuth D.J.;
RT "zfp-37, a new murine zinc finger encoding gene, is expressed in a
RL developmentally regulated pattern in the male germ line.";
RL Nucleic Acids Res. 20:2827-2834(1992).
RN [3]
RP SEQUENCE OF 219-594 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=90301500; PubMed=21114017;
RA Nelki D., Dudley K., Cunningham P., Akhavan M.;
RT "Cloning and sequencing of a zinc finger cDNA expressed in mouse
RL testis".
RL Nucleic Acids Res. 18:3655-3655(1990).
CC -!- FUNCTION: MAY HAVE A ROLE IN REGULATING SPERMIOGENESIS.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND BRAIN.
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.

CC -!- SIMILARITY: Contains 1 KRAB domain.

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CC EMBL; X89264; CAA61539.1; -.
CC EMBL; X64413; CAA45758.1; -.
CC EMBL; X52533; CAA36769.1; ALT_INIT.
CC HSSP; R25490; IUBD.
CC MGD; MGI:99181; Zfp37.
CC InterPro; IPR001909; KRAB.
CC InterPro; IPR007087; Znf C2H2.
CC InterPro; IPR007086; Znf_C2H2_sub.
CC Pfam; PF01352; KRAB; 1.
CC Pfam; PF00096; zf-C2H2; 12.
CC PRINTS; PR00048; ZINC_FINGER.
CC ProDom; PD000003; Znf C2H2; 10.
CC SMART; SM00349; KRAB; 1.
CC SMART; SM00355; Znf C2H2; 12.
CC PROSITE; PS50805; KRAB; 1.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 11.
CC PROSITE; PS50157; ZINC_FINGER_C2H2_2; 12.

KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat; Developmental protein; Spermatogenesis.

FT DOMAIN 3 74 KRAB

FT ZN_FING 255 277 C2H2-TYPE.
FT ZN_FING 283 305 C2H2-TYPE.
FT ZN_FING 311 324 C2H2-TYPE.
FT ZN_FING 339 361 C2H2-TYPE.
FT ZN_FING 367 389 C2H2-TYPE.
FT ZN_FING 395 417 C2H2-TYPE.
FT ZN_FING 423 445 C2H2-TYPE.
FT ZN_FING 451 473 C2H2-TYPE.
FT ZN_FING 479 501 C2H2-TYPE.
FT ZN_FING 507 529 C2H2-TYPE.
FT ZN_FING 535 557 C2H2-TYPE.
FT ZN_FING 563 585 C2H2-TYPE.
FT CONFLICT 101 101 S -> T (IN REF. 1).
FT CONFLICT 572 572 F -> V (IN REF. 3).

SQ SEQUENCE 594 AA; 67254 MW; B6CA2F9F53B70455 CRC64;

Query Match 35.5%; Score 43; DB 1; Length 594;

Best Local Similarity 38.9%; Pred. No. 46;

Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 4 SKKTNDINSHQTPKRTK 21

Db 175 SHSASDVNKDEIPTRKC 192

RESULT 15

YE02_SCHPO
ID YE02 SCHPO STANDARD; PRT; 1030 AA.
AC O13759;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative helicase Cl7H9.02 (EC 3.6.1.-).
GN SPAC17H9.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vansreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Leirach H., Wambutt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McComb W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
CC -----
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CC -----
DR EMBL: Z98597; CAB11211.1; -.
DR FIR: T37868; T37868.
DR GenDB_SPombe; SPAC17H9.02; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
FT NP BIND 147 154 ATP (POTENTIAL).
FT SITE 238 241 DEVH BOX
SQ SEQUENCE 1030 AA; 118460 MW; 1E08BCE01118789 CRC64;
Query Match 35.5%; Score 43; DB 1; Length 1030;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 FSKKTNDINSHQTPK 17
Db 378 FSKKECEINAHQFGK 392

```

Search completed: October 15, 2003, 16:58:14
 Job time : 10.6509 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 43.006 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-10
Perfect score: 121
Sequence: 1 CYFSKKTNDINSHQTPRKTC 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	54	44.6	690	13 Q05951	Q05951 gallus gall
2	51	42.1	236	10 Q94KH9	Q94KH9 avicennia m
3	50	41.3	88	8 Q98451	Q98451 spirogyra m
4	49.5	40.9	1470	5 Q9VF24	Q9VF24 drosophila
5	49	40.5	299	16 Q97N22	Q97N22 streptococc
6	49	40.5	299	16 Q8DNK3	Q8DNK3 streptococc
7	49	40.5	715	10 Q49424	Q49424 arabidopsis
8	48	39.7	971	11 Q8CDJ7	Q8CDJ7 mus musculu
9	47	38.8	113	13 Q90VZ4	Q90VZ4 oreochromis
10	47	38.8	329	12 Q91QY8	Q91QY8 chinese whe
11	47	38.8	2379	5 Q8IQW3	Q8IQW3 plasmodium
12	46	38.0	389	6 Q8WMG9	Q8WMG9 aus scrofa
13	46	38.0	482	16 Q9PPP0	Q9PPP0 ureaplasma
14	46	38.0	674	11 Q90979	Q90979 mus musculu
15	45.5	37.6	366	16 Q99TQ2	Q99TQ2 staphylococ
16	45.5	37.6	366	16 Q8NWA0	Q8NWA0 staphylococ

17	45.5	37.6	366	16	Q8CSB9	Q8csb9 staphylococ
18	45	37.2	120	5	Q8T6A0	Q8t6a0 aplysia cal
19	45	37.2	131	13	Q9W6X7	Q9w6x7 oryzias lat
20	45	37.2	173	4	Q9UKC5	Q9ukc5 homo sapien
21	45	37.2	315	16	Q97KP7	Q97kp7 clostridium
22	45	37.2	471	4	Q9H0V2	Q9h0v2 homo sapien
23	45	37.2	1297	5	Q8IC22	Q8ic22 plasmodium
24	44.5	36.8	635	5	Q8IJY1	Q8ijy1 plasmodium
25	44	36.4	133	5	Q9BML2	Q9bml2 strongyloce
26	44	36.4	195	16	Q8CQZ3	Q8cqz3 staphylococ
27	44	36.4	501	5	Q8IKG6	Q8ikg6 plasmodium
28	44	36.4	629	5	Q07997	Q07997 chironomus
29	44	36.4	766	5	Q8T9E6	Q8t9e6 drosophila
30	44	36.4	1005	5	Q8IJK0	Q8ijk0 plasmodium
31	44	36.4	1463	5	Q9GYZ0	Q9gyz0 strongyloce
32	44	36.4	1843	5	Q8IC40	Q8ic40 plasmodium
33	44	36.4	1883	5	Q8ILJ0	Q8ilj0 plasmodium
34	44	36.4	2803	6	Q9XS53	Q9xs53 potorous tr
35	43.5	36.0	163	8	Q9SV98	Q9sv98 gymnostachy
36	43.5	36.0	328	16	Q95AX3	Q95ax3 staphylococ
37	43.5	36.0	328	16	Q8NXD5	Q8nxd5 staphylococ
38	43	35.5	73	4	Q9P145	Q9p145 homo sapien
39	43	35.5	234	10	Q94BR2	Q94br2 arabidopsis
40	43	35.5	257	5	Q8I3L9	Q8i3l9 plasmodium
41	43	35.5	302	5	Q96125	Q96125 plasmodium
42	43	35.5	433	12	Q91L91	Q91l91 white spot
43	43	35.5	526	11	Q8R1B1	Q8r1b1 mus musculu
44	43	35.5	531	10	Q9FLU1	Q9flul arabidopsis
45	43	35.5	537	13	Q8JHG0	Q8jhg0 brachydanio

ALIGNMENTS

RESULT 1

ID Q05951 PRELIMINARY; PRT; 690 AA.
AC Q05951;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SKI-related oncogene SNON.
GN C-SNO.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149607; PubMed=8426750;
RA Boyer P.L., Colmenares C., Stavnezer E., Hughes S.H.;
RT "Sequence and biological activity of chicken snON cDNA clones.";
RL Oncogene 8:457-466(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95278756; PubMed=7758967;
RA Givol I, Boyer P.L., Hughes S.H.;
RT "Isolation and characterization of the chicken c-sno gene.";
RL Gene 156:271-276(1995).
CC -!- SIMILARITY: TO H-SKI AND V-SKI ONCOGENES.
DR EMBL; S78406; AAD14280.1; JOINED.
DR EMBL; S78394; AAD14280.1; JOINED.
DR EMBL; S78395; AAD14280.1; JOINED.
DR EMBL; S78398; AAD14280.1; JOINED.
DR EMBL; S53899; AAB25175.1; JOINED.
DR InterPro; IPR003380; Transform_Ski.
DR Pfam; PF02437; Ski_Sno; 1..
KW Oncogene.
SQ SEQUENCE 690 AA; 78143 MW; 8D48977D477D349F CRC64;

Query Match 44.6%; Score 54; DB 13; Length 690;
Best Local Similarity 43.5%; Pred. No. 3.8;

RT	"Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";			
RT	KL	Science 293:498-506(2001).		
DR	ENBL; AE007477; AAK75929.1; -.			
DR	TIGR; SPL857; -.			
DR	InterPro; IPR002524; Cation_efflux.			
DR	Pfam; PF01545; Cation_efflux; 1.			
DR	TIGRFAMs; TIGR01297; CDF; 1.			
KW	Complete proteome.			
Q	SEQUENCE 299 AA; 33528 MW; 62C23A92323E23DB CRC64;			
	Query Match	40.5%;	Score 49; DB 16; Length 299;	
	Best Local Similarity	61.5%;	Pred. No. 10;	
	Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;			
QY	9 DINSHOTPKRKTC 21			
	:-:			
Db	277 DLETHQTHKRKVC 289			
	:-:			
RESULT 6				
Q8DNK3	PRELIMINARY; PRT; 299 AA.			
ID	Q8DNK3			
AC	Q8DNK3;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Cation diffusion facilitator transporter-heavy metal transport.			
GN	CZCD OR SPRI672.			
OS	Streptococcus pneumoniae (strain ATCC BAA-255 / R6).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=171101;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21429245; PubMed=11544234;			
RA	Hoskins J., Alborn W.B. Jr., Arnold J., Blaszcak L.C., BURGESS S.,			
RA	DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,			
RA	Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,			
RA	LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,			
RA	McAhen S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,			
RA	Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,			
RA	Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,			
RA	Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,			
RA	Glass J.I.;			
RT	"Genome of the bacterium Streptococcus pneumoniae strain R6.";			
RL	J. Bacteriol. 183:5709-5717(2001).			
DR	ENBL; AE008532; AAL00475.1; -.			
KW	Complete proteome.			
Q	SEQUENCE 299 AA; 33528 MW; 62C23A92323E23DB CRC64;			
	Query Match	40.5%;	Score 49; DB 16; Length 299;	
	Best Local Similarity	61.5%;	Pred. No. 10;	
	Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;			
QY	9 DINSHOTPKRKTC 21			
	:-:			
Db	277 DLETHQTHKRKVC 289			
	:-:			
RESULT 7				
Q49424	PRELIMINARY; PRT; 715 AA.			
ID	Q49424			
AC	Q49424;			
DT	01-JUN-1998 (TrEMBLrel. 06, Created)			
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Hypothetical 82.1 kDa protein.			
GN	F18F4.70 OR AT4G19970			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.			

```

OX NCBI_TaxID=3702;
RN [1] SEQUENCE FROM N.A.
RP Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
RA Bancroft I., Mewes H.W., Mayer K., Schueller C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2] SEQUENCE FROM N.A.
RP Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3] SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021637; CAA1605.1; -
DR EMBL; AL161552; CAB78997.1; -
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 2.
KW Hypothetical protein.
SQ SEQUENCE 715 AA; 82075 MW; E7E1EFFBD3B5211A CRC64;

Query Match 40.5%; Score 49; DB 10; Length 715;
Best Local Similarity 47.4%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRX 19
Db 79 CYASKLTNESSSKTEPKKE 97

RESULT 8
Q8CDJ7 PRELIMINARY; PRT; 971 AA.
ID Q8CDJ7;
AC Q8CDJ7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical RNA-binding region RNP-1 (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK029961; BAC26701.1; -
DR InterPro; IPR001064; Crystallin.
KW Hypothetical protein.
FT NON TER 971
SQ SEQUENCE 971 AA; 108726 MW; B82DA55E5027C9B CRC64;

Query Match 39.7%; Score 48; DB 11; Length 971;
Best Local Similarity 52.8%; Pred. No. 48;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CYFSKKTNDINSHQTPKRX 19
Db 627 CQPAKKVDPNHPQPRQ 645

RESULT 9
Q90VZ4 PRELIMINARY; PRT; 113 AA.
ID Q90VZ4;
AC Q90VZ4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Follicle stimulating hormone beta subunit.
OS Plasmodium falciparum (isolate 3D7).

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OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8127;
RN [1] SEQUENCE FROM N.A.
RP Rosenfeld H., Levavi-Sivan B., Gur G., Melamed P., Meiri I., Yaron Z.,
RA Elizur A.;
RT "Characterization of tilapia FSHb gene and analysis of its 5'-flanking
RT region.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289174; AAK83080.1; -
DR EMBL; AF289173; AAK83079.1; -
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
SQ SEQUENCE 113 AA; 12389 MW; 500285A9FDBF231D CRC64;

Query Match 38.8%; Score 47; DB 13; Length 113;
Best Local Similarity 47.4%; Pred. No. 8.3;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 FSKKTNDINSHQTPKRTK 21
Db 48 FQDENFIHTDDWPKQKTC 66

RESULT 10
Q91QY8 PRELIMINARY; PRT; 329 AA.
ID Q91QY8;
AC Q91QY8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Movement protein.
OS Chinese wheat mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Furovirus.
OX NCBI_TaxID=83544;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=Rongcheng;
RA Yang J., Chen J., Chen J., Jiang H., Zhao Q., Adams M.J.;
RT "Sequence of a second isolate of Chinese wheat mosaic furovirus.";
RL J. Phytopathol. 149:135-140(2001).
DR EMBL; AJ271838; CAC39428.1; -
DR InterPro; IPR000603; 3A_mov.
DR Pfam; PF00803; 3A; 1.
SQ SEQUENCE 329 AA; 37364 MW; 2285379946336A6F CRC64;

Query Match 38.8%; Score 47; DB 12; Length 329;
Best Local Similarity 35.0%; Pred. No. 24;
Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 YFSKKTNDINSHQTPKRTK 21
Db 172 YWTRQGDHSSYSEFORSTC 191

RESULT 11
Q81JW3 PRELIMINARY; PRT; 2379 AA.
ID Q81JW3;
AC Q81JW3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF10_0078.
OS Plasmodium falciparum (isolate 3D7).

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RC STRAIN=3D7;
RX SEQUENCE FROM N.A.
RL MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McCadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrall B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum";
RL Nature 419:498-511(2002).
DR EMBL; AEO14830; AAN35276.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2379 AA; 282225 MW; 9CE33F320CD8B5D1 CRC64;

Query Match 38.8%; Score 47; DB 5; Length 2379;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 YFSKKTNDINSHQTPKPK 19
| | | | | | | | | | | | | | | | | | | | |
DB 187 YIKKINEINYFIQKK 204
| | | | | | | | | | | | | | | | | | | | |

RESULT 12
Q8WMG9 PRELIMINARY; PRT; 389 AA.
AC Q8WMG9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CD34 antigen.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RC TISSUE=Mesenteric lymph node;
RA Sun J., Butler J.E.;
RT "Cloning, sequencing and expression of swine CD34 gene.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461503; AAL67838.1; -.
SQ SEQUENCE 389 AA; 40544 MW; 8B1BEE7F045F3C5 CRC64;

Query Match 38.0%; Score 46; DB 6; Length 389;
Best Local Similarity 52.8%; Pred. No. 41;
Matches 10; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 2 YFSKKTNDINSHQTPKPK 20
| | | | | | | | | | | | | | | | | | | | |
DB 278 HFSKQ--DVRSHQSYRK 294
| | | | | | | | | | | | | | | | | | | | |

RESULT 13
Q9PPPO PRELIMINARY; PRT; 482 AA.
AC Q9PPPO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutamy1-tRNA synthetase.
GN GLTX OR UUS99.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
```

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RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Setovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum.";
RL Nature 407:757-762(2000).
DR EMBL; AE002158; AAF31013.1; -.
DR InterPro; IPR004527; GLTX_bact.
DR InterPro; IPR000524; GLU_trna-synt_1c.
DR Pfam; PF00749; tRNA-synt_1c; 1.
DR PRINTS; PRO0987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Complete proteome.
SQ SEQUENCE 482 AA; 55908 MW; 3977C1BCFA31C16C CRC64;

Query Match 38.0%; Score 46; DB 16; Length 482;
Best Local Similarity 44.0%; Pred. No. 50;
Matches 11; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

QY 1 CYFSKKTNDIN-----SHQTPKPK 19
| | | | | | | | | | | | | | | | | | | | |
DB 106 CFCSEQLDADRELAEKSHQTPKPK 130
| | | | | | | | | | | | | | | | | | | | |

RESULT 14
Q60979 PRELIMINARY; PRT; 674 AA.
AC Q60979; Q64741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SKI-like protein SKIL (SKI/SNO related protein).
GN SKIL OR SKIR OR SNO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=SWISS WEBSTER; TISSUE=Trunk;
RX MEDLINE=97351167; PubMed=9207045;
RA Pearson-White S., Crittenden R.;
RT "Proto-oncogene SNO expression, alternative isoforms and immediate
RT early serum response.";
RL Nucleic Acids Res. 25:2930-2937(1997).
RN [2]
RC SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=Brain, and Heart;
RX MEDLINE=96431390; PubMed=8834472;
RA Pelzer T., Lyons G.E., Kim S., Moreadith R.W.;
RT "Cloning and characterization of the murine homolog of the sno proto-
RT oncogene reveals a novel splice variant.";
RL Dev Dyn. 205:114-125(1996).
CC -!- FUNCTION: MAY HAVE REGULATORY ROLE IN CELL DIVISION OR
CC DIFFERENTIATION IN RESPONSE TO EXTRACELLULAR SIGNALS.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYO, NEONATE AND ADULT.
CC -!- SIMILARITY: TO THE SKI ONCOGENE.
DR EMBL; U36203; AAB65848.1; -.
DR EMBL; U10532; AAB50267.1; -.
DR EMBL; U10531; AAB50584.1; -.
DR MGI; MGI:106203; Skil.
DR InterPro; IPR003380; Transform_Ski.
DR Pfam; PF02437; Ski_Sno; 1.
KW Proto-oncogene.
FT CONFLICT 63 65 RAR -> GEHA (IN REF. 2).
FT CONFLICT 129 129 T -> P (IN REF. 2).
FT CONFLICT 149 149 T -> S (IN REF. 2).
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115a-11
Perfect score: 102
Sequence: 1 CYFSSKDNVGVTKGKTC 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	18	20	Staphylococcal gro
2	102	100.0	18	24	Staphylococcal ent
3	102	100.0	18	24	Staphylococcal ent
4	102	100.0	238	12	Staphylococcal ent
5	102	100.0	238	14	Staphylococcal ent
6	102	100.0	238	22	Staphylococcus aur
7	102	100.0	238	23	Staphylococcus aur
8	102	100.0	239	12	Staphylococcal ent
9	102	100.0	239	14	Staphylococcal ent

10	102	100.0	239	20	AA06255	Staphylococcal gro
11	102	100.0	239	20	AA06256	Staphylococcal gro
12	102	100.0	239	20	AA06251	Staphylococcal gro
13	102	100.0	239	20	AA06252	Staphylococcal gro
14	102	100.0	239	20	AA06253	Staphylococcal gro
15	102	100.0	239	22	AA067342	Staphylococcus aur
16	102	100.0	239	23	ABB76238	Staphylococcus aur
17	102	100.0	240	24	ABG71367	Staphylococcal ent
18	102	100.0	240	24	ABG71368	Staphylococcal ent
19	102	100.0	240	24	ABG71369	Staphylococcal ent
20	102	100.0	240	24	ABG71371	Staphylococcal ent
21	102	100.0	240	24	ABG71372	Staphylococcal ent
22	102	100.0	266	21	AA070108	Staphylococcal ent
23	102	100.0	266	23	ABB79507	Staphylococcal SEC
24	96	94.1	18	20	AA06250	Staphylococcal ent
25	96	94.1	18	24	ABG71378	Staphylococcal ent
26	96	94.1	239	20	AA06254	Staphylococcal gro
27	96	94.1	239	20	AA06257	Staphylococcal gro
28	96	94.1	240	24	ABG71370	Staphylococcal ent
29	96	94.1	240	24	ABG71373	Staphylococcal ent
30	93	91.2	18	24	ABG71379	Staphylococcal ent
31	87	85.3	239	20	AA06258	Staphylococcal gro
32	87	85.3	240	24	ABG71374	Staphylococcal ent
33	66	64.7	14	20	AA06259	Staphylococcal ent
34	66	64.7	14	24	ABG71381	Staphylococcal ent
35	47	46.1	77	21	AA061245	Arabidopsis thalia
36	47	46.1	103	21	AA061244	Arabidopsis thalia
37	46	45.1	374	20	AA043983	Human alcohol dehy
38	46	45.1	374	20	AA043984	Human alcohol dehy
39	46	45.1	375	23	ABG79657	Invertebrate forag
40	46	45.1	395	21	AA058159	Lung cancer associ
41	45	44.1	277	23	ABB97515	Novel human protei
42	45	44.1	513	22	AA073600	Zinc finger protei
43	44	43.1	299	21	AA06436	Arabidopsis thalia
44	44	43.1	315	21	AA06435	Arabidopsis thalia
45	44	43.1	340	21	AA06434	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AA06249
ID AA06249 standard; Peptide; 18 AA.
XX
AC AA06249;
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group C enterotoxin disulfide loop.
XX
KW Enterotoxin; SEC1; SEC2; SEC3 FRI 913; SEC3 4446; SEC-Bovine;
KW SEC-Ovine; toxin; disulfide loop; protein engineering.
XX
OS Staphylococcus aureus.
XX
PN WO927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25107.
XX
PR 02-DEC-1997; 97US-0067357.
XX
PA (IDAH-) JDAHO RES FOUND INC.
XX
PI Bohach GI;
XX
DR WPI; 1999-358008/30.
XX
N-PSDB; AA058884.
XX
Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 3; 25pp; English.

XX This peptide corresponds to the disulfide loop, i.e. amino acids

CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,

CC SEC3 FRI 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AAY06251-53

CC and AAY06255-58). The invention relates to pyrogenic toxins, such as

CC staphylococcal enterotoxins, modified in the disulfide loop region.

CC Typically, the modification involves deletions within the disulfide

CC loop region of SEC (see AAY06261). The modified toxins retain useful

CC biological properties, such as the ability to induce cytokine

CC production, but have substantially reduced toxicity compared to the

CC corresponding unmodified native toxin. Emetic response inducing

CC activity and fever inducing activity are typically decreased by at

CC least about 100-fold, while LD50 (in Dutch Belted rabbits) is at

CC least 100-fold higher than the native toxin.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 102; DB 20; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18

Db 1 CYFSSKDNVKGVTGGKTC 18

RESULT 2

ABG71377

ID ABG71377 standard; Peptide; 18 AA.

XX

AC ABG71377;

XX

DT 29-JAN-2003 (first entry)

XX

DE Staphylococcal enterotoxin disulphide loop region.

XX

KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;

KW emetic response-inducing activity; staphylococcal enterotoxin;

KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;

KW SEC1; SEC2; SEC3-FRI913; SEC-4446; SEC-bovine.

XX

OS Staphylococcus aureus.

XX

XX WO200283169-A1.

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-US11619.

XX

PR 13-APR-2001; 2001US-283720P.

XX

PA (IDAH-) IDAHO RES FOUND INC.

XX

PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;

XX

DR WPI; 2003-058608/05.

DR N-PSDB; ABS56822.

XX

PT New modified staphylococcal enterotoxin derived from a native disulfide

PT loop-containing pyrogenic toxin, useful for non-specifically enhancing

PT an immune function and as a vaccine against toxic shock syndrome or

PT food poisoning -

XX

PS Example 1; Fig 1; 67pp; English.

XX

CC The invention relates to a modified pyrogenic toxin derived from a native

CC disulphide loop-containing pyrogenic toxin where the modified toxin

CC comprises a disulphide loop having no more than 10 amino acids. The

CC modified toxin has a fever-inducing activity or an emetic

CC response-inducing activity decreased by about 100-fold in comparison to a

CC native toxin. The modified pyrogenic toxin, that is a staphylococcal

CC enterotoxin, is useful for non-specifically enhancing an immune function

CC and for vaccination against diseases such as toxic shock syndrome and

CC food poisoning. This sequence represents a staphylococcal enterotoxin

CC protein fragment.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 102; DB 24; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18

Db 1 CYFSSKDNVKGVTGGKTC 18

RESULT 3

ABG71380

ID ABG71380 standard; Peptide; 18 AA.

XX

AC ABG71380;

XX

DT 29-JAN-2003 (first entry)

XX

DE Staphylococcal enterotoxin C1 (SEC1) protein fragment.

XX

KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;

KW emetic response-inducing activity; staphylococcal enterotoxin; SEC1;

KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.

XX

OS Staphylococcus aureus.

XX

XX WO200283169-A1.

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-US11619.

XX

PR 13-APR-2001; 2001US-283720P.

XX

PA (IDAH-) IDAHO RES FOUND INC.

XX

PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;

XX

DR WPI; 2003-058608/05.

DR N-PSDB; ABS56822.

XX

PT New modified staphylococcal enterotoxin derived from a native disulfide

PT loop-containing pyrogenic toxin, useful for non-specifically enhancing

PT an immune function and as a vaccine against toxic shock syndrome or

PT food poisoning -

XX

PS Example 1; Fig 1; 67pp; English.

XX

CC The invention relates to a modified pyrogenic toxin derived from a native

CC disulphide loop-containing pyrogenic toxin where the modified toxin

CC comprises a disulphide loop having no more than 10 amino acids. The

CC modified toxin has a fever-inducing activity or an emetic

CC response-inducing activity decreased by about 100-fold in comparison to a

CC native toxin. The modified pyrogenic toxin, that is a staphylococcal

CC enterotoxin, is useful for non-specifically enhancing an immune function

CC and for vaccination against diseases such as toxic shock syndrome and

CC food poisoning. This sequence represents a staphylococcal enterotoxin

CC protein fragment.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 102; DB 24; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18

Db 1 CYFSSKDNVKGVTGGKTC 18

RESULT 4
AAR13208
ID AAR13208 standard; Protein; 238 AA.
XX
AC AAR13208;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C3.
XX
KW SEC3; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1991; 91WO-US000342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SEC3 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
XX
CC See AAR13203-R13211.
XX
SQ Sequence 238 AA;

Query Match 100.0%; Score 102; DB 12; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
||| ||||| ||||| |||||
DB 92 CYFSSKDNVKGVTGGKTC 109

RESULT 5
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
AC AAR45016;
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEC3.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX

PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US05213.
XX
PR 01-JUN-1992; 92US-0891718.
XX
PA (STON/) STONE J L.
PA (TERM/) Terman D S.
XX
PI Stone JL, Terman DS;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumoricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumoricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 238 AA;

Query Match 100.0%; Score 102; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
0 ||||| ||||| |||||
DB 92 CYFSSKDNVKGVTGGKTC 109

RESULT 6
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
AC AAB67343;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin C3 protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-0183437.
XX
PR 31-JAN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91WO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX

DR WPI; 2001-158657/16.
 XX
 PT Tumor cell capable of stimulating antitumor immune reactivity in vitro
 PT or in vivo comprises exogenous nucleic acids encoding a superantigen
 PT and a costimulatory molecule -
 XX
 PS Disclosure; Fig 2; 16pp; English.
 XX
 CC The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule
 CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 XX
 SQ Sequence 238 AA;
 Query Match 100.0%; Score 102; DB 22; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGVTGGKTC 18
 Db |||||
 92 CYFSSKDNVKGVTGGKTC 109
 RESULT 7
 ABB76239
 ID ABB76239 standard; Protein; 238 AA.
 XX
 AC ABB76239;
 XX
 XX 09-AUG-2002 (first entry)
 DT Staphylococcus aureus enterotoxin C3.
 DE
 DE Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
 KW antitumour; therapy.
 KW
 XX Staphylococcus aureus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 208
 FT /note= "given as 'O' in the specification"
 FT
 XX US2002051765-A1.
 PN
 XX 02-MAY-2002.
 PD
 XX 19-DEC-2000; 2000US-0741503.
 PF
 XX 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 XX (TERM/) Terman D S.
 PA
 XX Terman DS;
 PI
 XX WPI; 2002-415198/44.
 DR
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens -
 XX
 XX Disclosure; Fig 2; 17pp; English.
 PS
 XX

CC The present sequence is the protein sequence of enterotoxin C3
 CC (SEC3) of Staphylococcus aureus. Similarity is shown, in several
 CC stretches of sequence, between staphylococcal enterotoxins,
 CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative
 CC toxins (see ABB76234-44). In the present invention, synthetic
 CC polypeptides useful in tumour therapy and in blocking or destroying
 CC autoreactive T and B lymphocyte populations are characterised by
 CC substantial structural homology to staphylococcal enterotoxin A and
 CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
 CC statistically significant sequence homology and similarity (Z value
 CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
 CC 6) to include alignment of cysteine residues and similar hydropathy
 CC profiles. These superantigens are used to treat solid tumours,
 CC including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient
 CC with one or more superantigens ex vivo to generate stimulated cells,
 CC selecting a specific V beta subset of cells, and reintroducing
 CC these cells into the patient to induce an in vivo therapeutic,
 CC tumoricidal reaction.
 XX
 SQ Sequence 238 AA;
 Query Match 100.0%; Score 102; DB 23; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGVTGGKTC 18
 Db |||||
 92 CYFSSKDNVKGVTGGKTC 109
 RESULT 8
 AAR13207
 ID AAR13207 standard; Protein; 239 AA.
 XX
 AC AAR13207;
 XX
 XX 15-OCT-1991 (first entry)
 DT Staphylococcal enterotoxin C1.
 XX
 DE SEC1; cancer treatment; pyrogen; tumouricide.
 KW
 XX Staphylococcus aureus.
 OS
 XX WO9110680-A.
 PN
 XX 25-JUL-1991.
 PD
 XX 17-JAN-1991; 91WO-US00342.
 PF
 XX 17-JAN-1990; 90US-0466577.
 PR (TERM/) Terman D S.
 XX
 XX Terman DS;
 PI
 XX WPI; 1991-237984/32.
 DR
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 XX
 XX Disclosure; Fig 1; 74pp; English.
 PS
 XX SEC1 was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEC1. Synthetic
 CC polypeptides having structural homology to staphylococcal
 CC are claimed, provided the homology includes statistically

CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydropathy profiles.
 CC See AAR13203-R13211.

SQ Sequence 239 AA;

Query Match 100.0%; Score 102; DB 12; Length 239;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
 |||||
 DB 93 CYFSSKDNVKGVTGGKTC 110

RESULT 9

AAR45015
 ID AAR45015 standard; protein; 239 AA.

XX AC AAR45015;

XX DT 25-MAR-2003 (updated)
 DT 08-JUN-1994 (first entry)

XX DE Staphylococcal enterotoxin SEC1.

XX KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.

XX OS Staphylococcus aureus.

XX PN W09324136-A1.

XX PD 09-DEC-1993.

XX PF 01-JUN-1993; 93WO-US05213.

XX PR 01-JUN-1992; 92US-0891718.

XX PA (STONE/) STONE J L.

XX PA (TERM/) TERMAN D S.

XX PI Stone JL, Terman DS;

XX DR WPI; 1993-405418/50.

XX PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases

XX PS Disclosure; Fig 1; 90pp; English.

XX CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 239 AA;

Query Match 100.0%; Score 102; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
 |||||
 DB 93 CYFSSKDNVKGVTGGKTC 110

RESULT 10

AAY06255

ID AAY06255 standard; Protein; 239 AA.

XX AC AAY06255;

XX DT 23-AUG-1999 (first entry)

XX DE Staphylococcal group C enterotoxin SEC-MNCopeland.

XX KW Enterotoxin; SEC-MNCopeland; toxin; disulfide loop;
 KW protein engineering.

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

FT Disulfide-bond 93..110

XX PN W09927889-A2.

XX PD 10-JUN-1999.

XX PF 01-DEC-1998; 98WO-US25107.

XX PR 02-DEC-1997; 97US-0067357.

XX PA (IDAH-) IDAHO RES FOUND INC.

XX PI Bohach GI;

XX DR WPI; 1999-358008/30.

XX PT Non-toxic modified staphylococcal enterotoxins

XX PS Disclosure; Page 17; 25pp; English.

XX CC This protein represents the Staphylococcus aureus type C
 CC enterotoxin SEC-MNCopeland. The invention relates to pyrogenic
 CC toxins, such as staphylococcal enterotoxins, modified in the
 CC disulfide loop region. Typically, the modification involves
 CC deletions within the disulfide loop region of SEC (see AAY06261).
 CC The modified toxins retain useful biological properties, such as
 CC the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native
 CC toxin. Emetic response inducing activity and fever inducing
 CC activity are typically decreased by at least about 100-fold, while
 CC LD50 (in Dutch Belted rabbits) is at least 100-fold higher than
 CC the native toxin.

XX SQ Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18

|||||

DB 93 CYFSSKDNVKGVTGGKTC 110

RESULT 11

AAY06256

ID AAY06256 standard; Protein; 239 AA.

XX AC AAY06256;

XX DT 23-AUG-1999 (first entry)

XX DE Staphylococcal group C enterotoxin SEC-4446.

XX KW Enterotoxin; SEC-4446; toxin; disulfide loop;
 KW protein engineering.

XX OS Staphylococcus aureus.

```

XX Key Location/Qualifiers
FH Disulfide-bond 93..110
PT WO9927889-A2.
PN 10-JUN-1999.
PD 01-DEC-1998; 98WO-US25107.
PF 02-DEC-1997; 97US-0067357.
PR (IDAH-) IDAHO RES FOUND INC.
XX PA Bohach GI;
XX WPI; 1999-358008/30.
XX Non-toxic modified staphylococcal enterotoxins
PT Disclosure; Page 17; 25pp; English.
PS This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC1. The invention relates to pyrogenic toxins,
CC such as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.
XX Sequence 239 AA;
SQ Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGVTGGKTC 18
DB 93 CYPSSKDNVKGVTGGKTC 110

RESULT 12
AAY06251
ID AAY06251 standard; Protein; 239 AA.
XX AC AAY06251;
XX DT 23-AUG-1999 (first entry)
XX DE Staphylococcal group C enterotoxin SEC1.
XX KW Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FT Disulfide-bond 93..110
PN WO9927889-A2.
PD 10-JUN-1999.
PF 01-DEC-1998; 98WO-US25107.
XX PF 02-DEC-1997; 97US-0067357.
XX PR (IDAH-) IDAHO RES FOUND INC.
XX PA Bohach GI;
XX PI Bohach GI;
XX WPI; 1999-358008/30.
XX Non-toxic modified staphylococcal enterotoxins
PT Disclosure; Page 17; 25pp; English.
PS This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC2. The invention relates to pyrogenic toxins, such
CC as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.
XX Sequence 239 AA;
SQ Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGVTGGKTC 18
DB 93 CYPSSKDNVKGVTGGKTC 110

RESULT 13
AAY06252
ID AAY06252 standard; Protein; 239 AA.
XX AC AAY06252;
XX DT 23-AUG-1999 (first entry)
XX DE Staphylococcal group C enterotoxin SEC2.
XX KW Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FT Disulfide-bond 93..110
PN WO9927889-A2.
PD 10-JUN-1999.
PF 01-DEC-1998; 98WO-US25107.
XX PF 02-DEC-1997; 97US-0067357.
XX PR (IDAH-) IDAHO RES FOUND INC.
XX PA Bohach GI;
XX PI Bohach GI;
XX WPI; 1999-358008/30.
XX Non-toxic modified staphylococcal enterotoxins
PT Disclosure; Page 17; 25pp; English.
PS This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC2. The invention relates to pyrogenic toxins, such
CC as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic

```

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XX WPI; 1999-358008/30.
XX Non-toxic modified staphylococcal enterotoxins
PT Disclosure; Page 17; 25pp; English.
XX This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC1. The invention relates to pyrogenic toxins, such
CC as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.
XX Sequence 239 AA;
SQ Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGVTGGKTC 18
DB 93 CYPSSKDNVKGVTGGKTC 110

RESULT 13
AAY06252
ID AAY06252 standard; Protein; 239 AA.
XX AC AAY06252;
XX DT 23-AUG-1999 (first entry)
XX DE Staphylococcal group C enterotoxin SEC2.
XX KW Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FT Disulfide-bond 93..110
PN WO9927889-A2.
PD 10-JUN-1999.
PF 01-DEC-1998; 98WO-US25107.
XX PF 02-DEC-1997; 97US-0067357.
XX PR (IDAH-) IDAHO RES FOUND INC.
XX PA Bohach GI;
XX PI Bohach GI;
XX WPI; 1999-358008/30.
XX Non-toxic modified staphylococcal enterotoxins
PT Disclosure; Page 17; 25pp; English.
PS This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC2. The invention relates to pyrogenic toxins, such
CC as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:51:46 ; Search time 13.7964 Seconds
(without alignments)
55.202 Million cell updates/sec

Title: US-09-555-115A-11
Perfect score: 102
Sequence: 1 CVFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	89	US-09-144-776B-21	Sequence 21, Appl
2	102	100.0	89	US-09-144-776B-22	Sequence 22, Appl
3	102	100.0	89	US-09-144-776B-23	Sequence 23, Appl
4	102	100.0	238	US-08-896-933-28	Sequence 28, Appl
5	102	100.0	238	US-09-314-235-28	Sequence 28, Appl
6	102	100.0	239	US-08-896-933-27	Sequence 27, Appl
7	102	100.0	239	US-09-314-235-27	Sequence 27, Appl
8	102	100.0	266	US-09-144-776B-14	Sequence 14, Appl
9	48	47.1	170	US-09-252-991A-23047	Sequence 29047, A
10	46	45.1	263	US-08-892-690-3	Sequence 3, Appl
11	46	45.1	374	US-07-857-224B-82	Sequence 82, Appl
12	46	45.1	374	US-07-857-224B-83	Sequence 83, Appl
13	46	45.1	375	US-09-347-878-56	Sequence 56, Appl
14	44	43.1	134	US-08-482-728A-14	Sequence 14, Appl
15	44	43.1	176	US-08-145-995A-4	Sequence 4, Appl
16	44	43.1	176	US-08-451-747-4	Sequence 4, Appl
17	44	43.1	176	US-09-134-852-4	Sequence 4, Appl
18	42	41.2	514	US-08-361-920-21	Sequence 21, Appl
19	42	41.2	514	US-08-479-939-21	Sequence 21, Appl
20	42	41.2	514	US-08-483-432-21	Sequence 21, Appl
21	40.5	39.7	155	US-09-252-991A-19995	Sequence 19995, A
22	40	39.2	210	US-09-247-155-121	Sequence 121, App
23	40	39.2	264	US-08-924-570A-2	Sequence 2, Appl
24	40	39.2	320	US-09-092-437-2	Sequence 2, Appl
25	40	39.2	374	US-07-857-224B-80	Sequence 80, Appl
26	40	39.2	374	US-07-857-224B-81	Sequence 81, Appl
27	40	39.2	374	US-07-857-224B-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1

US-09-144-776B-21
; Sequence 21, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MPMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Query Match

100.0%; Score 102; DB 4; Length 89;

Sequence 85, Appl
Sequence 86, Appl
Sequence 2, Appl
Sequence 29429, A
Sequence 6788, Appl
Sequence 24791, A
Sequence 35, Appl
Sequence 37, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 6140, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl

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Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 54 CYFSSKDNVKGVTGGKTC 71

RESULT 2
US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-144-776B-23
Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 54 CYFSSKDNVKGVTGGKTC 71

RESULT 4
US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28
Query Match 100.0%; Score 102; DB 3; Length 238;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 54 CYFSSKDNVKGVTGGKTC 71

RESULT 3
US-09-144-776B-23
; Sequence 23, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
```

Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGGKTC 18
Db 92 CYFSSKDNVKGVTGGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-09-314-235-28

Query Match 100.0%; Score 102; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGGKTC 18
Db 92 CYFSSKDNVKGVTGGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-08-896-933-27

Query Match 100.0%; Score 102; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGGKTC 18
Db 93 CYFSSKDNVKGVTGGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-09-314-235-27

Query Match 100.0%; Score 102; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGGKTC 18
Db 93 CYFSSKDNVKGVTGGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC-504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998

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/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/882,431
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Charles H. Harris
/ REGISTRATION NUMBER: 34,616
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 619-2065
/ TELEFAX: (301) 619-7714
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 266
/ TYPE: Amino Acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-7768-14

Query Match 100.0%; Score 102; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 120 CYFSSKDNVGVKVTGKTC 137

RESULT 9
US-09-252-991A-29047
/ Sequence 29047, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 29047
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29047

Query Match 47.1%; Score 48; DB 4; Length 170;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTG 14
Db 116 CSPARDNAGRATG 129

RESULT 10
US-08-892-690-3
/ Sequence 3, Application US/08892690
/ Patent No. 5932420
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Lal, Preeti
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

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/ STREET: 3174 Porter Drive
/ CITY: oPalo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/892,690
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION NUMBER:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0339 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 263 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 624778
US-08-892-690-3

Query Match 45.1%; Score 46; DB 2; Length 263;
Best Local Similarity 43.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGCK 16
Db 90 CFFDSEDPVNSIPGGE 105

RESULT 11
US-07-857-224B-82
/ Sequence 82, Application US/07857224B
/ Patent No. 5958784
/ GENERAL INFORMATION:
/ APPLICANT: Benner, Steven A.
/ TITLE OF INVENTION: Predicting Folded Structures of Proteins
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Steven A. Benner
/ STREET: Hadlaubstrasse 151
/ CITY: Zurich
/ STATE: none
/ COUNTRY: Switzerland
/ ZIP: (note: this is an international post code) CH-8092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
/ OPERATING SYSTEM: Macintosh
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/857,224B
/ FILING DATE: 03/25/92
/ CLASSIFICATION: 436
/ PRIOR APPLICATION DATA: none
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (International) 41 1 632 2830
/ TELEFAX: (International) 41 1 262 2437
/ TELEX: none
```


NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-14

Query Match 43.1%; Score 44; DB 2; Length 134;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKTC 18
Db 21 CLCSGEKGLGKTKKLC 38

RESULT 15

US-08-145-995A-4
Sequence 4, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-4

Query Match 43.1%; Score 44; DB 1; Length 176;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKTC 18
Db 41 CLCSGEKGLGKTKKLC 58
Search completed: October 15, 2003, 17:08:31
Job time : 14.7964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 27.2695 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115A-11

Perfect score: 102

Sequence: 1 CYFSSKDNVKGVTGGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	89	15	US-10-002-784A-36
2	102	100.0	89	15	US-10-002-784A-37
3	102	100.0	89	15	US-10-002-784A-38
4	102	100.0	266	8	US-08-882-431-14
5	102	100.0	266	10	US-09-870-759-12
6	102	100.0	266	12	US-09-751-708A-12
7	102	100.0	266	15	US-10-002-784A-14
8	46	45.1	263	9	US-09-265-710-3
9	46	45.1	263	12	US-10-366-020-3
10	46	45.1	375	10	US-09-981-353-113
11	46	45.1	375	12	US-09-738-630-92
12	46	45.1	395	9	US-09-925-302-497
13	42	41.2	211	15	US-10-156-761-8802
14	42	41.2	332	15	US-10-021-811-54
15	41.5	40.7	993	15	US-10-128-714-3467

16	41.5	40.7	1105	15	US-10-128-714-8467	Sequence 8467, Ap
17	41	40.2	163	12	US-10-238-075-786	Sequence 786, App
18	41	40.2	307	11	US-09-764-891-4188	Sequence 4188, Ap
19	40.5	39.7	1139	15	US-10-156-761-10856	Sequence 10856, A
20	40	39.2	152	12	US-10-040-895-2	Sequence 2, Appli
21	40	39.2	210	12	US-09-903-190-121	Sequence 121, App
22	40	39.2	263	9	US-09-823-356-13	Sequence 13, Appl
23	40	39.2	263	11	US-09-946-374-43	Sequence 43, Appl
24	40	39.2	263	12	US-10-015-387A-43	Sequence 43, Appl
25	40	39.2	263	12	US-10-006-130A-43	Sequence 43, Appl
26	40	39.2	263	12	US-10-199-672-184	Sequence 184, App
27	40	39.2	263	12	US-10-006-172A-43	Sequence 43, Appl
28	40	39.2	263	12	US-10-187-749-184	Sequence 184, App
29	40	39.2	263	12	US-10-194-457-184	Sequence 184, App
30	40	39.2	263	12	US-10-184-642-184	Sequence 184, App
31	40	39.2	263	12	US-10-196-747-184	Sequence 184, App
32	40	39.2	263	12	US-10-015-392A-43	Sequence 43, Appl
33	40	39.2	263	12	US-10-017-253A-43	Sequence 43, Appl
34	40	39.2	263	12	US-10-173-689-184	Sequence 184, App
35	40	39.2	263	12	US-10-173-690-184	Sequence 184, App
36	40	39.2	263	12	US-10-173-691-184	Sequence 184, App
37	40	39.2	263	12	US-10-173-692-184	Sequence 184, App
38	40	39.2	263	12	US-10-173-694-184	Sequence 184, App
39	40	39.2	263	12	US-10-173-698-184	Sequence 184, App
40	40	39.2	263	12	US-10-173-699-184	Sequence 184, App
41	40	39.2	263	12	US-10-173-707-184	Sequence 184, App
42	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
43	40	39.2	263	12	US-10-174-583-184	Sequence 184, App
44	40	39.2	263	12	US-10-174-587-184	Sequence 184, App
45	40	39.2	263	12	US-10-174-589-184	Sequence 184, App

ALIGNMENTS

RESULT 1
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match 100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
DB 54 CYFSSKDNVKGVTGGKTC 71

RESULT 2
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33

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; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-37

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
Db      54 CYFSSKDNVKGVTGGKTC 71

RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-38

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
Db      54 CYFSSKDNVKGVTGGKTC 71

RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
```

```
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match      100.0%; Score 102; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
Db      120 CYFSSKDNVKGVTGGKTC 137

RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US2002017751A1
; GENERAL INFORMATION:
; APPLICANT: FERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-12

Query Match      100.0%; Score 102; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
Db      120 CYFSSKDNVKGVTGGKTC 137

RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
```

```

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match 100.0%; Score 102; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 7
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 100.0%; Score 102; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 8
US-09-265-710-3
; Sequence 3, Application US/09265710
; Patent No. US20020042126A1
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

Query Match 100.0%; Score 46; DB 9; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGK 16
Db 90 CFFDSEDPVNSIPGGE 105

RESULT 9
US-10-366-020-3
; Sequence 3, Application US/10366020
; Publication No. US20030152989A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/366,020
; FILING DATE: 11-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,161
; FILING DATE: 1998-12-07
; APPLICATION NUMBER: US/08/791,338
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/892,690
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0339 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624778
US-09-265-710-3

Query Match 45.1%; Score 46; DB 9; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGK 16
Db 90 CFFDSEDPVNSIPGGE 105

RESULT 9
US-10-366-020-3
; Sequence 3, Application US/10366020
; Publication No. US20030152989A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/366,020
; FILING DATE: 11-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,161
; FILING DATE: 1998-12-07
; APPLICATION NUMBER: US/08/791,338
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

```
;
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0208 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624778
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-366-020-3

Query Match 45.1%; Score 46; DB 12; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGK 16
Db 90 CFFDSEDPVNSIPGE 105

RESULT 10
US-09-981-353-113
; Sequence 113, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laese, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 2512879CD1
US-09-981-353-113

Query Match 45.1%; Score 46; DB 10; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 175 CGFSTGYGSANVAVKVTGPGSTC 196

RESULT 11
US-09-738-630-92
; Sequence 92, Application US/09738630
; Publication No. US20030166213A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; APPLICANT: Shaw, Paul J.
; TITLE OF INVENTION: Methods For Identifying Compounds That
; TITLE OF INVENTION: Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
; TITLE OF INVENTION: Protein Kinase Signaling
; FILE REFERENCE: P-NI 3906
; CURRENT APPLICATION NUMBER: US/09/738,630
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92

;
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-630-92

Query Match 45.1%; Score 46; DB 12; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVKGVTGGKTC 18
Db 175 CGFSTGYGSANVAVKVTGPGSTC 196

RESULT 12
US-09-925-302-497
; Sequence 497, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 497
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-497

Query Match 45.1%; Score 46; DB 9; Length 395;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVKGVTGGKTC 18
Db 195 CGFSTGYGSANVAVKVTGPGSTC 216

RESULT 13
US-10-156-761-8802
; Sequence 8802, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8802
; LENGTH: 211
; TYPE: PRT
```

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; ORGANISM: Streptomyces avermitilis
US-10-156-761-8802

Query Match      41.2%; Score 42; DB 15; Length 211;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 YFSSKDNVGVKT 13
       :|||||:
Db      58 HFSSKDNLTAKT 69

RESULT 14
US-10-021-811-54
; Sequence 54, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odell, Joan
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: B01294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 54
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Glycine max
US-10-021-811-54

Query Match      41.2%; Score 42; DB 15; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 CYFSSKDNVGVKTGG 15
       |||||:
Db      197 CYASSADNIARMLKG 211

RESULT 15
US-10-128-714-3467
; Sequence 3467, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3467
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; LENGTH: 993
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3467

Query Match      40.7%; Score 41.5; DB 15; Length 993;
Best Local Similarity 40.9%; Pred. No. 4.3e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 9; Gaps 1;

QY      5 SKDNV-----GKVTGGKT 17
       :|||:
Db      102 TKDNICFQIDAEEGTITGGKT 123

Search completed: October 15, 2003, 17:46:59
Job time : 27.2695 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 13.6886 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115A-11
Perfect score: 102
Sequence: 1 CYFSSKDNVGVTKGKTC 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	266	1 ENSAC1	enterotoxin C-1 pr
2	102	100.0	266	2 A60114	enterotoxin C-2 pr
3	102	100.0	266	2 S11885	enterotoxin C3 - S
4	46	45.1	199	2 AG1583	weakly phosphoglyc
5	46	45.1	375	1 DEHUA	alcohol dehydrogen
6	46	45.1	375	1 DEHUA	alcohol dehydrogen
7	44	43.1	246	2 JQ1472	trypsin (EC 3.4.21
8	44	43.1	246	2 JQ1471	trypsin (EC 3.4.21
9	44	43.1	275	2 T32005	hypothetical prote
10	44	43.1	1403	1 A47328	natural killer cel
11	44	43.1	1507	2 B47328	natural killer cel
12	43	42.2	274	2 T13010	hypothetical prote
13	43	42.2	346	2 AE3434	lytB protein (impo
14	43	42.2	368	2 T26338	hypothetical prote
15	42	41.2	212	2 T05336	agglutinin isolect
16	42	41.2	235	2 E91097	hypothetical prote
17	42	41.2	235	2 A85943	hypothetical prote
18	42	41.2	260	2 B96944	2 deoxy-D-gluconat
19	42	41.2	358	2 T08477	inclusion membrane
20	42	41.2	375	1 A38405	alcohol dehydrogen
21	42	41.2	378	2 AC1454	protein gp18 from
22	42	41.2	378	2 AD1090	protein gp18 from
23	42	41.2	40	2 A70734	peptidase, M20/M25
24	41	40.2	57	2 S70473	neurotoxin Ts-kapp
25	41	40.2	97	2 T08573	hypothetical prote
26	41	40.2	199	2 AD1230	phosphoglycerate m
27	41	40.2	269	2 B97113	protein serine/thr
28	41	40.2	368	1 DEHUA6	alcohol dehydrogen
29	41	40.2	375	1 A33909	alcohol dehydrogen

30 41 40.2 746 2 AD1622 probable integral
31 41 40.2 750 2 G81361 probable flagellin
32 41 40.2 1127 2 T03105 major single-stran
33 40.5 39.7 333 2 D83585 hypothetical prote
34 40.5 39.7 725 2 T17732 helicase-like prot
35 40.5 39.7 1102 2 A84480 probable retroelem
36 40 39.2 99 2 G84242 hypothetical prote
37 40 39.2 242 2 H69066 ribosomal protein
38 40 39.2 266 1 S18159 ribosomal protein
39 40 39.2 320 2 H95136 ribonucleoside-dip
40 40 39.2 320 2 B99005 hypothetical prote
41 40 39.2 348 2 D70195 hypothetical prote
42 40 39.2 374 1 DEHOAS alcohol dehydrogen
43 40 39.2 375 1 I55359 alcohol dehydrogen
44 40 39.2 375 1 DEHUAG alcohol dehydrogen
45 40 39.2 375 1 DEHOAL alcohol dehydrogen

ALIGNMENTS

RESULT 1
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
C:Accession: S06356; A01816
R:Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness t
A:Reference number: S06356; MUID:88038352; PMID:2823067
A:Accession: S06356
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Cross-references: EMBL:X05815; NID:G46566; PIDN:CAA29260.1; PID:G46567
R.Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A:Reference number: A01816; MUID:83213327; PMID:6189824
A:Accession: A01816
A:Molecule type: Protein
A:Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C:Genetics:
C:Gene: entC1
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-1 #status experimental <MAT>
F:120-137/Diaulfide bonds: #status experimental

Query Match 100.0%; Score 102; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
|||||
DB 120 CYFSSKDNVGVTKGKTC 137

RESULT 2
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A:Reference number: A60114; MUID:89277549; PMID:2543637
A:Accession: A60114
A:Status: not compared with conceptual translation
A:Molecule type: DNA

A;Residues: 1-266 <BOH>
A;Accession: B60114
A;Molecule type: protein
A;Residues: 28-66 <BOH2>
J;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests the
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:gi53003; PIDN:AAA26624.1; PID:gi53004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>
Query Match 100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
QY 1 CYFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 120 CYFSSKDNVGVGTGGKTC 137
RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S11885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison
A;Reference number: S11885; MUID:90220508; PMID:2325627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
A;Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B
Query Match 100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 120 CYFSSKDNVGVGTGGKTC 137
RESULT 4
AG1583
weakly phosphoglycerate mutase 1 homolog lin1208 [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1583
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <GLA>
A;Cross-references: GB:AL59202; PIDN:CAC96439.1; PID:gi6413682; GSPDB:GN00178

A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1208
Query Match 45.1%; Score 46; DB 2; Length 199;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 2 YFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 151 YWETSKIGKVTGLKNC 167
RESULT 5
DEHUA
alcohol dehydrogenase (EC 1.1.1.1) 1 - human
N;Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
C;Accession: S02265; A25428; A24408; I39398; I39397
R;Matsuo, Y.; Yokoyama, S.
FEBS Lett. 243, 57-60, 1989
A;Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
A;Reference number: S02265; MUID:89153548; PMID:2920825
A;Accession: S02265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 16375 <MATS>
R;Ikuta, T.; Szeto, S.; Yoshida, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
A;Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and ev
A;Reference number: A94120; MUID:86120595; PMID:2935875.
A;Accession: A25428
A;Molecule type: mRNA
A;Residues: 1-375 <IKU>
A;Cross-references: GB:M12271; NID:gi178091; PIDN:AAA68131.1; PID:gi178092
R;von Bahr-Lindstrom, H.; Hoog, J.O.; Heden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K.
Biochemistry 25, 2465-2470, 1986
A;Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
A;Reference number: A24408; MUID:86243367; PMID:3013304
A;Accession: A24408
A;Molecule type: mRNA
A;Residues: 1-375 <VON>
A;Cross-references: GB:M12963; NID:gi178089; PIDN:AAA51590.1; PID:gi178090
R;Yasunami, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
Genomics 7, 152-158, 1990
A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
A;Reference number: I39398; MUID:90269803; PMID:2347582
A;Accession: I39398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <YAS>
A;Cross-references: GB:M37066; NID:gi178095; PIDN:AAA51591.1; PID:gi178096
R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
Gene 90, 271-279, 1990
A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
A;Reference number: I39397; MUID:90382676; PMID:2169444
A;Accession: I39397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <STE>
A;Cross-references: GB:M32656; NID:gi178093; PIDN:AAA52276.1; PID:gi178094
C;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
C;Genetics:
A;Gene: GDB:ADH1
A;Cross-references: GDB:119650; OMIM:103700
A;Map position: 4q21-4q23
A;Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
C;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: ethanol degradation
A;Note: human alcohol dehydrogenase 1 is expressed predominately in fetal and neonatal li

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F:2-375/Product: alcohol dehydrogenase 1 #status predicted <MAT>
 F:32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F:195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F:47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 45.1%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVKVTGGK 18
 |||||
 DB 175 CGFSTGYGSVNVKVTGPGSTC 196

RESULT 6
 DEHUAB

N:Alternate names: alcohol dehydrogenase beta chain; class I alcohol dehydrogenase
 C:Species: Homo sapiens (man)
 C:Date: 25-FEB-1985 #sequence_revision 02-Aug-1994 #text_change 15-Sep-2000
 C:Accession: A23607; A38916; I39399; A26281; I39402; I39401; S05202; S10621; I39400; A000000000
 R:Heden, L.O.; Hoog, J.O.; Larsson, K.; Lake, M.; Lagerholm, E.; Holmgren, A.; Vallee, B.
 FEBS Lett. 194, 327-332, 1986

A:Title: cDNA clones coding for the beta-subunit of human liver alcohol dehydrogenase ha
 A:Reference number: A23607; MUID:86082371; PMID:3000832
 A:Accession: A23607

A:Molecule type: mRNA
 A:Residues: 1-375 <HE>
 A:Cross-references: EMBL:X03350; NID:g28415; PIDN:CAA27056.1; PID:g28416
 R:Ikuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2703-2707, 1985

A:Title: Molecular cloning of a full-length cDNA for human alcohol dehydrogenase.
 A:Reference number: A38916; MUID:85190565; PMID:2986130
 A:Accession: A38916

A:Molecule type: mRNA
 A:Residues: 1-375 <IK>
 A:Cross-references: GB:M24317; NID:gl78097
 A:Note: this sequence has been revised in reference A38917
 R:Ikuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5578, 1985

A:Reference number: A38917
 A:Contents: annotation; erratum
 R:Yokoyama, S.; Yokoyama, R.; Rotwein, P.
 Jpn. J. Genet. 62, 241-256, 1987

A:Title: Molecular characterization of cDNA clones encoding the human alcohol dehydrogen
 A:Reference number: I39399
 A:Accession: I39399

A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-375 <YK>
 A:Cross-references: GB:D00137; NID:g219427; PIDN:BA000084.1; PID:g219428
 R:Duester, G.; Smith, M.; Bilanchone, V.; Hatfield, G.W.
 J. Biol. Chem. 261, 2027-2033, 1986

A:Title: Molecular analysis of the human class I alcohol dehydrogenase gene family and n
 A:Reference number: A26281; MUID:86111889; PMID:2935533
 A:Accession: A26281

A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-229, 'K', 231-375 <DUE>
 A:Cross-references: GB:M24317; GB:K01883; NID:gl78097; PIDN:AAA51894.1; PID:gl78098
 A:Note: the authors translated the codon AAA for residue 230 as Phe
 R:Yasunami, M.; Kikuchi, I.; Sarapat, D.; Yoshida, A.
 Genomics 7, 152-158, 1990

A:Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly
 A:Reference number: I39398; MUID:90269803; PMID:2347582
 A:Accession: I39402

A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-6 <YAS>
 A:Cross-references: GB:M37067; NID:gl78114; PIDN:AAA51593.1; PID:gl78115

R:Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990

A:Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: intera
 A:Reference number: I39397; MUID:90382676; PMID:2169444
 A:Accession: I39401

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <STE>
 A:Cross-references: GB:M32657; NID:gl78112; PIDN:AAA52277.1; PID:gl78113
 R:Matsumoto, Y.; Yokoyama, R.; Yokoyama, S.
 Eur. J. Biochem. 163, 317-320, 1989

A:Title: The genes for human alcohol dehydrogenases beta(1) and beta(2) differ by only or
 A:Reference number: S05202; MUID:89338401; PMID:2547609
 A:Accession: S05202

A:Molecule type: DNA
 A:Residues: 1-47, 'H', 49-375 <MATS>
 A:Cross-references: EMBL:X15447; NID:g28385
 A:Note: allelic beta-2 variant found predominately in oriental populations
 A:Note: the sequence in GenBank entry HSADH221, release 103 (PID:g228260), has an incorr
 R:Ehrig, T.; von Wartburg, J.P.; Wermuth, B.
 FEBS Lett. 234, 53-55, 1988

A:Title: cDNA sequence of the beta(2)-subunit of human liver alcohol dehydrogenase.
 A:Reference number: S10621; MUID:88271624; PMID:2968918
 A:Accession: S10621

A:Molecule type: mRNA
 A:Residues: 1-47, 'H', 49-343 <EHR>
 A:Note: only a list of differences from various previously published sequences is shown
 R:Xu, Y.L.; Cart, L.G.; Bosron, W.F.; Li, T.K.; Edenberg, H.J.
 Genomics 2, 209-214, 1988

A:Title: Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci following I
 A:Reference number: I39400; MUID:88284699; PMID:3397059
 A:Accession: I39400

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7, 'M', 9-56, 'K', 58-165, 'K', 167-234, 'V', 236-375 <RE3>
 A:Cross-references: GB:M21692; NID:gl78099; PIDN:AAA51592.1; PID:gl78100
 R:Hempel, J.; Buhler, R.; Kaiser, R.; Holmquist, B.; de Zalsenki, C.; von Wartburg, J.P.;
 Eur. J. Biochem. 145, 437-445, 1984

A:Title: Human liver alcohol dehydrogenase. 1. The primary structure of the beta-1beta-1
 A:Reference number: A00335; MUID:85076637; PMID:6391920
 A:Accession: A00335

A:Molecule type: protein
 A:Residues: 2-129, 131-375 <HEM>
 A:Note: allelic beta-1 variant found predominately in caucasian and negroid populations
 R:Buhler, R.; Hempel, J.; Kaiser, R.; von Wartburg, J.P.; Vallee, B.L.; Jornvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6320-6324, 1984

A:Title: Human alcohol dehydrogenase: structural differences between the beta and gamma s
 ndants in livers of different mammals.
 A:Reference number: A05182; MUID:85038508; PMID:6387702
 A:Accession: A05182

A:Molecule type: protein
 A:Residues: 12-34, 'V', 36-38, 41-85, 101-114, 131-160, 170-213, 273-313, 317-331, 341-367 <BUH>
 R:Burnell, J.C.; Carr, L.G.; Dwulet, F.E.; Edenberg, H.J.; Li, T.K.; Bosron, W.F.
 Biochem. Biophys. Res. Commun. 146, 1227-1233, 1987

A:Title: The human beta-3 alcohol dehydrogenase subunit differs from beta-1 by a Cys for
 A:Reference number: A26826
 A:Accession: A26826

A:Molecule type: protein
 A:Residues: 368-369, 'C', 371-375 <BUR>
 A:Note: allelic beta-3 variant found as a minor form occurring to a greater extent in neg
 R:Hurler, T.D.; Bosron, W.F.; Hamilton, J.A.; Amzel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8149-8153, 1991

A:Title: Structure of human beta-1beta-1 alcohol dehydrogenase: catalytic effects of non
 A:Reference number: A40987; MUID:91376103; PMID:1896463
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms
 A:Note: Structure of beta-1 variant dimer
 R:Hurler, T.D.; Bosron, W.F.; Hamilton, J.A.; Amzel, L.M.
 submitted to the Brookhaven Protein Data Bank, January 1993

A:Reference number: A52127; PDB:3HJD
 A:Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 2-375
 C:Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C:Genetics:
 A:Gene: GDB:ADH2

A;Cross-references: GDB:119651; OMIM:103720
A;Map position: 4q22-4q22
A;Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded b
C;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
A;Pathway: alcohol degradation
A;Note: human alcohol dehydrogenase beta is expressed predominantly in fetal lung and ne
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
F;2-375/Product: alcohol dehydrogenase 2 #status experimental <MAT>
F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match 45.1%; Score 46; DB 1; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVKVTGGKTC 18
Db 175 CGFSTGYGSAVNVAKVTPGSTC 196

RESULT 7
JQ1472
trypsin (EC 3.4.21.4) V precursor, b-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: JQ1472
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: JQ1471; MUID:92165057; PMID:1537555
A;Accession: JQ1472
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59013; NID:g57414; PIDN:CAA41752.1; PID:g57415
A;Experimental source: pancreas
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, b-form #status predicted <MAT>
F;25-239/Domain: trypsin homology <TRY>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGGKTC 18
Db 16 FPTDNDNRIVGGYTC 31

RESULT 8
JQ1471
trypsin (EC 3.4.21.4) V precursor, a-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: JQ1471; S23784
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: JQ1471; MUID:92165057; PMID:1537555
A;Accession: JQ1471
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59012; NID:g57412; PIDN:CAA41751.1; PID:g57413

A;Experimental source: pancreas
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, a-form #status predicted <MAT>
F;25-239/Domain: trypsin homology <TRY>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
Db 193 CYINSGKPGNIPGMKYC 210

RESULT 10
A47328
natural killer cell tumor-recognition protein - human
N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: A47328
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
A;Reference number: A47328; MUID:93133824; PMID:8421688
A;Accession: A47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1403 <AND>
A;Cross-references: GB:I04288; NID:g181251; PIDN:AAA35734.1; PID:g181252
A;Experimental source: NK killer cells from adult blood
A;Note: sequence extracted from NCBI backbone (NCBIN:122798, NCBIPI:122800)
C;Genetics:
A;Gene: GDB:NKTR
A;Cross-references: GDB:137171; OMIM:161565
A;Map position: 3p23+3p21
C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C;Keywords: alternative splicing; lymphocyte

F:60-230/Domain: cyclophilin homology <CYP>

Query Match 43.1%; Score 44; DB 1; Length 1403;

Best Local Similarity 44.4%; Pred. No. 1.3e+02; Mismatches 8; Indels 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18

DB 95 CLCSGKGLGKTTGKTLIC 112

RESULT 11

B47328

natural killer cell tumor-recognition protein - mouse

N:Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 05-Nov-1999

C/Accession: B47328; 177662

R:Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.

Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993

A>Title: A cyclophilin-related protein involved in the function of natural killer cells.

A/Reference number: A47328; PMID:93133824; PMID:8421688

A/Accession: B47328

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1507 <AND>

A/Cross-references: GB:104289; NID:g192866

A/Note: authors translated the codon AGT for residue 972 as Arg

R:Rintfel, A.; Anderson, S.K.

Mol. Immunol. 30, 1307-1313, 1993

A>Title: IL-2 regulates the expression of the NK-TR gene via an alternate RNA splicing m

A/Reference number: 157820; PMID:94019422; PMID:8413330

A/Accession: 177662

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 235-237; 263-294 <RIN>

A/Cross-references: GB:s65998; NID:g425701; PIDN:AAB28500.1; PID:g425702

C/Genetics:

C/Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology

C/Keywords: alternative splicing; lymphocyte

F:60-230/Domain: cyclophilin homology <CYP>

Query Match 43.1%; Score 44; DB 2; Length 1507;

Best Local Similarity 44.4%; Pred. No. 1.4e+02; Mismatches 8; Indels 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18

DB 95 CLCSGKGLGKTTGKTLIC 112

RESULT 12

T13010

hypothetical protein T24C20.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999

C/Accession: T13010

R:Choiang, N.; Robert, C.; Brothier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: 217586

A/Accession: T13010

A/Molecule type: DNA

A/Residues: 1-274 <CHO>

A/Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.90

A/Experimental source: cultivar Columbia; BAC clone T24C20

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match 42.2%; Score 43; DB 2; Length 368;

Best Local Similarity 43.8%; Pred. No. 54; Mismatches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGKTC 18

DB 144 FASKNNTGNTGTLIC 159

RESULT 13

AE3434

lytB protein [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C/Accession: AE3434

R:DeVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Loz, T.; Ivanova, I.

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AE3434

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-346 <KUR>

A/Cross-references: GB:AE008917; PIDN:AAL52640.1; PID:g17983462; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Map position: I

C/Superfamily: penicillin tolerance protein

Query Match 42.2%; Score 43; DB 2; Length 346;

Best Local Similarity 53.8%; Pred. No. 51; Mismatches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVT 13

DB 161 CHFDDEDNLGFTV 173

RESULT 14

T26338

hypothetical protein Y102A5B.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T26338

R:Gardner, A.

submitted to the EMBL Data Library, June 1998

A/Reference number: Z20203

A/Accession: T26338

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match 42.2%; Score 43; DB 2; Length 368;

Best Local Similarity 43.8%; Pred. No. 54; Mismatches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGKTC 18

DB 144 FASKNNTGNTGTLIC 159

RESULT 15

T05936

agglutinin isolectin 1 precursor - barley

C:Species: Hordeum vulgare (barley)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000

C/Accession: T05936

R:Lerner, D.R.; Raikhel, N.V.

Plant Physiol. 91, 124-129, 1989
A;Title: Cloning and characterization of root-specific barley lectin.
A;Reference number: Z15461
A;Accession: T05936
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <LER>
A;Cross-references: EMBL:M29280; NID:G167070; PID:AAA32969.1; PID:G167071
C;Superfamily: wheat agglutinin; hevein chitin-binding domain homology
C;Keywords: lectin
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-212/Product: agglutinin isolectin I #status predicted <MAT>
F;27-69/Domain: hevein chitin-binding domain homology <HCB>

Query Match 41.2%; Score 42; DB 2; Length 212;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CYSSKDNVGVKVTGKTC 18
|||:|||||
Db 66 CYTSKR--CGTQAGKTC 81

Search completed: October 15, 2003, 17:06:23
Job time : 15.6886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 7.32934 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-11

Perfect score: 102
Sequence: 1 CYFSSMDNVGKVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	266	1 ETC1_STAAU	P01553 staphylococ
2	102	100.0	266	1 ETC2_STAAU	P34071 staphylococ
3	102	100.0	266	1 ETC3_STAAU	P23313 staphylococ
4	46	45.1	263	1 ITMA_MOUSE	O61500 mus musculu
5	46	45.1	374	1 ADHA_HUMAN	P07327 homo sapien
6	46	45.1	374	1 ADHB_HUMAN	P00325 homo sapien
7	44	43.1	246	1 TRVA_RAT	P32821 rattus norv
8	44	43.1	246	1 TRVB_RAT	P32822 rattus norv
9	44	43.1	1453	1 NKCR_MOUSE	P30415 mus musculu
10	44	43.1	1462	1 NKCR_MOUSE	P30414 mus musculu
11	43	42.2	346	1 ISPH_BRIME	O8YF11 bruceella me
12	42	41.2	212	1 AGI_HORVU	P15312 hordeum vul
13	42	41.2	358	1 INCI_ECOLI	O52312 escherichia
14	42	41.2	375	1 ADHI_RANPE	P22797 rana perezi
15	42	41.2	514	1 GUXC_FUSOX	P46238 fusarium ox
16	41	40.2	35	1 SCKK_TITSE	P56219 cilius serr
17	41	40.2	336	1 OTCC_STRPY	P16944 streptococ
18	41	40.2	368	1 ADH6_HUMAN	P28332 homo sapien
19	41	40.2	374	1 ADH_PAPPA	P14139 papilio hamad
20	41	40.2	905	1 YD83_HUMAN	O9P244 homo sapien
21	40	39.2	127	1 ACPS_THETN	O8R857 thermoanaer
22	40	39.2	242	1 RS4E_MERTH	O26123 methanobact
23	40	39.2	263	1 ITMA_HUMAN	O43376 homo sapien
24	40	39.2	265	1 RL7A_CHICK	P32429 gallus galli
25	40	39.2	373	1 ADH1_HORSE	P00338 equus caball
26	40	39.2	374	1 ADH1_RABIT	O03505 onycotlagus
27	40	39.2	374	1 ADHA_MOUSE	P16030 mus musculu
28	40	39.2	374	1 ADHA_PERMA	P41680 peromyscus
29	40	39.2	374	1 ADHE_HORSE	P00327 equus caball
30	40	39.2	374	1 ADHG_HUMAN	P00326 homo sapien
31	40	39.2	374	1 ADH1_MACMU	P28469 macaca mula
32	40	39.2	375	1 ADHA_RAT	P67571 rattus norv
33	40	39.2	412	1 FKBA_SPOFR	Q26486 spodoptera

34	40	39.2	523	1 TYD5_PAPSO	P54771 papaver som
35	40	39.2	528	1 ACH2_CHICK	P09480 gallus galli
36	40	39.2	612	1 UNJ7_CAEEL	O02482 caenorhabdi
37	40	39.2	761	1 VPA_BPE2	O06419 bacterioph
38	40	39.2	867	1 PHM1_MOUSE	O54890 mus musculu
39	40	39.2	1170	1 TSPI_MOUSE	P35441 mus musculu
40	40	39.2	1235	1 DNBI_HCMVA	P17147 human cytom
41	39.5	38.7	664	1 SYM_LISIN	O92490 listeria in
42	39.5	38.7	664	1 SYM_LISMO	O8YAF2 listeria mo
43	39	38.2	187	1 RECX_YERPE	P37867 yerinia pe
44	39	38.2	256	1 Y0EC_ECOLI	O46809 escherichia
45	39	38.2	259	1 KLR2_RAT	P00759 rattus norv

ALIGNMENTS

RESULT 1	ID	ETC1_STAAU	STANDARD;	PRT;	266 AA.
AC	P01553;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Enterotoxin type C-1 precursor (SEC1).				
GN	ENTC1.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8038352; PubMed=2823067;				
RA	Bohach G.A., Schlievert P.M.;				
RT	"Nucleotide sequence of the staphylococcal enterotoxin C1 gene and				
RL	relatedness to other pyrogenic toxins.";				
RM	Mol. Gen. Genet. 209:15-20(1987).				
RN	[2]				
RP	SEQUENCE OF 28-266.				
RX	MEDLINE=83213327; PubMed=6189824;				
RA	Schmidt J.J., Spero L.;				
RT	"The complete amino acid sequence of staphylococcal enterotoxin C1.";				
RL	J. Biol. Chem. 258:6300-6306(1983).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION				
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.				
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN				
CC	FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: X05815; CAA29260.1; -				
DR	PIR: S06356; ENSACI.				
DR	HSSP: P34071; ISE2.				
DR	InterPro: IPR006177; Bcst1_cox.				
DR	InterPro: IPR006123; Staph/Strep_toxin.				
DR	InterPro: IPR006126; Staph/Strep_tox.				
DR	InterPro: IPR006173; Staph_tox_OB.				
DR	Pfam: PR02876; Staph_Strep_cox_C1.				
DR	Pfam: PR01123; Staph_Strep_toxin; 1.				
DR	PRINTS: PR00279; BACTRLTOXIN.				
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.				
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.				
KW	Enterotoxin; Toxin; Signal; Superantigen.				
FT	STGNAL	1			
FT	CHAIN	28	266		ENTEROTOXIN TYPE C-1.
FT	DISULFID	120	137		
FT	CONFLICT	177	177		D -> N (IN REF. 2).

SO SEQUENCE 266 AA; 30546 MW; 3A7AB59A86853B CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGVTGKTC 18
 |||||
 DB 120 CYFSSKDNVKGVTGKTC 137

RESULT 2
 ETC2 STAAU STANDARD; PRT; 266 AA.
 AC P3407;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN ENT2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 RT enterotoxins C1 and C2."
 RL Infect. Immun. 57:2249-2252 (1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Traher H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RT Staphylococcus aureus reveals a zinc-binding site."
 RL Structure 3:769-779 (1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins."
 RL Nat. Struct. Biol. 2:680-686 (1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schlad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity."
 RL J. Mol. Biol. 269:270-280 (1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC PIR; A60114; A60114.
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR PDB; 1COV; 19-SEP-01.
 DR PDB; 114Q; 19-SEP-01.
 DR PDB; 114Q; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR InterPro; IPR006123; Bctrl tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF02876; Staph_strep_tox_Cf_1.

DR Pfam; PF01123; Staph Strep toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DE Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT STRAND 44 44
 FT TURN 48 48
 FT STRAND 49 49
 FT STRAND 60 65
 FT STRAND 69 69
 FT STRAND 73 74
 FT TURN 75 79
 FT STRAND 83 86
 FT TURN 90 94
 FT STRAND 98 104
 FT HELIX 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT STRAND 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT STRAND 146 147
 FT TURN 149 149
 FT STRAND 151 153
 FT HELIX 156 164
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT STRAND 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SO SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGVTGKTC 18
 |||||
 DB 120 CYFSSKDNVKGVTGKTC 137

RESULT 3
 ETC3 STAAU STANDARD; PRT; 266 AA.
 ID ETC3 STAAU
 AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN ENT3 OR SAAV2005 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 RN NCBI_TaxID=158878, 158879, 1280;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=MUS0 / ATCC 700699, and N315;
 RA MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunami H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancer 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT sequence comparison of all three type C staphylococcal
 RT enterotoxins.";
 RL Mol. Gen. Genet. 220:329-333(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=97064178; PubMed=8906797;
 RA Fields B.A., Matchodi E.L., Li H., Yseern X., Stauffacher C.V.,
 RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen.";
 RL Nature 384:188-192(1996).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -|- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL: AP003364; BAB58171.1; -
 DR EMBL: AP003135; BAB43097.1; -
 DR EMBL: X51661; CAA35972.1; -
 DR PIR: S11885; S11885.
 DR PDB: 1JCK; 12-NOV-97.
 DR PDB: 1KLG; 02-AUG-02.
 DR PDB: 1KLU; 14-AUG-02.
 DR InterPro: IPR006177; Bactrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph_strep_tox_C1.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLETOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
 KM Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 1 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137
 SQ SEQUENCE 266 AA; 30671 MW; SED8A32D11FFCA59 CRC64;
 Qy Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3; 7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
 Db 120 CYFSSKDNVKGVTGKTC 137
 RESULT 4
 ID ITMA MOUSE STANDARD; PRT; 263 AA.
 AC 061500;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integral membrane protein 2A (E25 protein).
 GN ITM2A OR ITM2 OR E25.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Mandible;
 RX MEDLINE=96325063; PubMed=8702637;
 RA Deleersnijder W., Hong G., Cortvriendt R., Poirier C., Tydzanowski P.,
 RA Pitlois K., Vanmarck E., Merregaert J.;
 RT "Isolation of markers for chondro-osteogenic differentiation using
 RT cDNA library subtraction. Molecular cloning and characterization of a
 RT gene belonging to a novel multigene family of integral membrane
 RT proteins.";
 RL J. Biol. Chem. 271:19475-19482(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=99111395; PubMed=9892734;
 RA Pitlois K., Wauters J., Bossuyt P., Deleersnijder W., Merregaert J.;
 RT "Genomic organization and chromosomal localization of the Itm2a
 RT gene.";
 RL Mamm. Genome 10:54-56(1999).
 CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN MANDIBULAR CONDYLES, IN BONE AND
 CC IN HAIR FOLLICLES. STRONG EXPRESSION IN OSTEOGENIC TISSUES, SUCH
 CC AS NEONATAL CALVARIA, PAWS, TAIL AND SKIN.
 CC -|- SIMILARITY: BELONGS TO THE ITM2 FAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL: L38971; AAC37700.1; -
 DR EMBL: AF074020; AAD14549.1; -
 DR MGD: MGI:107706; Itm2a.
 DR Pfam: PF04089; BRICHOS; 1.
 KM Transmembrane; Signal-anchor.
 FT TRANSMEM 54 74
 FT CARBOHYD 166 166
 SQ SEQUENCE 263 AA; 29705 MW; CF809834ABCDB85A CRC64;
 Qy Query Match 45.1%; Score 46; DB 1; Length 263;
 Best Local Similarity 43.8%; Pred. No. 4.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

RESULT 5
 ADHA HUMAN STANDARD; PRT; 374 AA.
 ID ADHA_HUMAN

AC P07327;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase alpha chain (EC 1.1.1.1).
 GN ADH1A OR ADH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=86243367; PubMed=3013304;
 RA von Bahr-Lindstrom K., Hoeoeg J.-O., Heden L.-O., Kaiser R.,
 RA Fleetwood L., Larsson K., Lake M., Holmquist B., Holmgren A.,
 RA Hempel U., Vallee B.L., Joernvall H.;
 RT "cDNA and protein structure for the alpha subunit of human liver
 RT alcohol dehydrogenase.";
 RL Biochemistry 25:2465-2470(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89153548; PubMed=2920825;
 RA Matsuo Y., Yokoyama S.;
 RT "Molecular structure of the human alcohol dehydrogenase 1 gene.";
 RL FEBS Lett. 243:57-60(1989).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=90269803; PubMed=2347582;
 RA Yasunami M., Kikuchi I., Sarapata D., Yoshida A.;
 RT "The human class I alcohol dehydrogenase gene cluster: three genes
 RT are tandemly organized in an 80-kb-long segment of the genome.";
 RL Genomics 7:152-158(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC P1, ONE TO CLASS-III: CHI, ONE TO CLASS-IV, ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL; M12271; AAA68131.1; -;
 DR EMBL; M12963; AAA51590.1; -;
 DR EMBL; M37066; AAA51591.1; -;
 DR PIR; S02265; DEHUA.
 DR PDB; 1HSO; 27-APR-01.
 DR Genew; HGNC:249; ADH1A.
 DR GK; P07327; -;
 DR MIM; 103700; -;
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; NAS.
 DR GO; GO:0006066; P:alcohol metabolism; NAS.
 DR InterPro; IPR002328; ADH_zinc.

DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF0107; ADH_zinc_N; 1.
 DR PROSITE; PROS00058; ADH_ZINC; 1.
 KW Oxidoreductase, zinc, metal-binding, NAD, Multigene family;
 FT Acetylation; 3D-structure.
 FT INIT MET 0
 FT MOD RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 174 174 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 374 AA; 39727 MW; 5D2F5F6B31C4962C CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CYFS---SKDNVGVTKGKTC 18
 Db 174 CGFSTGYGSANVAKVTPGSTC 195
 RESULT 6
 ID ADHB_HUMAN STANDARD; PRT; 374 AA.
 AC P00325; Q13711; Q96K17;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase beta chain (EC 1.1.1.1).
 GN ADH1B OR ADH2
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yokoyama S., Yokoyama R., Rotwein P.;
 RT "Molecular characterization of cDNA clones encoding the human alcohol
 RT dehydrogenase beta 1 and the evolutionary relationship to the other
 RT class I subunits alpha and gamma.";
 RL Jpn. J. Genet. 62:241-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=86082371; PubMed=300832;
 RA Heden L.-O., Hoeoeg J.-O., Larsson K., Lake M., Lagerholm E.,
 RA Holmgren A., Vallee B.L., Joernvall H., von Bahr-Lindstrom H.;
 RT "cDNA clones coding for the beta-subunit of human liver alcohol
 RT dehydrogenase have differently sized 3'-non-coding regions.";
 RL FEBS Lett. 194:327-332(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=8611889; PubMed=2935533;
 RA Diester G., Smith M., Bilanhone V., Hatfield G.W.;
 RT "Molecular analysis of the human class I alcohol dehydrogenase gene
 RT family and nucleotide sequence of the gene encoding the beta
 RT subunit.";
 RL J. Biol. Chem. 261:2027-2033(1986).
 RN [5]
 RP SEQUENCE (BETA-1).
 RX MEDLINE=85076637; PubMed=6391920;
 RA Hempel U., Buhler R., Kaiser R., Holmquist B., de Zalenski C.,
 RA von Wartburg J.-P., Vallee B.L., Joernvall H.;

RT "Human liver alcohol dehydrogenase. 1. The primary structure of the
 RT beta 1 beta 1 isoenzyme.";
 RL Eur. J. Biochem. 145:437-445(1984).
 RN [6]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=89338401; Pubmed=2547609;
 RA Matsuo Y., Yokoyama R., Yokoyama S.;
 RT "The genes for human alcohol dehydrogenases beta 1 and beta 2 differ
 RT by only one nucleotide.";
 RL Eur. J. Biochem. 183:317-320(1989).
 RN [7]
 RP SEQUENCE FROM N.A. (BETA-3).
 RC TISSUE=Liver;
 RX MEDLINE=90024225; Pubmed=2679216;
 RA Carr L.G., Xu Y., Ho W.H., Ederberg H.J.;
 RT "Nucleotide sequence of the ADH2(3) gene encoding the human alcohol
 RT dehydrogenase beta 3 subunit.";
 RL Alcohol. Clin. Exp. Res. 13:594-596(1989).
 RN [8]
 RP SEQUENCE FROM N.A. (BETA-2).
 RC TISSUE=Liver;
 RA Polin L., Hey-Chi H.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88284639; Pubmed=3397059;
 RA Xu Y.L., Carr L.G., Bosron W.F., Li T.K., Ederberg H.J.;
 RT "Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci
 RT following DNA sequence amplification.";
 RL Genomics 2:209-214(1988).
 RN [10]
 RP SEQUENCE OF 40-85 FROM N.A.
 RA Oster M., Speed W.C., Seaman M.I., Kidd K.K.;
 RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP VARIANT BETA-2.
 RX MEDLINE=84221897; Pubmed=6374651;
 RA Joernvall H., Hempel J., Vallee B.L., Bosron W.F., Li T.-K.;
 RT "Human liver alcohol dehydrogenase: amino acid substitution in the
 RT beta 2 beta 2 Oriental isoenzyme explains functional properties;
 RT establishes an active site structure, and parallels mutational
 RT exchanges in the yeast enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3024-3028(1984).
 RN [12]
 RP VARIANT BETA-3.
 RX MEDLINE=87298549; Pubmed=3619918;
 RA Burnell J.C., Carr L.G., Dwulet F.E., Ederberg H.J., Li T.-K.,
 RA Bosron W.F.;
 RT "The human beta 3 alcohol dehydrogenase subunit differs from beta 1
 RT by a Cys for Arg-369 substitution which decreases NAD(H) binding.";
 RL Biochem. Biophys. Res. Commun. 146:1127-1133(1987).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=91376103; Pubmed=1896463;
 RA Hurley T.D., Bosron W.F., Hamilton J.A., Amzel L.M.;
 RT "Structure of human beta 1 beta 1 alcohol dehydrogenase: catalytic
 RT effects of non-active-site substitutions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8149-8153(1991).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94260547; Pubmed=8201622;
 RA Hurley T.D., Bosron W.F., Stone C.L., Amzel L.M.;
 RT "Structures of three human beta 1 alcohol dehydrogenase variants.
 RT Correlations with their functional differences.";
 RL J. Mol. Biol. 239:415-429(1994).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=96291846; Pubmed=8663387;
 RA Davis G.J., Bosron W.F., Stone C.L., Onusu-Dekyi K., Hurley T.D.;
 RT "X-ray structure of human betabeta3 alcohol dehydrogenase. The
 RT contribution of ionic interactions to coenzyme binding.";
 RL J. Biol. Chem. 271:17057-17061(1996).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +

CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
 CC MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
 CC ORIENTALS.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMS IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL; D00137; BAA00084.1; -;
 DR EMBL; X03350; CAA27056.1; -;
 DR EMBL; M24316; AAB59496.1; -;
 DR EMBL; M24308; AAB59496.1; JOINED.
 DR EMBL; M24309; AAB59496.1; JOINED.
 DR EMBL; M24310; AAB59496.1; JOINED.
 DR EMBL; M24311; AAB59496.1; JOINED.
 DR EMBL; M24312; AAB59496.1; JOINED.
 DR EMBL; M24313; AAB59496.1; JOINED.
 DR EMBL; M24314; AAB59496.1; JOINED.
 DR EMBL; M24317; AAB51884.1; -;
 DR EMBL; X15447; CAA33487.1; -;
 DR EMBL; X15448; CAA33487.1; JOINED.
 DR EMBL; X15449; CAA33487.1; JOINED.
 DR EMBL; X15450; CAA33487.1; JOINED.
 DR EMBL; X15451; CAA33487.1; JOINED.
 DR EMBL; X15452; CAA33487.1; JOINED.
 DR EMBL; X15453; CAA33487.1; JOINED.
 DR EMBL; X15454; CAA33487.1; JOINED.
 DR EMBL; X15455; CAA33487.1; JOINED.
 DR EMBL; X138290; AAB48003.1; -;
 DR EMBL; L38284; AAB48003.1; JOINED.
 DR EMBL; L38285; AAB48003.1; JOINED.
 DR EMBL; L38286; AAB48003.1; JOINED.
 DR EMBL; L38287; AAB48003.1; JOINED.
 DR EMBL; L38288; AAB48003.1; JOINED.
 DR EMBL; L38289; AAB48003.1; JOINED.
 DR EMBL; AF153821; AAD37446.1; -;
 DR EMBL; M21692; AAA51592.1; -;
 DR EMBL; AF040967; AAB96912.1; -;
 DR PIR; A23607; DEHUAB.
 DR PDB; 1HDY; 3I-JAN-94.
 DR PDB; 1HDZ; 3I-JAN-94.
 DR PDB; 3HDD; 3I-JAN-94.
 DR PDB; 1DEH; 08-MAR-96.
 DR PDB; 1HTB; 07-DEC-95.
 DR PDB; 1HSZ; 27-APR-01.
 DR Genew; HGNC:250; ADH1B.
 DR GKI; P00325; -;
 DR MIM; 103720; -;
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; TAS.
 DR GO; GO:0005489; F:electron transporter activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR GO; GO:0006069; P:ethanol oxidation; TAS.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.

KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 KM Acetylation; Polymorphism; 3D-structure.
 FT INIT MET 0 0
 FT MOD RES 1 1 ACETYLATION
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 Oy 1 CYS-----SKDNVKGVTGKTC 18
 Db 174 CGFSTGYSANVAKVTPGSGTC 195

RESULT 7
 TRVA RAT STANDARD; PRT; 246 AA.
 AC P3282;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin V-A precursor (EC 3.4.21.4).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=92165057; PubMed=1537555;
 RA Kang J., Wiegand U., Mueller-Hill B.;
 RT "Identification of cDNAs encoding two novel rat pancreatic serine
 proteases.";
 RL Gene 110:181-187(1992).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -----
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 CC -----
 CC EMBL; X59012; CAA41751.1; -;
 DR PIR; J01471; J01471.
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.092; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPsin.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; FALSE NEG.
 KM Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
 KW Multigene family.
 FT SIGNAL 1 15
 FT PROPEP 16 24
 FT CHAIN 25 246
 FT ACT_SITE 64 64 TRYPSIN V-A.
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 160
 FT DISULFID 49 65
 FT DISULFID 133 233
 FT DISULFID 133 233 BY SIMILARITY.
 FT DISULFID 133 233 BY SIMILARITY.

FT DISULFID 140 206 BY SIMILARITY.
 FT DISULFID 171 185 BY SIMILARITY.
 FT DISULFID 196 220 BY SIMILARITY.
 FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 246 AA; 26900 MW; 1EBB59DB8AB1715 CRC64;
 Query Match 43.1%; Score 44; DB 1; Length 246;
 Best Local Similarity 43.8%; Pred. No. 8.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Oy 3 FSSKDNVKGVTGKTC 18
 Db 16 PTFEDNDRLVGGVTC 31

RESULT 8
 TRVB RAT STANDARD; PRT; 246 AA.
 AC P3282;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin V-B precursor (EC 3.4.21.4).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=92165057; PubMed=1537555;
 RA Kang J., Wiegand U., Mueller-Hill B.;
 RT "Identification of cDNAs encoding two novel rat pancreatic serine
 proteases.";
 RL Gene 110:181-187(1992).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -----
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 CC -----
 CC EMBL; X59013; CAA41752.1; -;
 DR PIR; J01472; J01472.
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.093; -;
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00089; trypsin_1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; FALSE NEG.
 KM Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
 KW Multigene family.
 FT SIGNAL 1 15
 FT PROPEP 16 24
 FT CHAIN 25 246
 FT ACT_SITE 64 64 TRYPSIN V-B.
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 160
 FT DISULFID 49 65
 FT DISULFID 133 233
 FT DISULFID 140 206
 FT DISULFID 171 185
 FT DISULFID 196 220
 FT SITE 194 194
 FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 246 AA; 26819 MW; 1EB899CAlBAb0025 CRC64;

Query Match 43.1%; Score 44; DB 1; Length 246;
 Best Local Similarity 43.8%; Pred. No. 8.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVKGVTGKTC 18
 ID NKR_MOUSE STANDARD; PRT; 1453 AA.
 Db 16 FPFEDNDNDRIVGGYTC 31

RESULT 9

NKR_MOUSE
 ID NKR_MOUSE STANDARD; PRT; 1453 AA.
 AC P30415;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NK-tumor recognition protein (Natural-Killer cells cyclophilin-
 related protein) (NK-TR protein).
 GN NKTR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93133824; PubMed=8421688;
 RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,
 RT "A cyclophilin-related protein involved in the function of natural
 killer cells.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RC STRAIN=BALB/c; TISSUE=Blood;
 RA Anderson S.K.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
 CC INVOLVED IN THE FUNCTION OF NK CELLS.
 CC -1- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L04289; AAA37500.2; ALT_INT.
 DR HSSP; Q27450; 1A33.
 DR MCD; MG1; 97346; NKTR.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; Pro_Isoamrase; 1.
 DR PRINTS; PR00153; CSAPPISMPASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PSS0072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Repeat; Transmembrane.
 FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.
 FT DOMAIN 222 241 ARG/LYS-RICH (BASIC).
 FT DOMAIN 422 459 ARG/LYS-RICH (BASIC).
 FT DOMAIN 964 1003 ARG/LYS-RICH (BASIC).
 FT DOMAIN 198 273 ARG/SER-RICH.
 FT DOMAIN 468 565 ARG/SER-RICH.
 FT DOMAIN 658 812 ARG/SER-RICH.
 FT DOMAIN 1303 1453 ARG-SER TANDEN REPEAT-RICH.
 SQ SEQUENCE 1453 AA; 163439 MW; DF1173FF814B283E CRC64;

Query Match 43.1%; Score 44; DB 1; Length 1453;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
 ID NKR_MOUSE STANDARD; PRT; 1453 AA.
 Db 16 FPFEDNDNDRIVGGYTC 31

Db 41 CLCSGKGLGKTKTKLC 58

RESULT 10

NKR_HUMAN
 ID NKR_HUMAN STANDARD; PRT; 1462 AA.
 AC P30414;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NK-tumor recognition protein (Natural-Killer cells cyclophilin-
 related protein) (NK-TR protein).
 GN NKTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93133824; PubMed=8421688;
 RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,
 RT "A cyclophilin-related protein involved in the function of natural
 killer cells.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).
 RN [2]
 RP REVISIONS.
 RA Anderson S.K.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
 CC INVOLVED IN THE FUNCTION OF NK CELLS.
 CC -1- SUBCELLULAR LOCATION: Membrane-anchored. Attached to the membrane
 CC via its N-terminus.
 CC -1- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.
 CC -----
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 CC -----
 CC EMBL; L04288; AAA35734.2; -.
 DR EMBL; AF184110; AAD56402.1; -.
 DR HSSP; Q27450; 1A33.
 DR Genew; HGNC:7833; NKTR.
 DR MIM; 161565; -.
 DR GO; GO:0004600; F:cyclophilin; TAS.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; Pro_Isoamrase; 1.
 DR PRINTS; PR00153; CSAPPISMPASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PSS0072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Repeat; Membrane.
 FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.
 FT DOMAIN 219 240 ARG/LYS-RICH (BASIC).
 FT DOMAIN 421 457 ARG/LYS-RICH (BASIC).
 FT DOMAIN 970 1010 ARG/LYS-RICH (BASIC).
 FT DOMAIN 194 244 ARG/SER-RICH.
 FT DOMAIN 466 574 ARG/SER-RICH.
 FT DOMAIN 664 814 ARG/SER-RICH.
 FT DOMAIN 1311 1348 ARG-SER TANDEN REPEAT-RICH.
 SQ SEQUENCE 1462 AA; 165676 MW; D98A1147763E527 CRC64;

Query Match 43.1%; Score 44; DB 1; Length 1462;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
 ID NKR_HUMAN STANDARD; PRT; 1462 AA.
 Db 41 CLCSGKGLGKTKTKLC 58

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RESULT 11
ISPH_BRUME STANDARD; PRT; 346 AA.
AC Q8YFRI;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IspH protein.
GN IspH OR LYTB OR BMEI1459.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
NCBI_TaxID=29459;
RN
[1]
SEQUENCE FROM N.A.
RC STRAIN=16W / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kaparatou V., Redkar R.J., Patra G., Mujter C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldeman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Lelsson J.-U.,
RA Haelelorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
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-----
DR EMBL; AE009582; AAL52640.1; -.
DR PIR; AE3434; AE3434.
DR HAMAP; MF_00191; -.
DR InterPro; IPR003451; LYTB.
DR Pfam; PF02401; LYTB; 1.
DR TIGRFAMs; TIGR00216; isph_lytb; 1.
DR Isoprene biosynthesis; Complete proteome.
SQ SEQUENCE 346 AA; 37747 MW; EB9C1D60EF73421B CRC64;

Query Match 42.2%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CYFSSKDNVGVKVT 13
Db 161 CHFDDNDUGFVT 173

RESULT 12
AGI_HORVU STANDARD; PRT; 212 AA.
AC P15312;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Root-specific lectin precursor.
GN Hordeum vulgare (Barley).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
NCBI_TaxID=4513;
OX

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RN
[1]
SEQUENCE FROM N.A.
RA Lerner D.R., Raikhel N.V.;
RT "Cloning and characterization of root-specific barley lectin.";
RL Plant Physiol. 91:124-129(1989).
CC -1- FUNCTION: CARBOHYDRATE BINDING.
CC -1- SIMILARITY: Contains 4 chitin-binding domains.
-----
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-----
DR EMBL; M29280; AAA32969.1; -.
DR PIR; T05936; T05936.
DR HSSP; P10969; 1WGT.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00187; Chitin bind 1; 4.
DR PRINTS; PR00451; CHITINBINDING.
DR SMART; SM00270; CHTBD1; 4.
DR PROSITE; PS00026; CHITIN BINDING; 4.
KW Lectin; Repeat; Chitin-binding; Glycoprotein; Signal;
KW Pyroliidone carboxylic acid.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 212 ROOT-SPECIFIC LECTIN.
FT DOMAIN 27 69 CHITIN-BINDING 1.
FT DOMAIN 70 112 CHITIN-BINDING 2.
FT DOMAIN 113 155 CHITIN-BINDING 3.
FT DOMAIN 156 197 CHITIN-BINDING 4.
FT MOD_RES 27 27 PYROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
FT FT DISULFID 29 44 BY SIMILARITY.
FT FT DISULFID 38 50 BY SIMILARITY.
FT FT DISULFID 43 57 BY SIMILARITY.
FT FT DISULFID 61 66 BY SIMILARITY.
FT FT DISULFID 72 87 BY SIMILARITY.
FT FT DISULFID 81 93 BY SIMILARITY.
FT FT DISULFID 86 100 BY SIMILARITY.
FT FT DISULFID 104 109 BY SIMILARITY.
FT FT DISULFID 115 130 BY SIMILARITY.
FT FT DISULFID 124 136 BY SIMILARITY.
FT FT DISULFID 129 143 BY SIMILARITY.
FT FT DISULFID 147 152 BY SIMILARITY.
FT FT DISULFID 158 173 BY SIMILARITY.
FT FT DISULFID 167 179 BY SIMILARITY.
FT FT DISULFID 172 186 BY SIMILARITY.
FT FT DISULFID 190 195 BY SIMILARITY.
FT FT CARBOHYD 206 206 N-LINKED (GLCNAC...).
SQ SEQUENCE 212 AA; 21209 MW; BD948245D6B625A5 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 212;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Oy 1 CYFSSKDNVGVKVTGKTC 18
Db 66 CYTSKR--CTQAGKTC 81

RESULT 13
INCL_ECOLI STANDARD; PRT; 358 AA.
AC Q52312; P71175; Q52283;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein incC.
GN Escherichia coli.
OS Escherichia coli.
OG Plasmid Incp-beta R751.

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macartney D.P., Williams D.R., Stafford T., Foster A., Thomas C.M.;
 RT "Evolution of the partitioning and global regulation functions of
 the Incp central control region."
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-109 FROM N.A.
 RC STRAIN=K12 / C600;
 RX MEDLINE=95291464; PubMed=7773415;
 RA Thomas C.M., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;
 RT "Evolution of the korf-ori segment of promiscuous Incp plasmids."
 RL Microbiology 141:1201-1210(1995).
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS ENCODED BY THE TRPB OPERON;
 IT IS INVOLVED IN PLASMID MAINTENANCE AND REPLICATION (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY.
 CC -----
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 CC -----
 DR EMBL; U67194; AAC64421.1; -;
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 KW plasmid, DNA replication.
 SQ SEQUENCE 358 AA; 38246 MW; 44859F07844167BE CRC64;
 Query Match 41.2%; Score 42; DB 1; Length 358;
 Best Local Similarity 41.2%; Pred. No. 25;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CYFSKDNVKGKVTGGKT 17
 DB 45 CHFGADGGGAGGGS 61
 RESULT 14
 ADHI_RANPE STANDARD; PRT; 375 AA.
 ID ADHI_RANPE
 AC P22797;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase, major (EC 1.1.1.1).
 OS Rana perezi (Perez's frog) (Western Mediterranean green frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8403;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=91175722; PubMed=2007119;
 RA Cedergund E., Peralba J.M., Pares X., Joernvall H.;
 RT "Amphibian alcohol dehydrogenase, the major frog liver enzyme.
 RT Relationship to other forms and assessment of an early gene
 duplication separating vertebrate class I and class III alcohol
 dehydrogenases."
 RL Biochemistry 30:2811-2816(1991).
 RN [2]
 RP SEQUENCE OF 1-5.
 RX MEDLINE=90355571; PubMed=2387402;
 RA Egestad B., Estenius W., Danielsson O., Persson B., Cedergund E.,
 RA Kaiser R., Holmquist B., Vallee B., Pares X., Jefferey J.,
 RA Joernvall H.;
 RT "Fast atom bombardment mass spectrometry and chemical analysis in

RT determinations of acyl-blocked protein structures."
 RL FEBS Lett. 269:194-196(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 FAMILY. MORE CLOSELY RELATED TO CLASS I MAMMALIAN ENZYMES.
 DR PIR; A38405; A38405.
 DR HSSP; P00325; 1DEH.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Acetylation.
 FT MOD_RES 1
 FT METAL 46 46 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 68 68 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 98 98 ZINC 2 (BY SIMILARITY).
 FT METAL 101 101 ZINC 2 (BY SIMILARITY).
 FT METAL 104 104 ZINC 2 (BY SIMILARITY).
 FT METAL 112 112 ZINC 2 (BY SIMILARITY).
 FT METAL 175 175 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 375 AA; 40184 MW; 283E0A60E339195 CRC64;
 Query Match 41.2%; Score 42; DB 1; Length 375;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
 QY 1 CYFS---SKDNVKGKVTGGKT 18
 DB 175 CGFSTGSAVNTGKVPGSTC 196
 RESULT 15
 GUXC_FUSOX STANDARD; PRT; 514 AA.
 ID GUXC_FUSOX
 AC P46238;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Putative exoglucanase type C precursor (EC 3.2.1.91)
 DE (Exocellulohydrolase I) (1,4-beta-cellobiohydrolase)
 DE (Beta-glucanocellobiohydrolase).
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=5507;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95047531; PubMed=7959045;
 RA Sheppard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
 RA Hagen F.S., Upshall A., McKnight G.L., O'Hara P.J.;
 RT "The use of conserved cellulase family-specific sequences to clone
 RT cellulase homologue cDNAs from Fusarium oxysporum."
 RL Gene 150:163-167(1994).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 in cellulose and cellobiose, releasing cellobiose from the non-
 reducing ends of the chains.
 CC -1- SIMILARITY: Contains 1 fungal-type cellulose-binding (CBD) domain.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
 HYDROLASES).
 CC -----
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 CC -----
 DR EMBL; L29379; AAA65587.1; -;
 DR HSSP; P00725; 8CEL.

DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR01722; Glyco_hydro_7.
DR Pfam; PF00734; CBM_1; 1.
DR Pfam; PF00840; Glyco_hydro_7; 1.
DR ProDom; PD001821; CBD_fungal; 1.
DR ProDom; PD186135; Glyco_hydro_7; 1.
DR SMART; SM00236; fCBD; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
KM Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 514 PUTATIVE EXOGLUCANASE TYPE C.
FT DOMAIN 18 439 CATALYTIC.
FT DOMAIN 440 482 LINKER.
FT DOMAIN 483 514 CELLULOSE-BINDING (BY SIMILARITY).
FT ACT_SITE 229 229 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 234 234 PROTON DONOR (BY SIMILARITY).
FT DISULFID 486 503 BY SIMILARITY.
FT DISULFID 497 513 BY SIMILARITY.
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 514 AA; 54704 MW; 6A4617323A46E062 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 514;
Best Local Similarity 44.4%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVGAKTC 18
||| : | : |||
Db 66 CYTGKMDTSTICTDGKTC 83

Search completed: October 15, 2003, 16:58:15
Job time : 8.42934 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-11
Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	234	2	Q9RSX4
2	102	100.0	239	2	Q05157
3	102	100.0	239	2	Q53678
4	102	100.0	239	2	Q06532
5	102	100.0	239	2	Q06531
6	102	100.0	239	2	Q06533
7	102	100.0	266	16	Q8NXX6
8	102	100.0	271	2	Q9F0L6
9	96	94.1	239	2	Q06535
10	93	91.2	239	2	Q06534
11	55	53.9	511	16	Q8RI66
12	47	46.1	2108	5	Q815C7
13	46.5	45.6	505	2	Q50203
14	46	45.1	199	16	Q92CG4
15	46	45.1	233	11	Q9CRW4
16	46	45.1	263	11	Q8KH04

17	46	45.1	269	6	Q8MNN3	Q8MNN3 gorilla gor
18	45	44.1	276	4	Q9NBP0	Q9NBP0 homo sapien
19	44.5	43.6	107	4	Q9UB82	Q9UB82 homo sapien
20	44.5	43.6	457	12	Q9Y0Z1	Q9Y0Z1 randid herpe
21	44	43.1	275	5	Q16622	Q16622 caenorthabdi
22	44	43.1	299	10	Q8LAK6	Q8LAK6 arabidopsis
23	44	43.1	966	11	Q8CBP6	Q8CBP6 mus musculu
24	44	43.1	2301	5	Q95Z81	Q95Z81 oikopleura
25	43	42.2	126	5	Q95U05	Q95U05 branchiost
26	43	42.2	159	5	Q81TX7	Q81TX7 branchiost
27	43	42.2	274	10	Q9STR7	Q9STR7 arabidopsi
28	43	42.2	315	10	Q93VK9	Q93VK9 arabidopsi
29	43	42.2	368	5	Q9XXJ6	Q9XXJ6 caenorthabdi
30	43	42.2	372	16	Q8G257	Q8G257 bruceella su
31	43	42.2	765	5	Q26018	Q26018 plasmodium
32	43	42.2	765	5	Q81KT6	Q81KT6 plasmodium
33	43	42.2	1022	5	Q9W3E1	Q9W3E1 drosophila
34	42	41.2	148	16	Q8DRX5	Q8DRX5 streptococ
35	42	41.2	161	17	Q8TLN3	Q8TLN3 methanosarc
36	42	41.2	224	8	Q9ZGS7	Q9ZGS7 ceratocolen
37	42	41.2	235	16	Q8XET9	Q8XET9 escherichia
38	42	41.2	260	16	Q97M39	Q97M39 clostridium
39	42	41.2	278	2	Q51311	Q51311 nostoc punc
40	42	41.2	377	11	Q9QYY9	Q9QYY9 mus musculu
41	42	41.2	378	16	Q92FD6	Q92FD6 listeria in
42	42	41.2	378	16	Q8YAK1	Q8YAK1 listeria mo
43	42	41.2	430	16	Q9A3U5	Q9A3U5 caulobacter
44	42	41.2	1064	16	Q8XK16	Q8XK16 clostridium
45	41.5	40.7	731	16	Q8RG00	Q8RG00 fusobacteri

ALIGNMENTS

RESULT 1

Q9RSX4 PRELIMINARY; PRT; 234 AA.
ID Q9RSX4
AC Q9RSX4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; Pubmed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PR01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
DB 88 CYFSSKDNVKGVTGKTC 105

```
RESULT 2
005157 PRELIMINARY; PRT; 239 AA.
AC 005157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
  Berger P.H., Kapur V., Staefelcher C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
  Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro; IPR006177; Bcctl_tox.
DR InterPro; IPR006123; Scap/Strep_toxin.
DR InterPro; IPR006126; Scaph/Strep_tox.
DR InterPro; IPR006173; Scaph_tox_OB.
DR Pfam; PF01123; Scap_Strep_toxin; 1.
DR Pfam; PF02876; Scap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CYFSSKDNVKGVTGKTC 18
Db 93 CYFSSKDNVKGVTGKTC 110

RESULT 3
053678 PRELIMINARY; PRT; 239 AA.
AC 053678;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcctl_tox.
DR InterPro; IPR006123; Scap/Strep_toxin.
DR InterPro; IPR006126; Scaph/Strep_tox.
DR InterPro; IPR006173; Scaph_tox_OB.
DR Pfam; PF01123; Scap_Strep_toxin; 1.
DR Pfam; PF02876; Scap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;
```

```
Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CYFSSKDNVKGVTGKTC 18
Db 93 CYFSSKDNVKGVTGKTC 110

RESULT 4
006532 PRELIMINARY; PRT; 239 AA.
AC 006532;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcctl_tox.
DR InterPro; IPR006123; Scap/Strep_toxin.
DR InterPro; IPR006126; Scaph/Strep_tox.
DR InterPro; IPR006173; Scaph_tox_OB.
DR Pfam; PF01123; Scap_Strep_toxin; 1.
DR Pfam; PF02876; Scap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CYFSSKDNVKGVTGKTC 18
Db 93 CYFSSKDNVKGVTGKTC 110

RESULT 5
006531 PRELIMINARY; PRT; 239 AA.
AC 006531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; 1SE2.
```



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DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; B87BD6204731ED24 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 6
Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TIREMBLrel. 01, Created)
DT 01-NOV-1996 (TIREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TIREMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCOPEland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Robertson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL: L13378; AAA26622.1; -.
DR HSSP: P34071; 1STE.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386A8625 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 7
Q08XJ6 PRELIMINARY; PRT; 266 AA.
AC Q08XJ6;
DT 01-OCT-2002 (TIREMBLrel. 22, Created)
DT 01-OCT-2002 (TIREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TIREMBLrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
```

```
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
DR EMBL: AP004824; BAB94624.1; -.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 100.0%; Score 102; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 120 CYFSSKDNVGVKVTGKTC 137

RESULT 8
Q09F06 PRELIMINARY; PRT; 271 AA.
AC Q09F06;
DT 01-MAR-2001 (TIREMBLrel. 16, Created)
DT 01-MAR-2001 (TIREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TIREMBLrel. 23, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70 (2001).
DR EMBL: AF217235; AAG29599.1; -.
DR HSSP: P34071; 1SE2.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B0422F10 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 9.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
Db 125 CYFSSKDNVGVKVTGKTC 142
```

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RESULT 9
Q06535
ID Q06535 PRELIMINARY; PRT; 239 AA.
AC Q06535;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR1 909;
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; I13377; AAA26621.1; -.
DR HSSP; P2313; IUCK.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27648 MW; CC3CB04E4119E0 CRC64;

Query Match 94.1%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
Db 93 CYFSSKDNVKGVTGKTC 110

RESULT 10
Q06534
ID Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; I13379; AAA26623.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

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FT NON TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 91.2%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
Db 93 CYFSSKDNVKGVTGKTC 110

RESULT 11
Q08166
ID Q08166 PRELIMINARY; PRT; 511 AA.
AC Q08166;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Cysteine permease.
GN FN1747.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhatlacharya A., Bertain A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fornsstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018 (2002).
DR EMBL; AE010479; AAL93862.1; -.
DR InterPro; IPR002293; AA/re1_permeasel.
DR InterPro; IPR001463; Na/Ala_symport.
DR Pfam; PF01235; Na_Ala_sympt_1.
DR TIGRFAMs; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.
SQ SEQUENCE 511 AA; 56196 MW; 03D8A2859135EF3D CRC64;

Query Match 53.9%; Score 55; DB 16; Length 511;
Best Local Similarity 52.9%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 17
Db 128 CYRSKDETGRYFGGST 144

RESULT 12
Q08157
ID Q08157 PRELIMINARY; PRT; 2108 AA.
AC Q08157;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF1410C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

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RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shellenom S.J., Suh B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Salenog J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Sudramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RT "Genome sequence of the human malaria parasite *Plasmodium falciparum*.";
 RL Nature 419:498-511(2002).
 DR EMBL; AB014848; AAN36368.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 2108 AA; 248300 MW; 2B0464D22291B2D9 CRC64;
 QY Query March 46.1%; Score 47; DB 5; Length 2108;
 Db Best Local Similarity 32.4%; Pred. No. 1.3e+02;
 Matches 12; Conservative 2; Mismatches 3; Indels 20; Gaps 1;
 1 CYFSSKNDN-----VGRVTGKGT 17
 763 CYFSSKNDNDYILKNINLTLKNNSVLIIGVSGSKT 799
 RESULT 13
 ID 050203 PRELIMINARY; PRT; 505 AA.
 AC 050203;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Chloroacetaldehyde dehydrogenase.
 GN ALDA.
 OS Xanthobacter autotrophicus.
 OC plasmid linear plasmid pXAN1.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Xanthobacter.
 OX NCBI_TaxID=280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GT10;
 RX MEDLINE=98172729; PubMed=9511738;
 RA Bergeron H., Labbe D., Turmel C., Lau P.C.;
 RT "Cloning, sequence and expression of a linear plasmid-based and a
 RT chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
 RT in Xanthobacter autotrophicus GJ10.";
 RL Gene 207:9-18(1998).
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
 DR EMBL; AF029733; AAC13641.1; -.
 DR HSSP; P05091; 1CM3.
 DR InterPro: IPR002086; Aldehyde_dehydr.
 DR Pfam: PF001171; aldehyd; 1
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KM Oxidoreductase; Plasmid.
 SQ SEQUENCE 505 AA; 54945 MW; AD6A3EDB0297B04 CRC64;
 QY Query March 45.6%; Score 46.5; DB 2; Length 505;
 Db Best Local Similarity 58.8%; Pred. No. 33;
 Matches 10; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
 2 YFSSKDNVGVKGTGKTC 18
 34 YF---DNTSPVTGKIC 47
 RESULT 14
 ID 092CG4 PRELIMINARY; PRT; 199 AA.
 AC 092CG4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein lin1208.

GN LIN1208.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX PubMed=11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Ruanio C., Amend A.,
 RA Baquero F., Berche P., Bloecher H., Brande P., Chakraborty T.,
 RA Charbit A., Checouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeat O.,
 RA Entian K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkut G.,
 RA Medueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstrek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 DR EMBL; AL596168; CAC96439.1; -.
 DR ListList; LIN01208; -.
 DR InterPro: IPR001345; PG/BPGW_mutase.
 DR Pfam; PF00300; PGAM; 1.
 DR PROSITE; PS00175; PG_MUTASE; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 199 AA; 22902 MW; E14DD962F46BFE5 CRC64;
 QY Query March 45.1%; Score 46; DB 16; Length 199;
 Db Best Local Similarity 47.1%; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 2 YFSSKDNVGVKGTGKTC 18
 151 YWEKTSKIGKVTGKNC 167
 RESULT 15
 ID 09CRM4 PRELIMINARY; PRT; 233 AA.
 AC 09CRM4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Integral membrane protein 2 (Fragment).
 GN ITW2A OR ITW2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinsgawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Araiawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barz G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitlaxer C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;

```

RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
E EMBL; AK014024; BAB29119.1; -.
DR MGD; MGI:107706; Iem2a.
DR NON TER 1
FT 1
SQ SEQUENCE 233 AA; 26321 MW; B073D1FD94DEF2E9 CRC64;

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Query Match	45.1%	Score 46	DB 11	Length 233
Best Local Similarity	43.8%	Pred. No. 17		
Matches 7; Conservative	4	Mismatches 5	Indels 0	Gaps 0

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QY      1 CYFSSKDQNVGKVTGGK 16
        ||:||:| | :||:
Db      60 CFFDSEDPVNSIPGGE 75
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Search completed: October 15, 2003, 17:04:12
Job time : 39.8623 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-12

Sequence: 1 CYFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	18	20	AAV06249
2	102	100.0	18	20	ABG71377
3	102	100.0	18	24	ABG71380
4	102	100.0	238	12	AA13208
5	102	100.0	238	14	AA15016
6	102	100.0	238	22	AA17343
7	102	100.0	238	23	AA176239
8	102	100.0	239	12	AA13207
9	102	100.0	239	14	AA15015

10	102	100.0	239	20	AAV06255	Staphylococcal gro
11	102	100.0	239	20	AAV06256	Staphylococcal gro
12	102	100.0	239	20	AAV06251	Staphylococcal gro
13	102	100.0	239	20	AAV06252	Staphylococcal gro
14	102	100.0	239	20	AAV06253	Staphylococcal gro
15	102	100.0	239	22	AA167342	Staphylococcus aur
16	102	100.0	239	23	AB176238	Staphylococcus aur
17	102	100.0	240	24	AB171367	Staphylococcal ent
18	102	100.0	240	24	AB171368	Staphylococcal ent
19	102	100.0	240	24	AB171369	Staphylococcal ent
20	102	100.0	240	24	AB171371	Staphylococcal ent
21	102	100.0	240	24	AB171372	Staphylococcal ent
22	102	100.0	266	21	AA170108	Staphylococcal SEC
23	102	100.0	266	23	AB179507	Staphylococcal SEC
24	96	94.1	18	20	AAV06250	Staphylococcal gro
25	96	94.1	18	24	AB171378	Staphylococcal ent
26	96	94.1	239	20	AAV06254	Staphylococcal gro
27	96	94.1	239	20	AAV06257	Staphylococcal gro
28	96	94.1	240	24	AB171370	Staphylococcal ent
29	96	94.1	240	24	AB171373	Staphylococcal ent
30	93	91.2	18	24	AB171379	Staphylococcal ent
31	87	85.3	239	20	AAV06258	Staphylococcal gro
32	87	85.3	240	24	AB171374	Staphylococcal ent
33	66	64.7	14	20	AAV06259	Staphylococcal ent
34	66	64.7	14	24	AB171381	Staphylococcal ent
35	47	46.1	77	21	AA161245	Arabidopsis thalia
36	47	46.1	103	21	AA161244	Arabidopsis thalia
37	46	45.1	374	20	AA143983	Human alcohol dehy
38	46	45.1	374	20	AA143984	Human alcohol dehy
39	46	45.1	375	23	AB179657	Invertebrate forag
40	45	44.1	395	21	AA158159	Lung cancer associ
41	45	44.1	277	23	AA1597515	Novel human protei
42	45	44.1	513	22	AA173600	Zinc finger protei
43	44	43.1	299	21	AA160436	Arabidopsis thalia
44	44	43.1	315	21	AA160435	Arabidopsis thalia
45	44	43.1	340	21	AA160434	Arabidopsis thalia

ALIGNMENTS

RESULT 1
ID AAV06249 standard; Peptide: 18 AA.
XX AAV06249;
AC
XX 23-AUG-1999 (first entry)
DT
XX
XX Staphylococcal group C enterotoxin disulfide loop.
DE
XX Enterotoxin; SEC1; SEC2; SEC3 FRI 913; SEC3 4446; SEC-Bovine;
KW SEC-Ovine; toxin; disulfide loop; protein engineering.
XX
XX Staphylococcus aureus.
OS
XX
XX
XX W09927889-A2.
PN
XX
XX 10-JUN-1999.
PD
XX
XX 01-DEC-1998; 98WO-US25107.
PF
XX
XX 02-DEC-1997; 97US-0067357.
PR
XX
XX (IDAH-) IDAHO RES FOUND INC.
PA
XX Bohach GI;
PI
XX WPI: 1999-358008/30.
DR N-PSDB; AAX58884.
XX
XX Non-toxic modified staphylococcal enterotoxins
PT

CC	food poisoning. This sequence represents a staphylococcal enterotoxin
CC	disulphide loop region, occurring in several enterotoxins.
XX	
SQ	Sequence 18 AA;
OY	1 CYFSSKDNVKGKVTGKTC 18
Db	1 CYFSSKDNVKGKVTGKTC 18
RESULT 3	
ID	ABG71380 standard; Peptide; 18 AA.
XX	ABG71380;
XX	ABG71380;
XX	29-JAN-2003 (first entry)
XX	
DE	Staphylococcal enterotoxin C1 (SECI) protein fragment.
KW	Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW	emetic response-inducing activity; staphylococcal enterotoxin; SECI;
KW	toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
XX	
OS	Staphylococcus aureus.
XX	
FM	WO200283169-A1.
PD	24-OCT-2002.
XX	
PF	11-APR-2002; 2002WO-US11619.
XX	
PR	13-APR-2001; 2001US-283720P.
XX	
PA	(IDAH-) IDAHO RES POUND INC.
PI	Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX	
DR	WPI; 2003-058608/05.
XX	
XX	N-PSDB; ABS56822.
XX	
PT	New modified staphylococcal enterotoxin derived from a native disulphide
PT	loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT	an immune function and as a vaccine against toxic shock syndrome or
PT	food poisoning
XX	
PS	Example 1; Fig 1; 67pp; English.
XX	
CC	The invention relates to a modified pyrogenic toxin derived from a native
CC	disulphide loop-containing pyrogenic toxin where the modified toxin
CC	comprises a disulphide loop having no more than 10 amino acids. The
CC	modified toxin has a fever-inducing activity or an emetic
CC	response-inducing activity decreased by about 100-fold in comparison to a
CC	native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC	enterotoxin, is useful for non-specifically enhancing an immune function
CC	and for vaccination against diseases such as toxic shock syndrome and
CC	food poisoning. This sequence represents a staphylococcal enterotoxin
CC	protein fragment.
SQ	Sequence 18 AA;
OY	Query Match 100.0%; Score 102; DB 24; Length 18; Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Db	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	1 CYFSSKDNVKGKVTGKTC 18
XX	1 CYFSSKDNVKGKVTGKTC 18

```

RESULT 4
AAR13208
ID AAR13208 standard; Protein; 238 AA.
XX
AC AAR13208;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C3.
XX
KW SEC3; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1991; 91WO-US00342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SEC3 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydrophathy profiles.
CC See AAR13203-R13211.
XX
SQ Sequence 238 AA;
XX
Query Match 100.0%; Score 102; DB 12; Length 238;
Best Local Similarity 100.0%; Pred. No. 4,7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGKVTGKTC 18
Db 92 CYFSSKDNVKGKVTGKTC 109
XX
RESULT 5
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
AC AAR45016;
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEC3.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX

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PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US05213.
XX
PR 01-JUN-1992; 92US-0891718.
XX
PA (STON/) STONE J L.
PA (TERM/) Terman D S.
XX
PI Stone JL, Terman DS;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 238 AA;
XX
Query Match 100.0%; Score 102; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 4,7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGKVTGKTC 18
Db 92 CYFSSKDNVKGKVTGKTC 109
XX
RESULT 6
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
AC AAB67343;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin C3 protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-0183437.
XX
PR 31-JAN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91WO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX

```

DR WPI; 2001-158657/16.
XX
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro
PT or in vivo comprises exogenous nucleic acids encoding a superantigen
PT and a costimulatory molecule -
XX
XX Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and
CC expresses an exogenous nucleic acid molecule encoding a superantigen
CC or its active fragment and an exogenous nucleic acid molecule
CC encoding a costimulatory molecule that activates T cells in
CC conjunction with an antigenic stimulus. The invention may be used
CC for cancer therapy by stimulating an anticancer immune response
CC in vivo or ex vivo.
XX
SQ Sequence 238 AA;
Query Match 100.0%; Score 102; DB 22; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTGKTC 18
|||
DB 92 CYFSSKDNVGVKVTGKTC 109
RESULT 7
ABR76239
ID ABR76239 standard; Protein; 238 AA.
XX
AC ABR76239;
XX
DT 09-AUG-2002 (first entry)
XX
DE Staphylococcus aureus enterotoxin C3.
XX
KM Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
KM antitumour; therapy.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 208 /note= "given as 'O' in the specification"
XX
FN US2002051765-A1.
XX
PD 02-MAY-2002.
XX
PE 19-DEC-2000; 2000US-0741503.
XX
PR 31-JAN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91WO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2002-415198/44.
XX
PT Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens -
XX
XX Disclosure; Fig 2; 17pp; English.

CC The present sequence is the protein sequence of enterotoxin C3
CC (SEC3) of Staphylococcus aureus. Similarity is shown, in several
CC stretches of sequence, between staphylococcal enterotoxins,
CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative
CC toxins (see ABR76234-44). In the present invention, synthetic
CC polypeptides useful in tumour therapy and in blocking or destroying
CC autoreactive T and B lymphocyte populations are characterized by
CC substantial structural homology to staphylococcal enterotoxin A and
CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
CC statistically significant sequence homology and similarity (Z value
CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
CC 6) to include alignment of cysteine residues and similar hydrophathy
CC profiles. These superantigens are used to treat solid tumours,
CC including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient
CC with one or more superantigens ex vivo to generate stimulated cells,
CC selecting a specific V beta subset of cells, and reintroducing
CC these cells into the patient to induce an in vivo therapeutic,
CC tumoricidal reaction.
XX
SQ Sequence 238 AA;
Query Match 100.0%; Score 102; DB 23; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTGKTC 18
|||
DB 92 CYFSSKDNVGVKVTGKTC 109
RESULT 8
AAR13207
ID AAR13207 standard; Protein; 239 AA.
XX
AC AAR13207;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C1.
XX
KM SEC1; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
FN W09110680-A.
XX
PD 25-JUL-1991.
XX
PE 17-JAN-1991; 91WO-US00342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
XX Disclosure; Fig 1; 74pp; English.
XX
CC SEC1 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC1. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically

CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
CC See AAR13203-R13211.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 93 CYFSSKDNVKGKVTGKTC 110

RESULT 9

AAR45015 standard; protein; 239 AA.

XX AAR45015;

DT 25-MAR-2003 (updated)

DT 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SEC1.

KM Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KM autoimmune disease; toxicity; Protein A; perfusion system.

Staphylococcus aureus.

MO9324136-A1.

PD 09-DEC-1993.

PF 01-JUN-1993; 93MO-US05213.

PR 01-JUN-1992; 92US-0891718.

PA (STON/) STONE J L.
(TERM/) TERMAN D S.

PI Stone JL, Terman DS;

DR WPI; 1993-405418/50.

PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases

PS Disclosure; Fig 1; 90pp; English.

CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 239 AA;

Query Match 100.0%; Score 102; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 93 CYFSSKDNVKGKVTGKTC 110

RESULT 10

AAV06255
ID AAV06255 standard; Protein; 239 AA.

XX AAV06255;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-MNCopeland.

KM Enterotoxin; SEC-MNCopeland; toxin; disulfide loop;
KM protein engineering.

Staphylococcus aureus.

Key Location/Qualifiers
FT Disulfide-bond 93..110

PN WO9927889-A2.

PD 10-JUN-1999.

PF 01-DEC-1998; 98MO-US25107.

PR 02-DEC-1997; 97US-0067357.

PA (IDAH-) IDAHO RES FOUND INC.

PI Bohach GI;

DR WPI; 1999-358008/30.

PT Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 17; 25pp; English.

CC This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC-MNCopeland. The invention relates to pyrogenic
CC toxins, such as staphylococcal enterotoxins, modified in the
CC disulfide loop region. Typically, the modification involves
CC deletions within the disulfide loop region of SEC (see AAV06261).
CC The modified toxins retain useful biological properties, such as
CC the ability to induce cytokine production, but have substantially
CC reduced toxicity compared to the corresponding unmodified native
CC toxin. Emetic response inducing activity and fever inducing
CC activity are typically decreased by at least about 100-fold, while
CC LD50 (in Dutch Belted rabbits) is at least 100-fold higher than
CC the native toxin.

SO Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 93 CYFSSKDNVKGKVTGKTC 110

RESULT 11

AAV06256
ID AAV06256 standard; Protein; 239 AA.

XX AAV06256;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-4446.

KM Enterotoxin; SEC-4446; toxin; disulfide loop;
KM protein engineering.

Staphylococcus aureus.

```

XX Key Location/Qualifiers
FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX PS Disclosure; Page 17; 25pp; English.
XX
XX CC This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC-4446. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX belted rabbits) is at least 100-fold higher than the native toxin.
XX
XX SO Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGRVTGKTC 18
Db 93 CYFSSKDNVGRVTGKTC 110

RESULT 12
AAY06251
ID AAY06251 standard; Protein; 239 AA.
XX
XX AAY06251;
XX
XX 23-AUG-1999 (first entry)
XX
XX DE Staphylococcal group C enterotoxin SEC1.
XX
XX KM Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.
XX
XX OS Staphylococcus aureus.
XX
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 93..110
XX
XX PN WO9927889-A2.
XX
XX PD 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX

```

```

XX DR WPI; 1999-358008/30.
XX
XX FT Non-toxic modified staphylococcal enterotoxins
XX
XX PS Disclosure; Page 17; 25pp; English.
XX
XX CC This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC1. The invention relates to pyrogenic toxins, such
XX as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX belted rabbits) is at least 100-fold higher than the native toxin.
XX
XX SO Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGRVTGKTC 18
Db 93 CYFSSKDNVGRVTGKTC 110

RESULT 13
AAY06252
ID AAY06252 standard; Protein; 239 AA.
XX
XX AAY06252;
XX
XX 23-AUG-1999 (first entry)
XX
XX DE Staphylococcal group C enterotoxin SEC2.
XX
XX KM Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
XX
XX OS Staphylococcus aureus.
XX
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 93..110
XX
XX PN WO9927889-A2.
XX
XX PD 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX PI Bohach GI;
XX
XX DR WPI; 1999-358008/30.
XX
XX FT Non-toxic modified staphylococcal enterotoxins
XX
XX PS Disclosure; Page 17; 25pp; English.
XX
XX CC This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC2. The invention relates to pyrogenic toxins, such
XX as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX

```

CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGGKTC 18

DB 93 CYFSSKDNVKGKVTGGKTC 110

RESULT 14

AAV06253 standard; Protein; 239 AA.

XX AAV06253;

XX 23-AUG-1999 (first entry)

XX Staphylococcal group C enterotoxin SEC3-FRI913.

XX Enterotoxin; SEC3-FRI913; toxin; disulfide loop;

XX protein engineering.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Disulfide-bond 93..110

XX WO927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98MO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C

XX enterotoxin SEC3-FRI913. The invention relates to pyrogenic toxins,

XX such as staphylococcal enterotoxins, modified in the disulfide loop

XX region. Typically, the modification involves deletions within the

XX disulfide loop region of SEC (see AAV06261). The modified toxins

XX retain useful biological properties, such as the ability to induce

XX cytokine production, but have substantially reduced toxicity

XX compared to the corresponding unmodified native toxin. Emetic

XX response inducing activity and fever inducing activity are

XX typically decreased by at least about 100-fold, while LD50 (in Dutch

XX belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGGKTC 18

DB 93 CYFSSKDNVKGKVTGGKTC 110

RESULT 15

AA67342 standard; peptide; 239 AA.

XX AAB67342;

XX 23-APR-2001 (first entry)

XX Staphylococcus aureus enterotoxin C1 protein.

XX Tumour; cancer; immune; enterotoxin.

XX Staphylococcus aureus.

XX US6180097-B1.

XX 30-JAN-2001.

XX 30-OCT-1998; 98US-0183437.

XX 31-JAN-1994; 94US-0189424.

XX 19-JUN-1995; 95US-0491746.

XX 03-OCT-1989; 89US-0416530.

XX 17-JAN-1990; 90US-046577.

XX 17-JAN-1991; 91MO-US00342.

XX 01-JUN-1992; 92US-0891718.

XX 02-MAR-1993; 93US-0025144.

XX (TERM/) TERNAN D S.

XX Terman DS;

XX WPI; 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro

XX or in vivo comprises exogenous nucleic acids encoding a superantigen

XX and a costimulatory molecule

XX Disclosure; Fig 2; 16pp; English.

XX The present invention relates to a tumour cell capable of stimulating

XX antitumor immune reactivity in vitro or in vivo contains and

XX expresses an exogenous nucleic acid molecule encoding a superantigen

XX or its active fragment and an exogenous nucleic acid molecule

XX encoding a costimulatory molecule that activates T cells in

XX conjunction with an antigenic stimulus. The invention may be used

XX for cancer therapy by stimulating an anticancer immune response

XX in vivo or ex vivo.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 22; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGGKTC 18

DB 93 CYFSSKDNVKGKVTGGKTC 110

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Job time : 49.3575 sec

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Perfect score: 102
Sequence: 1 CYFSSKDNVGVTKGKTC 18

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Searched: 328717 seqs, 42310858 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	102	100.0	89	4	US-09-144-776B-21	Sequence 21, Appl
2	102	100.0	89	4	US-09-144-776B-22	Sequence 22, Appl
3	102	100.0	89	4	US-09-144-776B-23	Sequence 23, Appl
4	102	100.0	238	3	US-08-896-933-28	Sequence 28, Appl
5	102	100.0	238	4	US-09-114-235-28	Sequence 28, Appl
6	102	100.0	239	3	US-08-896-933-27	Sequence 27, Appl
7	102	100.0	239	4	US-09-114-235-27	Sequence 27, Appl
8	102	100.0	266	4	US-09-144-776B-14	Sequence 14, Appl
9	48	47.1	170	4	US-09-252-991A-29047	Sequence 29047, A
10	46	45.1	263	2	US-08-892-690-3	Sequence 3, Appl
11	46	45.1	374	2	US-07-857-224B-82	Sequence 82, Appl
12	46	45.1	374	2	US-07-857-224B-83	Sequence 83, Appl
13	46	45.1	375	4	US-09-347-878-56	Sequence 56, Appl
14	44	43.1	134	2	US-08-482-128A-14	Sequence 14, Appl
15	44	43.1	176	1	US-08-145-895A-4	Sequence 4, Appl
16	44	43.1	176	2	US-08-451-747-4	Sequence 4, Appl
17	44	43.1	176	3	US-09-134-852-4	Sequence 4, Appl
18	42	41.2	514	1	US-08-361-820-21	Sequence 21, Appl
19	42	41.2	514	1	US-08-479-939-21	Sequence 21, Appl
20	42	41.2	514	1	US-08-483-432-21	Sequence 21, Appl
21	40.5	39.7	155	4	US-09-252-991A-19995	Sequence 19995, A
22	40	39.2	210	4	US-09-247-155-121	Sequence 121, App
23	40	39.2	264	3	US-08-924-570A-2	Sequence 2, Appl
24	40	39.2	320	3	US-09-092-437-2	Sequence 2, Appl
25	40	39.2	374	2	US-07-857-224B-80	Sequence 80, Appl
26	40	39.2	374	2	US-07-857-224B-81	Sequence 81, Appl
27	40	39.2	374	2	US-07-857-224B-84	Sequence 84, Appl

28	40	39.2	374	2	US-07-857-224B-85	Sequence 85, Appl
29	40	39.2	375	2	US-07-857-224B-86	Sequence 86, Appl
30	40	39.2	412	2	US-08-741-134-2	Sequence 2, Appl
31	40	39.2	690	4	US-09-252-991A-29429	Sequence 29429, A
32	40	39.2	1053	4	US-09-328-352-67881	Sequence 6788, Ap
33	39.5	38.7	765	4	US-09-252-991A-24791	Sequence 24791, A
34	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
35	39	38.2	94	2	US-07-728-215-37	Sequence 37, Appl
36	39	38.2	94	4	US-08-938-085A-35	Sequence 35, Appl
37	39	38.2	94	4	US-08-938-085A-37	Sequence 37, Appl
38	39	38.2	94	4	US-10-072-844-35	Sequence 35, Appl
39	39	38.2	94	4	US-10-072-844-37	Sequence 37, Appl
40	39	38.2	95	4	US-09-107-532A-6140	Sequence 6140, Ap
41	39	38.2	228	1	US-08-483-859-7	Sequence 7, Appl
42	39	38.2	228	1	US-08-483-859-7	Sequence 7, Appl
43	39	38.2	228	1	US-08-472-173-7	Sequence 7, Appl
44	39	38.2	228	2	US-08-487-167-7	Sequence 7, Appl
45	39	38.2	228	2	US-08-482-816-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-144-776B-21
Sequence 21, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09144, 776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21
Query Match 100.0%; Score 102; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
Db 54 CYFSSKDNVKGVTGKTC 71

RESULT 2

US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-144-776B-22

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
Db 54 CYFSSKDNVKGVTGKTC 71

RESULT 3

US-09-144-776B-23
; Sequence 23, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson

Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
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; APPLICATION NUMBER: US/09/144,776B
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-144-776B-23

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
Db 54 CYFSSKDNVKGVTGKTC 71

RESULT 4

US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: Tumor Killing Effects of Enterotoxins,
; and Related Compounds
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28

Query Match 100.0%; Score 102; DB 3; Length 238;

Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 92 CYFSSKDNVGVGTGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-28

Query Match 100.0%; Score 102; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 92 CYFSSKDNVGVGTGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

Query Match 100.0%; Score 102; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 93 CYFSSKDNVGVGTGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-27

Query Match 100.0%; Score 102; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 93 CYFSSKDNVGVGTGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match 100.0%; Score 102; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
Db 120 CYFSSKDNVKGVTGKTC 137

RESULT 9
US-09-252-991A-29047
Sequence 29047, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29047
LENGTH: 170
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29047

Query Match 47.1%; Score 48; DB 4; Length 170;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTG 14
Db 116 CSFARNDNAGRATG 129

RESULT 10
US-08-892-690-3
Sequence 3, Application US/08892690
Patent No. 5932420
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,690
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0339 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 624778
US-08-892-690-3

Query Match 45.1%; Score 46; DB 2; Length 263;
Best Local Similarity 43.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGK 16
Db 90 CFTFSDPVSNIPIGE 105

RESULT 11
US-07-857-224B-82
Sequence 82, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none

INFORMATION FOR SEQ ID NO: 82;
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: human
FEATURE: Alcohol dehydrogenase, Table 3 Column 3
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Joernvall, H.
AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-82

Query Match 45.1%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18
DB 174 CGFSTGYGSAVNAVKTGSTC 195

RESULT 12
US-07-857-224B-83
Sequence 83, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICANT: Benner, Steven A.
FILING DATE: 03/25/92
CLASSIFICATION: 436
NUMBER OF SEQUENCES: 21
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
INFORMATION FOR SEQ ID NO: 83;
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: human
FEATURE: Alcohol dehydrogenase, Table 3 Column 4
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Joernvall, H.

AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-83

Query Match 45.1%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18
DB 174 CGFSTGYGSAVNAVKTGSTC 195

RESULT 13
US-09-347-878-56
Sequence 56, Application US/09347878C
Patent No. 6376210
GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-878-56

Query Match 45.1%; Score 46; DB 4; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGYTGKTC 18
DB 175 CGFSTGYGSAVNAVKTGSTC 196

RESULT 14
US-08-482-728A-14
Sequence 14, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802e1 Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Holbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Wang, Bruce
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-14

Query Match 43.1%; Score 44; DB 2; Length 134;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
| : : : : :
Db 21 CLCSGKGLGKTTGKKLC 38

RESULT 15

US-08-145-995A-4
Sequence 4, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-4

Query Match 43.1%; Score 44; DB 1; Length 176;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
| : : : : :
Db 41 CLCSGKGLGKTTGKKLC 58

Search completed: October 15, 2003, 17:08:31
Job time: 13.7964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 : Search time 27.2695 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115a-12

Perfect score: 102
Sequence: 1 CYFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: /cgn2_6/prodata/1/pubppa/PCR_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppa/PCRUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	89	15	US-10-002-784A-36 Sequence 36, Appl
2	102	100.0	89	15	US-10-002-784A-37 Sequence 37, Appl
3	102	100.0	89	15	US-10-002-784A-38 Sequence 38, Appl
4	102	100.0	266	8	US-08-882-431-14 Sequence 14, Appl
5	102	100.0	266	10	US-09-870-759-12 Sequence 12, Appl
6	102	100.0	266	12	US-09-751-708A-12 Sequence 12, Appl
7	102	100.0	266	15	US-10-002-784A-14 Sequence 14, Appl
8	46	45.1	263	9	US-09-265-710-3 Sequence 3, Appl
9	46	45.1	263	12	US-10-366-020-3 Sequence 13, Appl
10	46	45.1	375	10	US-09-981-353-113 Sequence 92, Appl
11	46	45.1	375	12	US-09-738-630-92 Sequence 97, Appl
12	46	45.1	395	9	US-09-925-302-497 Sequence 8802, Ap
13	42	41.2	211	15	US-10-156-761-8802 Sequence 54, Appl
14	42	41.2	332	15	US-10-021-811-54 Sequence 3467, Ap
15	41.5	40.7	993	15	US-10-128-714-3467

16	41.5	40.7	1105	15	US-10-128-714-8467	Sequence 8467, Ap
17	41	40.2	163	12	US-10-238-075-786	Sequence 786, App
18	41	40.2	307	11	US-09-764-891-4188	Sequence 4188, Ap
19	40.5	39.7	1139	15	US-10-156-761-10856	Sequence 10856, A
20	40	39.2	152	12	US-10-040-895-2	Sequence 2, Appl
21	40	39.2	210	12	US-09-903-190-121	Sequence 121, App
22	40	39.2	263	9	US-09-823-356-13	Sequence 43, Appl
23	40	39.2	263	12	US-09-946-374-43	Sequence 13, Appl
24	40	39.2	263	12	US-10-015-3872A-43	Sequence 43, Appl
25	40	39.2	263	12	US-10-006-120A-43	Sequence 184, App
26	40	39.2	263	12	US-10-199-672-184	Sequence 184, App
27	40	39.2	263	12	US-10-006-172A-43	Sequence 43, Appl
28	40	39.2	263	12	US-10-187-749-184	Sequence 184, App
29	40	39.2	263	12	US-10-194-457-184	Sequence 184, App
30	40	39.2	263	12	US-10-184-642-184	Sequence 184, App
31	40	39.2	263	12	US-10-196-747-184	Sequence 184, App
32	40	39.2	263	12	US-10-015-392A-43	Sequence 43, Appl
33	40	39.2	263	12	US-10-017-253A-43	Sequence 43, App
34	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
35	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
36	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
37	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
38	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
39	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
40	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
41	40	39.2	263	12	US-10-173-659-184	Sequence 184, App
42	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
43	40	39.2	263	12	US-10-174-583-184	Sequence 184, App
44	40	39.2	263	12	US-10-174-587-184	Sequence 184, App
45	40	39.2	263	12	US-10-174-589-184	Sequence 184, App

ALIGNMENTS

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RESULT 1
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36
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Query Match 100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
Db 54 CYFSSKDNVGVTKGKTC 71

RESULT 2
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
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; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO: 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in figure 3
; US-10-002-784A-37

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6,6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGGKTC 18
Db      54  CYFSSKDNVGVKVTGGKTC 71

RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO: 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in figure 3
; US-10-002-784A-38

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6,6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGGKTC 18
Db      54  CYFSSKDNVGVKVTGGKTC 71

RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
```

```

; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14

Query Match      100.0%; Score 102; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 2,2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGGKTC 18
Db      120  CYFSSKDNVGVKVTGGKTC 137

RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US2002017751A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-870-759-12

Query Match      100.0%; Score 102; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 2,2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGGKTC 18
Db      120  CYFSSKDNVGVKVTGGKTC 137

RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
```

GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match 100.0%; Score 102; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
DB 120 CYFSSKDNVKGKVTGKTC 137

RESULT 7
US-10-002-784A-14
Sequence 14, Application US/10002784A
Publication No. US2003003644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 14
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 100.0%; Score 102; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
DB 120 CYFSSKDNVKGKVTGKTC 137

RESULT 8
US-09-265-710-3
Sequence 3, Application US/09265710
Patent No. US20020042126A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lai, Preeti
APPLICANT: Shah, Purni
TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,690
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: o Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0339 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 624778
US-09-265-710-3

Query Match 45.1%; Score 46; DB 9; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGK 16
DB 90 CFFDSEDVNSIPGGE 105

RESULT 9
US-10-366-020-3
Sequence 3, Application US/10366020
Publication No. US20030152989A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/366,020
FILING DATE: 11-Feb-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/207,161
FILING DATE: 1998-12-07
APPLICATION NUMBER: US/08/791,338
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

```

;
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0208 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 263 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;       LIBRARY: GenBank
;       CLONE: 624778
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
US-10-366-020-3

Query Match      45.1%; Score 46; DB 12; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Cy      1  CYFS---SKDNVKGKVTGKTC 16
Db      90  CFFDSEDPVNSIPGGE 105

RESULT 10
US-09-981-353-113
; Sequence 113, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
;   APPLICANT: Lasek, Amy W.
;   APPLICANT: Jones, David A.
;   TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;   FILE REFERENCE: PA-0038 US
;   CURRENT APPLICATION NUMBER: US/09/981,353
;   CURRENT FILING DATE: 2001-10-11
;   NUMBER OF SEQ ID NOS: 194
;   SOFTWARE: PERL Program
;   SEQ ID NO 113
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: Incyte ID No. US20020160382A1 2512879CD1
US-09-981-353-113

Query Match      45.1%; Score 46; DB 10; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy      1  CYFS---SKDNVKGKVTGKTC 18
Db      175  CGFSTGYGSANVAKVTPGSTC 196

RESULT 11
US-09-738-630-92
; Sequence 92, Application US/09738630
; Publication No. US2003016621A1
; GENERAL INFORMATION:
;   APPLICANT: Greenspan, Ralph J.
;   APPLICANT: Shaw, Paul J.
;   TITLE OF INVENTION: Methods For Identifying Compounds That
;   TITLE OF INVENTION: Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
;   TITLE OF INVENTION: Protein Kinase Signaling
;   FILE REFERENCE: P-NI 3906
;   CURRENT APPLICATION NUMBER: US/09/738,630
;   CURRENT FILING DATE: 2000-12-15
;   NUMBER OF SEQ ID NOS: 105
;   SOFTWARE: PaetSeq for Windows Version 4.0
;   SEQ ID NO 92
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;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-738-630-92

Query Match      45.1%; Score 46; DB 12; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy      1  CYFS---SKDNVKGKVTGKTC 18
Db      175  CGFSTGYGSANVAKVTPGSTC 196

RESULT 12
US-09-925-302-497
; Sequence 497, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA104
;   CURRENT APPLICATION NUMBER: US/09/925,302
;   CURRENT FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: PCT/US00/05918
;   PRIOR FILING DATE: 2000-03-08
;   PRIOR APPLICATION NUMBER: 60/124,270
;   PRIOR FILING DATE: 1999-03-12
;   NUMBER OF SEQ ID NOS: 896
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 497
;   LENGTH: 395
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (164)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-497

Query Match      45.1%; Score 46; DB 9; Length 395;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy      1  CYFS---SKDNVKGKVTGKTC 18
Db      195  CGFSTGYGSANVAKVTPGSTC 216

RESULT 13
US-10-156-761-8802
; Sequence 8802, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;   APPLICANT: OMURA, SATOSHI
;   APPLICANT: IKEDA, HARUO
;   APPLICANT: ISHIKAWA, JUN
;   APPLICANT: HORIKAWA, HIROSHI
;   APPLICANT: SHIBA, TADAYOSHI
;   APPLICANT: SAKAKI, YOSHIYUKI
;   APPLICANT: HATTORI, MASAHIRA
;   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;   FILE REFERENCE: 249-262
;   CURRENT APPLICATION NUMBER: US/10/156,761
;   CURRENT FILING DATE: 2002-05-29
;   PRIOR APPLICATION NUMBER: JP 2001-204089
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-272697
;   PRIOR FILING DATE: 2001-08-02
;   NUMBER OF SEQ ID NOS: 15109
;   SEQ ID NO 8802
;   LENGTH: 211
;   TYPE: PRT
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-8802

Query Match 41.2%; Score 42; DB 15; Length 211;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YFSSKDNVGVKT 13
:|||||:|
Db 58 HFSSKDNLTAKT 69

RESULT 14

US-10-021-811-54
; Sequence 54, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Pang, Yiwen
; APPLICANT: Odell, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BSI294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 54
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Glycine max
US-10-021-811-54

Query Match 41.2%; Score 42; DB 15; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKTGG 15
|||:|:|
Db 197 CYASSADNIARMLKG 211

RESULT 15

US-10-128-714-3467
; Sequence 3467, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Meng
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3467

; LENGTH: 993
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3467

Query Match 40.7%; Score 41.5; DB 15; Length 993;
Best Local Similarity 40.9%; Pred. No. 4.3e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 9; Gaps 1;

QY 5 SKDNV-----GKVTGSKT 17
:||||:|
Db 102 TKDNICFQIDABEGTITGKT 123

Search completed: October 15, 2003, 17:47:00
Job time : 28.2695 secs

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A;Residues: 1-266 <BOH>
A;Accession: B60114
A;Molecule type: Protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA2624.1; PID:g153004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domin: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 120 CYFSSKDNVKGKVTGKTC 137

RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S11885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
A;Reference number: S11885; MUID:90220508; PMID:2235627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
A;Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B

Query Match 100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
Db 120 CYFSSKDNVKGKVTGKTC 137

RESULT 4
AG1583
weakly phosphoglycerate mutase 1 homolog lin1208 [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1583
R;Gasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baguerio, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreitel, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maltournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <GUA>
A;Cross-references: GB:AL592022; PIDN:CAC96439.1; PID:g16413682; GSPDB:GN00178

A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin1208

Query Match 45.1%; Score 46; DB 2; Length 199;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YFSSKDNVKGKVTGKTC 18
Db 151 YFSSKDNVKGKVTGKTC 167

RESULT 5
DEHUA
alcohol dehydrogenase (EC 1.1.1.1) 1 - human
N;Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
C;Accession: S02265; A25428; A24408; I39398; I39397
R;Matsumoto, Y.; Yokoyama, S.
FEBS Lett. 243, 57-60, 1989
A;Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
A;Reference number: S02265; MUID:89153548; PMID:2920825
A;Accession: S02265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-375 <MATS>
R;Ikuta, T.; Szeto, S.; Yoshida, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
A;Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and ev
A;Reference number: A94120; MUID:66120995; PMID:2935875
A;Accession: g25428
A;Molecule type: mRNA
A;Residues: 1-375 <IKU>
A;Cross-references: GB:M12271; NID:g178091; PIDN:AAA68131.1; PID:g178092
R;von Bahr-Lindstrom, H.; Hoeg, J.O.; Heden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K.
Biochemistry 25, 2465-2470, 1986
A;Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
A;Reference number: A24408; MUID:86243367; PMID:3013304
A;Accession: A24408
A;Molecule type: mRNA
A;Residues: 1-375 <VON>
A;Cross-references: GB:M12963; NID:g178089; PIDN:AAA51590.1; PID:g178090
R;Yasunami, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
Genomics 7, 152-158, 1990
A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
A;Reference number: I39398; MUID:90269803; PMID:2347582
A;Accession: I39398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <YAS>
A;Cross-references: GB:M37066; NID:g178095; PIDN:AAA51591.1; PID:g178096
R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
Gene 90, 271-279, 1990
A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: intere
A;Reference number: I39397; MUID:90382676; PMID:2169444
A;Accession: I39397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <STE>
A;Cross-references: GB:M32656; NID:g178093; PIDN:AAA52276.1; PID:g178094
C;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activit
C;Genetics:
A;Gene: GDB:ADH1
A;Cross-references: GDB:119650; OMIM:103700
A;Map position: 4q21-4q23
A;Intons: 6/3; 40/3; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
A;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: ethanol degradation
A;Note: human alcohol dehydrogenase 1 is expressed predominantly in fetal and neonatal li

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F1:2-375/Product: alcohol dehydrogenase 1 #status predicted <MAT>
 F1:2-366/Domains: long-chain alcohol dehydrogenase homology <LADH>
 F1:195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F1:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F1:47,66,115/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F1:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 45.1%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYS-----SKDNKGYTGCTC 18
 DB 175 CGFSTGYGSANVNAKVTGSGTC 196

RESULT 6

DEHUB

alcohol dehydrogenase (EC 1.1.1.1) 2 [validated] - human
 N:Alternate names: alcohol dehydrogenase beta chain; class I alcohol dehydrogenase
 C:Species: Homo sapiens (man)
 C:Date: 25-Feb-1985 #sequence revision 02-Aug-1994 #text change 15-Sep-2000
 C:Accession: A23607; A28916; I39399; A26281; I39401; S05202; S10621; I39400; A00
 R:Heden, L.O.; Hoog, J.O.; Larsson, K.; Lake, M.; Lagerholm, E.; Holmgren, A.; Vallée, H.
 FEBS Lett. 194, 327-332, 1986
 A>Title: cDNA clones coding for the beta-subunit of human liver alcohol dehydrogenase
 A:Reference number: A23607; MUID:86082371; PMID:3000832
 A:Accession: A23607
 A:Molecule type: mRNA
 A:Residues: 1-375 <HED>
 A:Cross-references: EMBL:X03350; NID:g28415; PIDN:CAA27056.1; PID:g28416
 R:Ikuta, T.; Fujiyoshi, T.; Kuwachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2703-2707, 1985
 A>Title: Molecular cloning of a full-length cDNA for human alcohol dehydrogenase.
 A:Reference number: A38916; MUID:85190565; PMID:2966130
 A:Accession: A38916
 A:Molecule type: mRNA
 A:Residues: 1-375 <IKU>
 A:Cross-references: GB:M24317; NID:g178097
 A>Note: this sequence has been revised in reference A38917
 R:Ikuta, T.; Fujiyoshi, T.; Kuwachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5578, 1985
 A:Reference number: A38917
 A:Contents: annotation; erratum
 R:Yokoyama, S.; Yokoyama, R.; Rotwein, P.
 Jpn. J. Genet. 62, 241-256, 1987
 A>Title: Molecular characterization of cDNA clones encoding the human alcohol dehydrogenase
 A:Reference number: I39399
 A:Accession: I39399
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-375 <YOK>
 A:Cross-references: GB:M24317; NID:g219427; PIDN:BA00084.1; PID:g219428
 R:Duester, G.; Smith, M.; Blanchone, V.; Hatfield, G.W.
 J. Biol. Chem. 261, 2027-2033, 1986
 A>Title: Molecular analysis of the human class I alcohol dehydrogenase gene family and n
 A:Reference number: A26281; MUID:8611189; PMID:2935533
 A:Accession: A26281
 A:Molecule type: DNA
 A:Residues: 1-229, 'K', 231-375 <DUE>
 A:Cross-references: GB:M24317; GB:K01883; NID:g178097; PIDN:AAA51884.1; PID:g178098
 A>Note: the authors translated the codon AAA for residue 230 as Phe
 R:Tasunuma, M.; Kikuchi, I.; Satrapata, D.; Yoshida, A.
 Genomics 7, 152-158, 1990
 A>Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly
 A:Reference number: I39398; MUID:90269803; PMID:2347582
 A:Accession: I39402
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-6 <YAS>
 A:Cross-references: GB:M37067; NID:g178114; PIDN:AAA51593.1; PID:g178115

R:Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990
 A>Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: intere
 A:Reference number: I39397; MUID:90382676; PMID:2169444
 A:Accession: I39401
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <STE>
 A:Cross-references: GB:M3657; NID:g178112; PIDN:AAA52277.1; PID:g178113
 R:Matsumoto, Y.; Yokoyama, R.; Yokoyama, S.
 Eur. J. Biochem. 183, 317-320, 1989
 A>Title: The genes for human alcohol dehydrogenases beta(1) and beta(2) differ by only or
 A:Reference number: S05202; MUID:89338401; PMID:2547609
 A:Accession: S05202
 A:Molecule type: DNA
 A:Residues: 1-47, 'H', 49-375 <MAT>
 A:Cross-references: EMBL:X15447; NID:g28385
 A>Note: allelic beta-2 variant found predominately in oriental populations
 A>Note: the sequence in GenBank entry HSADH221, release 103 (PID:g228260), has an incorre
 R:Brigg, T.; von Wartburg, J.P.; Wermuth, B.
 FEBS Lett. 234, 53-55, 1988
 A>Title: cDNA sequence of the beta(2)-subunit of human liver alcohol dehydrogenase.
 A:Reference number: S10621; MUID:88271624; PMID:2968918
 A:Accession: S10621
 A:Molecule type: mRNA
 A:Residues: 1-47, 'H', 49-343 <EHR>
 A>Note: only a list of differences from various previously published sequences is shown
 R:Xu, Y.L.; Carr, L.G.; Boston, W.F.; Li, T.K.; Edenberg, H.J.
 Genomics 2, 209-214, 1988
 A>Title: Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci following I
 A:Reference number: I39400; MUID:88284699; PMID:3397059
 A:Accession: I39400
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7, 'M', 9-56, 'K', 58-165, 'K', 167-234, 'V', 236-375 <RE3>
 A:Cross-references: GB:M21692; NID:g178099; PIDN:AAA51592.1; PID:g178100
 R:Hempel, J.; Buhler, R.; Kaiser, R.; Holmquist, B.; de Zalsenski, C.; von Wartburg, J.P.;
 Eur. J. Biochem. 145, 437-445, 1984
 A>Title: Human liver alcohol dehydrogenase. 1. The primary structure of the beta-1beta-1
 A:Reference number: A00335; MUID:85076537; PMID:6391920
 A:Accession: A00335
 A:Molecule type: protein
 A:Residues: 2-129, 131-375 <HEM>
 A>Note: allelic beta-1 variant found predominately in caucasian and negroid populations
 R:Buhler, R.; Hempel, J.; Kaiser, R.; von Wartburg, J.P.; Vallée, B.L.; Jorvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6320-6324, 1984
 A>Title: Human alcohol dehydrogenase: structural differences between the beta and gamma f
 ndants in livers of different mammals.
 A:Reference number: A05182; MUID:85038508; PMID:6387702
 A:Accession: A05182
 A:Molecule type: protein
 A:Residues: 12-34, 'V', 36-38, 41-85, 101-114, 131-160, 170-213, 273-313, 317-331, 341-367 <BUH>
 R:Burnell, J.C.; Carr, L.G.; Dwyer, F.E.; Edenberg, H.J.; Li, T.K.; Boston, W.F.
 Biochem. Biophys. Res. Commun. 146, 1227-1233, 1987
 A>Title: The human beta-3 alcohol dehydrogenase subunit differs from beta-1 by a Cys for
 A:Reference number: A26826
 A:Accession: A26826
 A:Molecule type: protein
 A:Residues: 368-369, 'C', 371-375 <BUR>
 A>Note: allelic beta-3 variant found as a minor form occurring to a greater extent in neg
 R:Huxley, T.D.; Boston, W.F.; Hamilton, J.A.; Amzel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8149-8153, 1991
 A>Title: Structure of human beta-1beta-1 alcohol dehydrogenase: catalytic effects of non
 A:Reference number: A40987; MUID:91376103; PMID:1896463
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms
 A>Note: structure of beta-1 variant dimer
 R:Huxley, T.D.; Boszon, W.F.; Hamilton, J.A.; Amzel, L.M.
 submitted to the Brookhaven Protein Data Bank, January 1993
 A:Reference number: A52127; PDB:3HND
 A:Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 2-375
 C:Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C:Genetics:
 A:Gene: GDB:ADH2

A;Cross-references: GDB:119651; OMIM:103720
 A;Map position: 4q22-4q22
 A;Intons: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
 C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by C;Function:
 A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and A;Pathway: alcohol degradation
 A;Note: human alcohol dehydrogenase beta is expressed predominantly in fetal lung and ne C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor F;2-375/Product: alcohol dehydrogenase 2 #status experimental <MAT>
 F;3-366/Domains: long-chain alcohol dehydrogenase homology <LADH>
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
 F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match 45.1%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Oy 1 CYFS---SKDNVKGKTKC 18
 Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 7
 JQ1472
 trypsin (EC 3.4.21.4) V precursor, b-form - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
 C;Accession: JQ1472
 R;Kang, J.; Miegand, U.; Mueller-Hill, B.
 Gene 110, 181-187, 1992
 A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
 A;Reference number: JQ1471; MUID:92165057; PMID:1537555
 A;Accession: JQ1472
 A;Molecule type: mRNA
 A;Residues: 1-246 <KAN>
 A;Cross-references: EMBL:X59013; NID:957414; PIDN:CAAA1752.1; PID:957415
 A;Experimental source: pancreas
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: hydrolyase; protein digestion; serine proteinase; zymogen
 F;1-15/Domains: signal sequence #status predicted <SIG>
 F;16-24/Domains: activation peptide #status predicted <ACT>
 F;25-246/Product: trypsin V, b-form #status predicted <MAT>
 F;25-239/Domains: trypsin homology <TRY>
 F;31-160,48-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
 F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
 Best Local Similarity 43.8%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 FFSKDNVKGKTKC 18
 Db 16 FPTEDNDRIVGXYTC 31

RESULT 8
 JQ1471
 trypsin (EC 3.4.21.4) V precursor, a-form - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
 C;Accession: JQ1471; S23784
 R;Kang, J.; Miegand, U.; Mueller-Hill, B.
 Gene 110, 181-187, 1992
 A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
 A;Reference number: JQ1471; MUID:92165057; PMID:1537555
 A;Accession: JQ1471
 A;Molecule type: mRNA
 A;Residues: 1-246 <KAN>
 A;Cross-references: EMBL:X59012; NID:957412; PIDN:CAAA1751.1; PID:957413

A;Experimental source: pancreas
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: hydrolyase; protein digestion; serine proteinase; zymogen
 F;1-15/Domains: signal sequence #status predicted <SIG>
 F;16-24/Domains: activation peptide #status predicted <ACT>
 F;25-246/Product: trypsin V, a-form #status predicted <MAT>
 F;25-239/Domains: trypsin homology <TRY>
 F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
 F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
 Best Local Similarity 43.8%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 FFSKDNVKGKTKC 18
 Db 16 FPTEDNDRIVGXYTC 31

RESULT 9
 T32005
 hypothetical protein F36H9.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T32005
 R;Dante, M.; Kramer, J.; Twyman, B.
 submitted to the EMBL Data Library, July 1997
 A;Description: The sequence of C. elegans cosmid F36H9.
 A;Reference number: Z21110
 A;Accession: T32005
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-275 <DAN>
 A;Cross-references: EMBL:AF016668; PIDN:AA66090.1; GSPDB:GN00020; CESP:F36H9.2
 A;Experimental source: strain Bristol N2; clone F36H9
 C;Genetics:
 A;Gene: CESP:F36H9.2
 A;Map position: 2
 A;Intons: 26/2; 54/3; 80/1; 128/3; 152/1; 212/1

Query Match 43.1%; Score 44; DB 2; Length 275;
 Best Local Similarity 38.9%; Pred. No. 29;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CYFSKDNVKGKTKC 18
 Db 193 CYTNSNKGPNIPGMKTC 210

RESULT 10
 A47328
 natural killer cell tumor-recognition protein - human
 N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
 C;Accession: A47328
 R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortolano, J.R.
 Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
 A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
 A;Reference number: A47328; MUID:93133824; PMID:8421688
 A;Accession: A47328
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1403 <AND>
 A;Cross-references: GB:I04288; NID:g181251; PIDN:AAA5734.1; PID:g181252
 A;Experimental source: NK killer cells from adult blood
 A;Note: sequence extracted from NCBI backbone (NCBI:122798, NCBI:122800)
 C;Genetics:
 A;Gene: GDB:NKTR
 A;Cross-references: GDB:137171; OMIM:161565
 A;Map position: 3p23-3p21
 C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
 C;Keywords: alternative splicing; lymphocyte

F:60-230/Domain: cyclophilin homology <CYP>

Query Match 43.1%; Score 44; DB 1; Length 1403;

Best Local Similarity 44.4%; Pred. No. 1,3e+02; Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
DB 95 CLCSGKGLGKTGKKLC 112

RESULT 11

B47328

natural killer cell tumor-recognition protein - mouse
N:Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 05-Nov-1999

C/Accession: B47328; 177662

R:Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortolano, J.R.

Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993

A>Title: A cyclophilin-related protein involved in the function of natural killer cells.

A:Reference number: A47328; MUID:93133824; PMID:8421688

A:Accession: B47328

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1507 <AND>

A:Cross-references: GB:I04289; NID:g192866

A>Note: authors translated the codon AGT for residue 972 as Arg

R:Rintrec, A.; Anderson, S.K.

Mol. Immunol. 30, 1307-1311, 1993

A>Title: IL-2 regulates the expression of the NK-TR gene via an alternate RNA splicing m

A:Reference number: 157820; MUID:94019422; PMID:8413330

A:Accession: 177662

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 235-237; 263-294 <RIN>

A:Cross-references: GB:S65988; NID:g425701; PIDN:AAB28500.1; PID:g425702

C:Genetics:

A:Gene: NK-TR

C:Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology

C:Keywords: alternative splicing; lymphocyte

F:60-230/Domain: cyclophilin homology <CYP>

Query Match 43.1%; Score 44; DB 2; Length 1507;

Best Local Similarity 44.4%; Pred. No. 1,4e+02; Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
DB 95 CLCSGKGLGKTGKKLC 112

RESULT 12

T13010

hypothetical protein T24C20.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999

C/Accession: T13010

R:Choine, N.; Robert, C.; Broctier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A:Reference number: 217586

A:Accession: T13010

A:Molecule type: DNA

A:Residues: 1-274 <CHO>

A:Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.90

A:Experimental source: cultivar Columbia; BAC clone T24C20

C:Genetics:

A:Gene: ATSP:T24C20.90

A:Map position: 3

A:Insertions: 62/1; 84/1; 133/1; 171/1; 201/1; 271/3

Query Match 42.2%; Score 43; DB 2; Length 274;

Best Local Similarity 75.0%; Pred. No. 41;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SKDNVKGVTGK 16

DB 137 SKDNAGKTEDEK 148

RESULT 13
AB3434
lyrB protein (imported) - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C/Accession: AB3434

R:DeIvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Ios, T.; Ivanova, J.

; Mazur, M.; Goldman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:1175688

A:Accession: AB3434

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 <KUR>

A:Cross-references: GB:AB008917; PIDN:AAL52640.1; PID:g17983462; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI1459

A:Map position: 1

C:Superfamily: penicillin tolerance protein

Query Match 42.2%; Score 43; DB 2; Length 346;

Best Local Similarity 53.8%; Pred. No. 51; Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVT 13
DB 161 CHFDDEDLGFPV 173

RESULT 14

T26338

hypothetical protein Y102A5B.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T26338

R:Gardner, A.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z20203

A:Accession: T26338

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-368 <WIL>

A:Cross-references: EMBL:AL023821; PIDN:CAA19437.1; CESP:Y102A5B.3

A:Experimental source: clone Y102A5B

C:Genetics:

A:Gene: CESP:Y102A5B.3

A:Insertions: 61/3; 76/3; 136/3; 185/1; 245/1

Query Match 42.2%; Score 43; DB 2; Length 368;

Best Local Similarity 43.8%; Pred. No. 54; Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVKGVTGKTC 18
DB 144 FASKNNIGNIWGLLC 159

RESULT 15
T05936
agglutinin isolectin I precursor - barley

C:Species: Hordeum vulgare (barley)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000

C/Accession: T05936

R:Lerner, D.R.; Ralshel, N.V.

Plant Physiol. 91, 124-129, 1989
A:Title: Cloning and characterization of root-specific barley lectin.
A:Reference number: Z15461
A:Accession: F053936
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <LER>
A:Cross-references: EMBL:M29280; NID:G167070; PIDN:AAA32969.1; PID:G167071
C:Superfamily: wheat agglutinin, hevein chitin-binding domain homology
C:Keywords: lectin
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-212/Product: agglutinin isolectin 1 #status predicted <MAT>
F:27-69/Domain: hevein chitin-binding domain homology <HCB>

Query March 41.2%; Score 42; DB 2; Length 212;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 1 CYFSSKDNVGVKVTGGKTC 18
|||:|
Db 66 CYTSKR--CCTQAGKTC 81

Search completed: October 15, 2003, 17:06:23
Job time : 13.6886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 7.32934 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-12
Perfect score: 102
Sequence: 1 CYFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	266	1 ETC1_STRAU	P01553 staphylococ
2	102	100.0	266	1 ETC2_STRAU	P34071 staphylococ
3	102	100.0	266	1 ETC3_STRAU	P23313 staphylococ
4	46	45.1	263	1 ITMA_MOUSE	O61500 mus musculu
5	46	45.1	374	1 ADHA_HUMAN	P07327 homo sapien
6	46	45.1	374	1 ADHE_HUMAN	P00325 homo sapien
7	44	43.1	246	1 TRVA_RAT	P32821 rattus norv
8	44	43.1	246	1 TRVB_RAT	P32822 rattus norv
9	44	43.1	1453	1 NKCR_MOUSE	P30415 mus musculu
10	44	43.1	1462	1 NKCR_HUMAN	P30414 homo sapien
11	43	42.2	346	1 ISPH_BRIME	O84f11 brucella me
12	42	41.2	212	1 AGI_HORVU	P15312 hordeum vul
13	42	41.2	358	1 INCI_ECOLI	O52312 escherichia
14	42	41.2	375	1 ADH1_RANPE	P22797 rana perezi
15	42	41.2	514	1 GUXC_FUSOX	P46238 fusarium ox
16	41	40.2	35	1 SCKK_TITSE	P56219 titys sarr
17	41	40.2	336	1 OTCC_STRPY	P16964 streptococ
18	41	40.2	368	1 ADHE_HUMAN	P28332 homo sapien
19	41	40.2	374	1 ADH_PAPHA	P14139 papio namad
20	41	40.2	905	1 YD83_HUMAN	O9P244 homo sapien
21	40	39.2	127	1 ACPS_THETN	O8R857 thermoaer
22	40	39.2	242	1 RS4E_MERTH	O26123 methanobac
23	40	39.2	263	1 ITMA_HUMAN	O43736 homo sapien
24	40	39.2	265	1 RL7A_CHICK	P32429 gallus gall
25	40	39.2	373	1 ADHS_HORSE	P00338 equus cabal
26	40	39.2	374	1 ADH1_RABIT	O03505 oryctolagus
27	40	39.2	374	1 ADHA_MOUSE	P00339 mus musculu
28	40	39.2	374	1 ADHA_PERMA	P41680 peromyscus
29	40	39.2	374	1 ADHE_HORSE	P00337 equus cabal
30	40	39.2	374	1 ADHG_HUMAN	P00336 homo sapien
31	40	39.2	374	1 ADH_MACMU	P28469 macaca mula
32	40	39.2	375	1 ADHA_RAT	P06757 rattus norv
33	40	39.2	412	1 FXB4_SPOFR	Q26486 spodoptera

34	40	39.2	523	1 TYD5_PAPSO	P54771 papaver som
35	40	39.2	528	1 ACH2_CHICK	P09480 gallus gall
36	40	39.2	612	1 UNJ7_CAEEL	O02482 caenorhabd
37	40	39.2	761	1 VPA_BRP2	O06419 bacterioph
38	40	39.2	867	1 PMLI_MOUSE	O54990 mus musculu
39	40	39.2	1170	1 TSPI_MOUSE	P35441 mus musculu
40	40	39.2	1235	1 DNBI_HCMVA	P17147 human cytom
41	39.5	38.7	664	1 SYM_LISIN	O92490 listeria in
42	39.5	38.7	664	1 SYM_LISMO	O8A452 listeria mo
43	39	38.2	197	1 BECC_YERPE	P37867 yersinia pe
44	39	38.2	256	1 Y0EC_ECOLI	O46809 escherichia
45	39	38.2	259	1 KLM2_RAT	P00759 rattus norv

ALIGNMENTS

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RESULT 1
ID ETC1_STRAU STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.U., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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CC -----
DR EMBL: X05815; CA29260.1; -.
DR PIR: S06356; ENSACT.
DR HSSP: P34071; ISE2.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph/Strep tox.
DR Pfam: PF02876; Staph_Strep_tox_C1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT FT 177 177
FT CONFLICT 177 177

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D -> N (IN REF. 2).

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SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;
Query Match 100.0%; Score 102; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
Db 120 CYFSSKDNVKGVTGKTC 137

RESULT 2
ETC3 STAAU STANDARD; PRT; 266 AA.
ID ETC3 STAAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-2 precursor (SEC2).
GN ENT2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_taxid=1280;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; Pubmed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RL Infect. Immun. 57:2249-2252(1989).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; Pubmed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Brehm R.D., Tracter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT Staphylococcus aureus reveals a zinc-binding site."
RL Structure 3:769-779(1995).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; Pubmed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RN COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=9734373; Pubmed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC PIR; A60114; A60114.
DR PDB; 1STE; 23-DEC-96.
DR PDB; 1SE2; 08-MAR-96.
DR PDB; 1COV; 19-SEP-01.
DR PDB; 1I4P; 19-SEP-01.
DR PDB; 1I4Q; 19-SEP-01.
DR PDB; 1I4R; 19-SEP-01.
DR PDB; 1I4X; 19-SEP-01.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_O8.
DR Pfam; PF02876; Staph_strep_tox_Cf_1.

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DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00227; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36
FT METAL 110 ZINC.
FT METAL 145 ZINC.
FT METAL 149 ZINC.
FT METAL 35 37
FT HELIX 41 43
FT STRAND 44 44
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 55
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT TURN 75 79
FT TURN 83 86
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 109 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 128 129
FT STRAND 136 139
FT STRAND 142 144
FT TURN 146 147
FT STRAND 149 149
FT HELIX 151 153
FT STRAND 156 164
FT TURN 167 176
FT STRAND 178 178
FT STRAND 180 182
FT HELIX 183 198
FT STRAND 208 216
FT TURN 218 219
FT STRAND 222 226
FT STRAND 232 232
FT STRAND 237 241
FT HELIX 242 246
FT HELIX 249 251
FT TURN 252 254
FT STRAND 256 263
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 100.0%; Score 102; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGVTGKTC 18
Db 120 CYFSSKDNVKGVTGKTC 137

RESULT 3
ETC3 STAAU STANDARD; PRT; 266 AA.
ID ETC3 STAAU STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN ENT3 OR SAV2009 OR SA1817.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.

```


OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=158878, 158879, 1280;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hatakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus".
 RL Lancet 357:1225-1240(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackert S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT enterotoxin C3".
 RL Mol. Gen. Genet. 220:329-333(1990).
 [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=97064178; PubMed=8905797;
 RA Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffer C.V.,
 RA Schlievert P.M., Karjalainen K., Martinza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen".
 RL Nature 384:188-192(1996).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 DR EMBL; AP003364; BAB58171.1; -;
 DR EMBL; AP003365; BAB43097.1; -;
 DR EMBL; X51661; CA35972.1; -;
 DR PIR; S11885; S11885.
 DR PDB; 1JCK; 12-NOV-97.
 DR PDB; 1KLG; 02-AUG-02.
 DR PDB; 1KLU; 14-AUG-02.
 DR InterPro: IPR006177; Bcst1 tox.
 DR InterPro: IPR006123; Staph/Strep toxin.
 DR InterPro: IPR006125; Staph/Strep tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_Scrt_tox_C; 1.
 DR Pfam; PF01123; Staph_Scrt_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
 KW Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137
 SQ SEQUENCE 266 AA; 30671 MW; SED8A32D11FCA59 CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3; 7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGYTGKTC 18
 ID ITMA MOUSE STANDARD; PRT; 263 AA.
 AC 061500;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integral membrane protein 2A (E25 protein).
 GN ITM2A OR ITM2 OR E25.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Mandible;
 RX MEDLINE=96325063; PubMed=8702637;
 RA Deleersnijder W., Hong G., Cortvriend R., Poirier C., Tylianowski P.,
 RA Pittois K., Vanmarck E., Merregaert J.;
 RT "Isolation of markers for chondro-osteogenic differentiation using
 RT cDNA library subtraction. Molecular cloning and characterization of a
 RT gene belonging to a novel multigene family of integral membrane
 RT proteins".
 RL J. Biol. Chem. 271:19475-19482(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=99111395; PubMed=9892734;
 RA Pittois K., Wauters J., Bessuyt P., Deleersnijder W., Merregaert J.;
 RT "Genomic organization and chromosomal localization of the Itm2a
 RT gene".
 RL Mamm. Genome 10:54-56(1999).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANDIBULAR CONDYLES, IN BONE AND
 CC IN HAIR FOLLICLES. STRONG EXPRESSION IN OSTEOGENIC TISSUES, SUCH
 CC AS NEONATAL CALVARIA, PAMS, TAIL AND SKIN.
 CC -1- SIMILARITY: BELONGS TO THE ITM2 FAMILY.
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 CC -----
 DR EMBL; U38971; AAC37700.1; -;
 DR EMBL; AF074020; AAD14549.1; -;
 DR MGD; MGI:107706; Itm2a.
 DR Pfam; PF04089; BRICHOS; 1.
 KW Transmembrane; Signal-anchor.
 FT TRANSMEM 54 74
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CARBOHYD 166 166
 SQ SEQUENCE 263 AA; 29705 MW; CFB09834ABECB85A CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 263;
 Best Local Similarity 43.8%; Pred. No. 4; 1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

RESULT 5
 ADHA_HUMAN STANDARD; PRT; 374 AA.
 ID ADHA_HUMAN

AC P07327; 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase alpha chain (EC 1.1.1.1).
 GN ADH1A OR ADH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=66243367; PubMed=3013304;
 RA von Bahrlindstrom H., Hoeoeg J.-O., Heden L.-O., Kaiser R.,
 RA Fleetwood L., Larsson K., Lake M., Holmquist B., Holmgren A.,
 RA Hempel J., Vallee B.L., Joernvall H.;
 RT "CDNA and protein structure for the alpha subunit of human liver
 alcohol dehydrogenase.";
 RL Biochemistry 25:2465-2470(1986).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89153548; PubMed=2920825;
 RA Matsuo Y., Yokoyama S.;
 RT "Molecular structure of the human alcohol dehydrogenase 1 gene.";
 RL FEBS Lett. 243:57-60(1989).
 RN (4)
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=90269803; PubMed=2347582;
 RA Yasunami M., Kituchi I., Sarapata D., Yoshida A.;
 RT "The human class I alcohol dehydrogenase gene cluster: three genes
 are tandemly organized in an 80-kb-long segment of the genome.";
 RL Genomics 7:152-158(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC P1, ONE TO CLASS-III: CH1, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL; M12271; AAA68131.1; -;
 DR EMBL; M12963; AAA51590.1; -;
 DR EMBL; M37066; AAA51591.1; -;
 DR PIR; S02265; DEHDA.
 DR PDB; 1HSO; 27-APR-01.
 DR Genew; HGNC:249; ADH1A.
 DR GK; P07327; -;
 DR MIM; 103700; -;
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; NAS.
 DR GO; GO:0006066; P:alcohol metabolism; NAS.
 DR InterPro; IPR002328; ADH_zinc.

DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 KW Acetylation; 3D-structure.
 FT INIT_MET 0
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 174 174 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 374 AA; 39727 MW; 5D2F5F6E31C4962C CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CVFS---SKDNVGRYTGKTC 18
 DB 174 CGFSTGYSAVNAKYTPSTC 195
 RESULT 6
 ADHB_HUMAN STANDARD; PRT; 374 AA.
 ID ADHB_HUMAN STANDARD; PRT; 374 AA.
 AC P00325; Q13711; Q96KIT;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase beta chain (EC 1.1.1.1).
 GN ADHB OR ADH2
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Yokoyama S., Yokoyama R., Rotwein P.;
 RT "Molecular characterization of cDNA clones encoding the human alcohol
 RT dehydrogenase beta 1 and the evolutionary relationship to the other
 RT class I subunits alpha and gamma.";
 RL Jpn. J. Genet. 62:241-256(1987).
 RN (3)
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=6082371; PubMed=3000832;
 RA Heden L.O., Hoeoeg J.-O., Larsson K., Lake M., Lagerholm B.,
 RA Holmgren A., Vallee B.L., Joernvall H., von Bahrlindstrom H.;
 RT "CDNA clones coding for the beta-subunit of human liver alcohol
 RT dehydrogenase have differentially sized 3'-non-coding regions.";
 RL FEBS Lett. 194:327-332(1986).
 RN (4)
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=6111889; PubMed=2935533;
 RA Diester G., Smith M., Blanche V., Hatfield G.W.;
 RT "Molecular analysis of the human class I alcohol dehydrogenase gene
 RT family and nucleotide sequence of the gene encoding the beta
 RT subunit.";
 RL J. Biol. Chem. 261:2027-2033(1986).
 RN (5)
 RP SEQUENCE (BETA-1).
 RX MEDLINE=85076637; PubMed=6391920;
 RA Hempel J., Buhler R., Kaiser R., Holmquist B., de Zalsenski C.,
 RA von Wartburg J.-P., Vallee B.L., Joernvall H.;

RT "human liver alcohol dehydrogenase. 1. The primary structure of the
 RL beta 1 beta 1 isoenzyme.";
 RT Eur. J. Biochem. 145:437-445(1984).
 RN [6]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=89338401; PubMed=2547609;
 RA Matsuo Y., Yokoyama R., Yokoyama S.;
 RT "The genes for human alcohol dehydrogenases beta 1 and beta 2 differ
 RL by only one nucleotide.";
 RN Eur. J. Biochem. 183:317-320(1989).
 RN [7]
 RP SEQUENCE FROM N.A. (BETA-3).
 RC TISSUE=Liver;
 RX MEDLINE=90024225; PubMed=2679216;
 RA Carr L.G., Xu Y., Ho W.H., Edenberg H.J.;
 RT "nucleotide sequence of the ADH2(3) gene encoding the human alcohol
 RL dehydrogenase beta 3 subunit.";
 RN Alcohol. Clin. Exp. Res. 13:594-596(1989).
 RP [8]
 RP SEQUENCE FROM N.A. (BETA-2).
 RC TISSUE=Liver;
 RA polin L., Hey-Chi H.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88284699; PubMed=3397059;
 RA Xu Y.L., Carr L.G., Bosron W.F., Li T.-K., Edenberg H.J.;
 RT "genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci
 RL following DNA sequence amplification.";
 RN Genomics 2:209-214(1988).
 RP [10]
 RP SEQUENCE OF 40-85 FROM N.A.
 RA Gaier M., Speed W.C., Seaman M.I., Kidd K.K.;
 RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP VARIANT BETA-2.
 RX MEDLINE=84221897; PubMed=6374651;
 RA Joernvall H., Hempel J., Vallee B.L., Bosron W.F., Li T.-K.;
 RT "human liver alcohol dehydrogenase: amino acid substitution in the
 RL beta 2 beta 2 Oriental isoenzyme explains functional properties,
 RT establishes an active site structure, and parallels mutational
 RL exchanges in the yeast enzyme.";
 RN Proc. Natl. Acad. Sci. U.S.A. 81:3024-3028(1984).
 RL [12]
 RP VARIANT BETA-3.
 RX MEDLINE=87298549; PubMed=3619918;
 RA Burnell J.C., Carr L.G., Dwyer F.E., Edenberg H.J., Li T.-K.,
 RA Bosron W.F.;
 RT "The human beta 3 alcohol dehydrogenase subunit differs from beta 1
 RL by a Cys for Arg-369 substitution which decreases NAD(H) binding.";
 RN Biochem. Biophys. Res. Commun. 146:1127-1133(1987).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=91376103; PubMed=1896463;
 RA Hurley T.D., Bosron W.F., Hamilton J.A., Amzel L.M.;
 RT "Structure of human beta 1 beta 1 alcohol dehydrogenase: catalytic
 RL effects of non-active-site substitutions.";
 RN Proc. Natl. Acad. Sci. U.S.A. 88:8149-8153(1991).
 RL [14]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94260547; PubMed=8201522;
 RA Hurley T.D., Bosron W.F., Stone C.L., Amzel L.M.;
 RT "structures of three human beta alcohol dehydrogenase variants.
 RL Correlations with their functional differences.";
 RN J. Mol. Biol. 239:415-429(1994).
 RL [15]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=96291846; PubMed=8663387;
 RA Davis G.J., Bosron W.F., Stone C.L., Omsu-Dekyi K., Hurley T.D.;
 RT "x-ray structure of human betabeta3 alcohol dehydrogenase. The
 RL contribution of ionic interactions to coenzyme binding.";
 CC J. Biol. Chem. 271:17057-17061(1996).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +

CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types:
 CC alpha, beta and gamma. Cytoplasmic.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
 CC MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
 CC ORIENTALS.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC PL, ONE TO CLASS-III: CH1, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL; D00137; BAA00084.1; -;
 DR EMBL; X03350; CAA27056.1; -;
 DR EMBL; M24316; AAB59496.1; -;
 DR EMBL; M24308; AAB59496.1; JOINED.
 DR EMBL; M24309; AAB59496.1; JOINED.
 DR EMBL; M24310; AAB59496.1; JOINED.
 DR EMBL; M24311; AAB59496.1; JOINED.
 DR EMBL; M24312; AAB59496.1; JOINED.
 DR EMBL; M24313; AAB59496.1; JOINED.
 DR EMBL; M24314; AAB59496.1; JOINED.
 DR EMBL; M24317; AAB51884.1; -;
 DR EMBL; X15447; CAA33487.1; -;
 DR EMBL; X15448; CAA33487.1; JOINED.
 DR EMBL; X15449; CAA33487.1; JOINED.
 DR EMBL; X15450; CAA33487.1; JOINED.
 DR EMBL; X15451; CAA33487.1; JOINED.
 DR EMBL; X15452; CAA33487.1; JOINED.
 DR EMBL; X15453; CAA33487.1; JOINED.
 DR EMBL; X15454; CAA33487.1; JOINED.
 DR EMBL; X15455; CAA33487.1; JOINED.
 DR EMBL; L38290; AAB48003.1; -;
 DR EMBL; L38283; AAB48003.1; JOINED.
 DR EMBL; L38284; AAB48003.1; JOINED.
 DR EMBL; L38285; AAB48003.1; JOINED.
 DR EMBL; L38286; AAB48003.1; JOINED.
 DR EMBL; L38287; AAB48003.1; JOINED.
 DR EMBL; L38288; AAB48003.1; JOINED.
 DR EMBL; L38289; AAB48003.1; JOINED.
 DR EMBL; AF153821; AAD37446.1; -;
 DR EMBL; M21692; AAA51592.1; -;
 DR EMBL; AF040967; AAB96912.1; -;
 DR PIR; A23607; DEHUBA.
 DR PDB; 1HDY; 31-JAN-94.
 DR PDB; 1HDY; 31-JAN-94.
 DR PDB; 1HDZ; 31-JAN-94.
 DR PDB; 3HDJ; 31-JAN-94.
 DR PDB; 1DEH; 08-MAR-96.
 DR PDB; 1HTB; 07-DEC-95.
 DR PDB; 1HSZ; 27-APR-01.
 DR Genew; HGNC:250; ADH1B.
 DR GK; P00325; -;
 DR MM; 103720; -;
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; TAS.
 DR GO; GO:0005489; F:electron transporter activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR GO; GO:0006069; P:ethanol oxidation; TAS.
 DR InterPro; IPR002328; Adh_zinc.
 DR InterPro; IPR002085; Adh_zinc_family.
 DR Pfam; PF00107; Adh_zinc_N; 1.
 DR PROSITE; PS00059; Adh_ZINC; 1.

KM Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 KM Acetylation; Polymorphism; 3d-structure.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 Oy 1 CYFS---SKDNVGYTGKTC 18
 Db 174 GPFSTGYGSANVAKVTPGSGTC 195

RESULT 7
 TRVA RAT STANDARD; PRT; 246 AA.
 AC P3282;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin V-A precursor (EC 3.4.21.4).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=92165057; PubMed=1537555;
 RA Kang J., Wiegand U., Mueller-Hill B.;
 RT "Identification of cDNAs encoding two novel rat pancreatic serine
 proteases.";
 RL Gene 110:181-187(1992).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Xaa, Lys|-Xaa.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -----
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 CC -----
 CC EMBL; X59012; CAA41751.1; -.
 DR PIR; JQ1471; JQ1471.
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.092; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser. Protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; tryp_SPC; 1.
 DR PROSITE; PS50240; TRYPsin DOM; 1.
 DR PROSITE; PS00134; TRYPsin HIS; 1.
 DR PROSITE; PS00135; TRYPsin SER; FALSE_NEG.
 KM Hydroxylase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
 KM Multigene family.
 FT SIGNAL 1 15
 FT PROPEP 16 24
 FT CHAIN 25 246
 FT ACT_SITE 64 64 TRYPsin V-A.
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 160
 FT DISULFID 49 65
 FT DISULFID 133 233
 FT DISULFID 133 233 BY SIMILARITY.
 FT DISULFID 133 233 BY SIMILARITY.

FT DISULFID 140 206 BY SIMILARITY.
 FT DISULFID 171 185 BY SIMILARITY.
 FT DISULFID 196 220 BY SIMILARITY.
 FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 246 AA; 26900 MW; 1EB859D88BA1715 CRC64;
 Query Match 43.1%; Score 44; DB 1; Length 246;
 Best Local Similarity 43.8%; Pred. No. 8.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Oy 3 FSKDNVGYTGKTC 18
 Db 16 FPFEDNDRIYGYTC 31

RESULT 8
 TRVB RAT STANDARD; PRT; 246 AA.
 AC P3282;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin V-B precursor (EC 3.4.21.4).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=92165057; PubMed=1537555;
 RA Kang J., Wiegand U., Mueller-Hill B.;
 RT "Identification of cDNAs encoding two novel rat pancreatic serine
 proteases.";
 RL Gene 110:181-187(1992).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Xaa, Lys|-Xaa.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X59013; CAA41752.1; -.
 DR PIR; JQ1472; JQ1472.
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.093; -.
 DR InterPro; IPR001254; Ser. Protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR SMART; SM00020; tryp_SPC; 1.
 DR PROSITE; PS50240; TRYPsin DOM; 1.
 DR PROSITE; PS00134; TRYPsin HIS; 1.
 DR PROSITE; PS00135; TRYPsin SER; FALSE_NEG.
 KM Hydroxylase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
 KM Multigene family.
 FT SIGNAL 1 15
 FT PROPEP 16 24
 FT CHAIN 25 246
 FT ACT_SITE 64 64 TRYPsin V-B.
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 160
 FT DISULFID 49 65
 FT DISULFID 133 233
 FT DISULFID 140 206
 FT DISULFID 171 185
 FT DISULFID 196 220
 FT DISULFID 194 194
 FT SITE 194 194
 SQ SEQUENCE 246 AA; 26819 MW; 1EB899CA1BA8025 CRC64;
 SQ SEQUENCE 246 AA; 26819 MW; 1EB899CA1BA8025 CRC64;

```

Query Match      43.1%; Score 44; DB 1; Length 246;
Best Local Similarity 43.8%; Pred. No. 8.1;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PSSKDNVGVKVTGKTC 18
   |::||::| |
Db 16 PFTEDNDRIVGXYTC 31

RESULT 9
ID NKCRCR MOUSE STANDARD; PRT; 1453 AA.
AC P30415;
DT 01-APR-1993 (Rel. 25, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NK-tumor recognition protein (Natural-killer cells cyclophilin-
DN related protein) (NK-TR protein).
GN NKTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93133824; PubMed=842168;
RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,
RA Ortolano J.R.;
RT "A cyclophilin-related protein involved in the function of natural
RT killer cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).
RN [2]
RC REVISIONS TO C-TERMINUS.
RC STRAIN=BALB/c; TISSUE=Blood;
RA Anderson S.K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
CC INVOLVED IN THE FUNCTION OF NK CELLS.
CC -!- SIMILARITY: Contains 1 cyclophilin-like p1ase domain.
CC -----
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CC -----
DR EMBL; L04289; AAA37500.2; ALT_INIT.
DR HSSP; Q27450; 1A33.
DR MGD; MGI:97346; Nktr.
DR InterPro; IPR002130; CSA_P1ase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PROSITE; PS00170; CSA_P1ase 1; 1.
DR PROSITE; PS50072; CSA_P1ase 2; 1.
KW Cyclosporin; Isomerase; Rotamase; Repeat; Transmembrane.
KW DOMAIN 1 176 P1ase CYCLOPHILIN-TYPE.
FT DOMAIN 222 241 ARG/LYS-RICH (BASIC).
FT DOMAIN 422 459 ARG/LYS-RICH (BASIC).
FT DOMAIN 964 1003 ARG/LYS-RICH (BASIC).
FT DOMAIN 198 273 ARG/SER-RICH.
FT DOMAIN 468 565 ARG/SER-RICH.
FT DOMAIN 658 812 ARG/SER-RICH.
FT DOMAIN 1303 1453 ARG-SER TANDUM REPEAT-RICH.
SQ SEQUENCE 1453 AA; 163439 MW; DFLI73FF814B283E CRC64;

Query Match      43.1%; Score 44; DB 1; Length 1453;
Best Local Similarity 44.4%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGKTC 18
   |::||::| |

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QY	1	CYFSSKDNVGVKTKGC	18
DB	41	CLCSGSEKGLGKTTGKCLC	58

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RESULT 11
ISPH_BRUME STANDARD; PRT; 346 AA.
ID AGI_HORVU
AC 08YFR;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
ISPH protein.
GN ISPH OR LYTB OR BME11459.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_Taxid=29459;
RN SEQUENCE FROM N.A.
RP STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; Pubmed=11756688;
RA DelVecchio V.G., Kaparatel V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lyridis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Leveson J.-J.,
RA Haselkorn R., Kyriides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
CC -----
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CC -----
DR EMBL: AE009582; AAL52640.1; -.
DR PIR: AE3434; AE3434.
DR HAMAP: MF_00191; -.
DR InterPro: IPR003451; LYTB.
DR Pfam: PF02401; LYTB.
DR TIGRfam: TIGR00216; isph_lytb.1.
KW Isoprene biosynthesis; Complete proteome.
SQ SEQUENCE 346 AA; 37747 MW; EB9C1D60EF73421B CRC64;

Query Match 42.2%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVT 13
DB 161 CHFDDENLGFVT 173

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RN [1]
RP SEQUENCE FROM N.A.
RA Lerner D.R., Rainel N.V.;
RT "Cloning and characterization of root-specific barley lectin.";
RL Plant Physiol. 91:124-129(1989).
CC -1- FUNCTION: CARBOHYDRATE BINDING.
CC -1- SIMILARITY: Contains 4 chitin-binding domains.
CC -----
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CC -----
DR EMBL: M28280; AA32969.1; -.
DR PIR: T05936; T05936.
DR HSPSP: P10969; 1WGT.
DR InterPro: IPR001002; Chitin binding_1.
DR Pfam: PF00187; Chitin bind 1; 4.
DR PRINTS: PRO0451; CHITNBINDG.
DR SMART: SM00270; CHTBD1; 4.
DR PROSITE: PS00026; CHITIN_BINDING; 4.
KW Lectin; Repeat; Chitin-binding; Glycoprotein; signal;
KM Pyrolidone carboxylic acid.
FT SIGNAL 1 26
FT CHAIN 27 212
FT DOMAIN 27 69
FT DOMAIN 70 112
FT DOMAIN 113 155
FT DOMAIN 156 197
FT MOD_RES 27 27
FT FT
FT DISULFID 29 44
FT DISULFID 38 50
FT DISULFID 43 57
FT DISULFID 61 66
FT DISULFID 72 87
FT DISULFID 81 93
FT DISULFID 86 100
FT DISULFID 104 109
FT DISULFID 115 130
FT DISULFID 124 136
FT DISULFID 129 143
FT DISULFID 147 152
FT DISULFID 158 173
FT DISULFID 167 179
FT DISULFID 172 186
FT DISULFID 190 195
FT CARBOHYD 206
SQ SEQUENCE 212 AA; 21209 MW; 8D948245DB625A5 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 212;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 CYFSSKDNVGVKGTGKTC 18
DB 66 CITSKR--CGTQAGKTC 81

```

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RESULT 13
INCL_ECOLI STANDARD; PRT; 358 AA.
ID INCL_ECOLI
AC Q52312; P71175; Q52283;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein incC.
GN INCC.
OS Escherichia coli.
OG Plasmid incP-Delta R751.

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxId=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macartney D.P., Williams D.R., Stafford T., Foster A., Thomas C.M.;
 RT "Evolution of the partitioning and global regulation functions of
 the incp central region."
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-109 FROM N.A.
 RC STRAIN=K12 / C600;
 RX MEDLINE=9529146; PubMed=7773415;
 RA Thomas C.M., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;
 RT "Evolution of the korA-oriV segment of promiscuous IncP plasmids."
 RL Microbiology 141:1201-1210 (1995).
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS ENCODED BY THE TRFB OPERON;
 IT IS INVOLVED IN PLASMID MAINTENANCE AND REPLICATION (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY.
 CC -----
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 CC -----
 DR EMBL: U67194; AAC64421.1; -
 DR InterPro: IPR00707; ATPase_Para.
 DR Pfam: PF00991; Para. 1.
 KM Plasmid: DNA replication.
 SQ SEQUENCE 358 AA; 38246 MW; 44859F07844167BE CRC64;
 QY Query Match 41.2%; Score 42; DB 1; Length 358;
 Best Local Similarity 41.2%; Pred. No. 25;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Db 1 CYFSKDNVGVKVGKTC 17
 45 CFFAGADGGGAGGAGG 61
 RESULT 14
 ADH1_RANPE STANDARD; PRT; 375 AA.
 ID ADH1_RANPE
 AC F22757;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase, major (EC 1.1.1.1).
 OS Rana perezi (Perez & frog) (Western Mediterranean green frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OC NCBI_TaxId=8403;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Liver;
 RX MEDLINE=91175722; PubMed=2007119;
 RA Cederlund E., Peralba J.M., Pares X., Joernvall H.;
 RT "Amphibian alcohol dehydrogenase, the major frog liver enzyme.
 Relationships to other forms and assessment of an early gene
 duplication separating vertebrate class I and class III alcohol
 dehydrogenases."
 RL Biochemistry 30:2811-2816 (1991).
 RN [2]
 RP SEQUENCE OF 1-5.
 RX MEDLINE=90353571; PubMed=2387402;
 RA Begerad B., Escornius M., Danielson O., Persson B., Cederlund E.,
 RA Kaiser R., Holmquist B., Vallee B., Pares X., Jellerey J.,
 RA Joernvall H.;
 RT "Fast atom bombardment mass spectrometry and chemical analysis in

RT determinations of acyl-blocked protein structures."
 RL FEBS Lett. 269:194-196 (1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 FAMILY. MORE CLOSELY RELATED TO CLASS I MAMMALIAN ENZYMES.
 DR PIR: A38405; A38405.
 DR HSSP: P00325; 1DEH.
 DR InterPro: IPR002328; ADH_zinc.
 DR InterPro: IPR002085; Adh_zn_family.
 DR Pfam: PF00107; ADH_zinc_N; 1.
 DR PROSITE: PS00059; ADH_ZINC; 1.
 KM Oxidoreductase; Zinc; Metal-binding; NAD; Acetylation.
 FT MOD RES 1 1
 FT METAL 46 46
 FT METAL 68 68
 FT METAL 98 98
 FT METAL 101 101
 FT METAL 104 104
 FT METAL 112 112
 FT METAL 175 175
 SQ SEQUENCE 375 AA; 40184 MW; 283E0A60E3339195 CRC64;
 QY Query Match 41.2%; Score 42; DB 1; Length 375;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
 Db 175 CFFSTGVSAVMTGVKPGSTC 196
 175 CFFSTGVSAVMTGVKPGSTC 196
 RESULT 15
 ID GUXC_FUSOX STANDARD; PRT; 514 AA.
 AC P46238;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Putative exoglucanase type C precursor (EC 3.2.1.91)
 DE (Exocellulohydrolase I) (1,4-beta-cellulohydrolase)
 DE (Beta-glucanocellulohydrolase).
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OC NCBI_TaxId=5507;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95047531; PubMed=7959045;
 RA Shepard P.O., Grant F.D., Oort P.J., Sprecher C.A., Foster D.C.,
 RA Hagen F.S., Upshall A., McKnight G.L., O'Hara P.J.;
 RT "The use of conserved cellulase family-specific sequences to clone
 RT cellulase homologue cDNAs from Fusarium oxysporum."
 RL Gene 150:163-167 (1994).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 in cellulose and cellotetraose, releasing cellobiose from the non-
 reducing ends of the chains.
 CC -1- SIMILARITY: Contains 1 fungal-type cellulose-binding (CBD) domain.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL
 HYDROLASES).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: U29379; AAA65587.1; -
 DR HSSP: P00725; 8CEL.

DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR01722; Glyco_hydro_7.
 DR Pfam; PF00734; CBM_1; 1.
 DR Pfam; PF00840; Glyco_hydro_7; 1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR ProDom; PD186135; Glyco_hydro_7; 1.
 DR SMART; SM00236; fCBD; 1.
 DR PROSITE; PS00562; CBD_FUNGAL; 1.
 KM Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 514 PUTATIVE EXOGLUCANASE TYPE C.
 FT DOMAIN 18 439 CATALYTIC.
 FT DOMAIN 440 482 LINKER.
 FT DOMAIN 483 514 CELLULOSE-BINDING (BY SIMILARITY).
 FT ACT_SITE 229 229 NUCEOPHILE (BY SIMILARITY).
 FT ACT_SITE 234 234 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 486 503 BY SIMILARITY.
 FT DISULFID 497 513 BY SIMILARITY.
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 514 AA; 54704 MW; 6A4617323A46E062 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 514;
 Best Local Similarity 44.4%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVGVKVGKTC 18
 DB 66 CYTGKMDTSICTDGKTC 83

Search completed: October 15, 2003, 16:58:16
 Job time : 8.42934 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-12
Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	102	100.0	234	2	Q9RSX4	Q9RSX4 staphylococ
2	102	100.0	239	2	O05157	O05157 staphylococ
3	102	100.0	239	2	Q53678	Q53678 staphylococ
4	102	100.0	239	2	Q06532	Q06532 staphylococ
5	102	100.0	239	2	Q06531	Q06531 staphylococ
6	102	100.0	239	2	Q06533	Q06533 staphylococ
7	102	100.0	266	16	Q8NXJ6	Q8NXJ6 staphylococ
8	102	100.0	271	2	Q9F0J6	Q9F0J6 staphylococ
9	96	94.1	239	2	Q06535	Q06535 staphylococ
10	93	91.2	239	2	Q06534	Q06534 staphylococ
11	55	53.9	511	16	Q8RI66	Q8RI66 fusobacteri
12	47	46.1	2108	5	Q815C7	Q815C7 plasmodium
13	46.5	45.6	505	2	Q50203	Q50203 xanthobacte
14	46	45.1	199	16	Q92CG4	Q92CG4 listeria in
15	46	45.1	233	11	Q9CRM4	Q9CRM4 mus musculu
16	46	45.1	263	11	Q8KH04	Q8KH04 mus musculu

17	46	45.1	269	6	Q8WMN3	Q8WMN3 gorilla gor
18	45	44.1	176	4	Q9NP00	Q9NP00 homo sapien
19	44.5	43.6	107	4	Q9UL82	Q9UL82 homo sapien
20	44.5	43.6	457	12	Q9Y0Z1	Q9Y0Z1 ranid herpe
21	44	43.1	275	5	O16622	O16622 caenorhabdi
22	44	43.1	299	10	Q8LAK6	Q8LAK6 arbidopsis
23	44	43.1	966	11	Q8CBP6	Q8CBP6 mus musculu
24	44	43.1	2201	5	Q95281	Q95281 oikopleura
25	43	42.2	126	5	Q95U05	Q95U05 branchiosto
26	43	42.2	159	5	Q817X7	Q817X7 branchiosto
27	43	42.2	274	10	Q9STR7	Q9STR7 arbidopsis
28	43	42.2	315	10	Q93VK9	Q93VK9 arbidopsis
29	43	42.2	368	5	Q9XXJ6	Q9XXJ6 caenorhabdi
30	43	42.2	372	16	Q8G257	Q8G257 bruceella su
31	43	42.2	765	5	Q26018	Q26018 plasmodium
32	43	42.2	765	5	Q8IKT6	Q8IKT6 plasmodium
33	43	42.2	1022	5	Q9W3E1	Q9W3E1 diosiphila
34	42	41.2	148	16	Q8DRX5	Q8DRX5 streptococ
35	42	41.2	161	17	Q8TLN3	Q8TLN3 methanosarc
36	42	41.2	224	8	Q9Z2S7	Q9Z2S7 ceratocolen
37	42	41.2	235	16	Q8XBI9	Q8XBI9 clostridium
38	42	41.2	260	16	Q97M39	Q97M39 clostridium
39	42	41.2	278	2	Q51311	Q51311 nostoc punc
40	42	41.2	377	11	Q9QYV9	Q9QYV9 mus musculu
41	42	41.2	378	16	Q92PD6	Q92PD6 listeria in
42	42	41.2	378	16	Q8YAK1	Q8YAK1 listeria mo
43	42	41.2	430	16	Q9A3U5	Q9A3U5 caulobacter
44	42	41.2	1064	16	Q8XK16	Q8XK16 clostridium
45	41.5	40.7	731	16	Q8RG00	Q8RG00 fusobacteri

ALIGNMENTS

RESULT 1
Q9RSX4 PRELIMINARY; PRT; 234 AA.
ID Q9RSX4
AC Q9RSX4;
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP: P34071; 1SE2.
DR InterPro: IPR006177; Bactrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGKTC 18
DB 88 CYFSSKDNVKGVTGKTC 105

RESULT 2

005157 ID 005157 PRELIMINARY; PRT; 239 AA.
 AC 005157;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type C enterotoxin (Fragment).
 OS Staphylococcus intermedius.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=95-011195;
 RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
 RA Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
 RT "Characterization of the type C enterotoxin (SEC-cantine) produced by
 RT Staphylococcus intermedius pyoderma isolates."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U91526; AAB50248.1; -.
 DR HSP; P23313; 11CK.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_toxin; 1.
 DR Pfam; PF02876; Staph_tox_C; 1.
 DR PRINTS; PR00279; BACTR1TOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
 Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 3

053678 ID 053678 PRELIMINARY; PRT; 239 AA.
 AC 053678;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13376; AAA26620.1; -.
 DR HSP; P34071; 1SE2.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_toxin; 1.
 DR Pfam; PF02876; Staph_tox_C; 1.
 DR PRINTS; PR00279; BACTR1TOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
 Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 4

006532 ID 006532 PRELIMINARY; PRT; 239 AA.
 AC 006532;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=740N;
 RA MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13375; AAA26619.1; -.
 DR HSP; P34071; 1SE2.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_toxin; 1.
 DR Pfam; PF02876; Staph_tox_C; 1.
 DR PRINTS; PR00279; BACTR1TOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
 Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 5

006531 ID 006531 PRELIMINARY; PRT; 239 AA.
 AC 006531;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4446;
 RA MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13374; AAA26618.1; -.
 DR HSP; P34071; 1SE2.

```
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 93 CYFSSKDNVGVKVTGKTC 110

RESULT 6
ID 006533 PRELIMINARY; PRT; 239 AA.
AC 006533;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCCopeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Mair J.C., Lyon J.D., Roberson J.R., Luyher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL: U13378; AAA26622.1; -.
DR HSSP: P34071; 1SE2.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE825 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 93 CYFSSKDNVGVKVTGKTC 110

RESULT 7
ID 08NXJ6 PRELIMINARY; PRT; 266 AA.
AC 08NXJ6;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
OS Staphylococcus aureus (strain MW2).
```

```
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22040717; PubMed=12044378;
RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94624.1; -.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA49120F CRC64;

Query Match 100.0%; Score 102; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 120 CYFSSKDNVGVKVTGKTC 137

RESULT 8
ID 09F0L6 PRELIMINARY; PRT; 271 AA.
AC 09F0L6;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20566668; PubMed=11114901;
RX Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70(2001).
DR EMBL: AF217235; AAG29599.1; -.
DR HSSP: P34071; 1SE2.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR SEQUENCE 271 AA; 31267 MW; 3493F622B8042F10 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 9.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
DB 125 CYFSSKDNVGVKVTGKTC 142
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RESULT 9
ID Q06535 PRELIMINARY; PRT; 239 AA.
AC Q06535;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 909;
RA MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13377; AAA26621.1; -.
DR HSSP; P23313; IUCK.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF02876; Staph_Strep_toxin_1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

Query Match 94.1%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 10
ID Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13379; AAA26623.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF02876; Staph_Strep_toxin_1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

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FT NON TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 91.2%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 11
ID Q8R166 PRELIMINARY; PRT; 511 AA.
AC Q8R166;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cysteinepermease.
GN FN1747.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Malinas T., Pusch G., Haeflorn R.,
RA Fossefin W., Kyrides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010479; AAL93862.1; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR001463; Na/Ala_sympor1.
DR Pfam; PF01235; Na_Ala_symp; 1.
DR TIGRFAMs; TIGR00835; agcS; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.
SQ SEQUENCE 511 AA; 56196 MW; 03DBA2859135EF3D CRC64;

Query Match 53.9%; Score 55; DB 16; Length 511;
Best Local Similarity 52.9%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 17
Db 128 CYRSDKDFGRYFGGST 144

RESULT 12
ID Q8I5C7 PRELIMINARY; PRT; 2108 AA.
AC Q8I5C7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF1410C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=6329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

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RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shellenom S.J., Sub B., Peterson J., Anginoli S.,
RA Perica M., Allen J., Shallogue J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairland A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum";
RL Nature 419:498-511(2002).
DR EMBL: AEO14848; AAN36368.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2108 AA; 248300 MW; 2B0464D22291B2D9 CRC64;

Query Match 46.1%; Score 47; DB 5; Length 2108;
Best Local Similarity 32.4%; Pred. No. 1.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 20; Gaps 1;

Qy 1 CYFSSKDN-----VGKVTGSKT 17
Db 763 CYFSSKNDYILKNTLNLTAKNSVILLGNVSGKT 799

RESULT 13
ID 050203 PRELIMINARY; PRT; 505 AA.
AC 050203;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chloroacetaldehyde dehydrogenase.
GN ALDA.
OS Xanthobacter autotrophicus.
OC Plasmid linear plasmid pXAL.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=GL10;
RX MEDLINE=98172729; PubMed=9511738;
RA Bergeron H., Labbe D., Turmel C., Lau P.C.,
RT "Cloning, sequence and expression of a linear plasmid-based and a
RT chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
RT in Xanthobacter autotrophicus GL10.";
RL Gene 207:9-18(1998).
CC -; SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL: AF029733; AAC13641.1; -.
DR HSSP: P05091; 1CM3.
DR InterPro: IPR002086; Aldenhyde_dehydr.
DR Pfam: PF001171; aldehyd.1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KM Oxidoreductase; Plasmid.
SQ SEQUENCE 505 AA; 54945 MW; AD6A9EDB0297B804 CRC64;

Query Match 45.6%; Score 46.5; DB 2; Length 505;
Best Local Similarity 58.8%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

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Db 34 YF--DNTSPVTGSKTC 47

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ID 092CG4 PRELIMINARY; PRT; 199 AA.
AC 092CG4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein lin1208.

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GN LIN1208.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Checonan F., Couve E., de Darvar A., Denoux P.,
RA Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunz F., Kurapkak G.,
RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueller T., Simoes N., Tietze A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:848-852(2001).
DR EMBL: AL596168; CAC96439.1; -.
DR ListList; LIN01208; -.
DR InterPro: IPR001345; PG/BPGM_mutase.
DR Pfam: PF00300; PGAM; 1.
DR PROSITE: PS00175; PG_MUTASE; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 199 AA; 22902 MW; E14DD962F4C6B85 CRC64;

Query Match 45.1%; Score 46; DB 16; Length 199;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YFSSKDNVKGVTGKTC 18
Db 151 YWEKTSKIGKVTGLKNC 167

RESULT 15
ID 09CRM4 PRELIMINARY; PRT; 233 AA.
AC 09CRM4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Integral membrane protein 2 (Fragment).
GN ITM2A OR ITM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Home D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;

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RT "Functional annotation of a full-length mouse cDNA collection." ;
PI Nature 408:685-690 (2001)

RL Nature 409:685-690 (2001).

DR EMBL; AK014024; BAB29119.1; -.
DR MCB; MCB.107706; T433

DR MGD; MGI:107706; Itm2a.

FT	NON_TER	1	1
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      NAME=
SQ SEQUENCE 233 AA; 26321 MW; B073D1FD94DEF2E9 CRC64;

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Query Match	Score	DB	Length
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Best Local Similarity 43.8%; Pred. No. 17;

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Matches      7; Conservative      4; Mismatches      5; Indels      0; Gaps      0;

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QY 1 CYFSSKDNVGVTTGGK 16

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Search completed: October 15, 2003, 17:04:12
Job time : 36.8623 secs

Job time : 36.8623 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds

(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-13

Perfect score: 102

Sequence: 1 CYSSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	18	20	AA196249
2	102	100.0	18	20	ABG71377
3	102	100.0	18	24	ABG71380
4	102	100.0	238	12	AA13208
5	102	100.0	238	14	AA15016
6	102	100.0	238	22	ABG7343
7	102	100.0	238	23	ABG76239
8	102	100.0	239	12	AA13207
9	102	100.0	239	14	AA15015

10	102	100.0	239	20	AA196255	Staphylococcal gro
11	102	100.0	239	20	AA196256	Staphylococcal gro
12	102	100.0	239	20	AA196257	Staphylococcal gro
13	102	100.0	239	20	AA196258	Staphylococcal gro
14	102	100.0	239	20	AA196259	Staphylococcal gro
15	102	100.0	239	22	ABG7342	Staphylococcus aur
16	102	100.0	239	23	ABG76238	Staphylococcus aur
17	102	100.0	240	24	ABG71367	Staphylococcal ent
18	102	100.0	240	24	ABG71368	Staphylococcal ent
19	102	100.0	240	24	ABG71369	Staphylococcal ent
20	102	100.0	240	24	ABG71371	Staphylococcal ent
21	102	100.0	240	24	ABG71372	Staphylococcal ent
22	102	100.0	266	21	AA170108	Staphylococcal ent
23	102	100.0	266	23	ABG79507	Staphylococcal SEC
24	96	94.1	18	20	AA196250	Staphylococcal gro
25	96	94.1	18	24	ABG71378	Staphylococcal ent
26	96	94.1	239	20	AA196254	Staphylococcal gro
27	96	94.1	239	20	AA196257	Staphylococcal gro
28	96	94.1	240	24	ABG71370	Staphylococcal ent
29	96	94.1	240	24	ABG71373	Staphylococcal ent
30	93	91.2	18	20	AA196258	Staphylococcal gro
31	87	85.3	239	20	AA196259	Staphylococcal ent
32	87	85.3	240	24	ABG71374	Staphylococcal ent
33	66	64.7	14	20	AA196259	Staphylococcal ent
34	66	64.7	14	24	ABG71381	Staphylococcal ent
35	47	46.1	77	21	AA196245	Arabidopsis thalia
36	47	46.1	103	21	AA196244	Arabidopsis thalia
37	46	45.1	374	20	AA196258	Human alcohol dehy
38	46	45.1	374	20	AA196259	Human alcohol dehy
39	46	45.1	375	23	ABG79657	Invertebrate forag
40	46	45.1	395	21	AA196259	Lung cancer associ
41	45	44.1	277	23	ABG79515	Novel human protei
42	45	44.1	513	22	ABG71600	Zinc finger protei
43	44	43.1	299	21	AA196258	Arabidopsis thalia
44	44	43.1	315	21	AA196259	Arabidopsis thalia
45	44	43.1	340	21	AA196254	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AA196249
ID AA196249 standard; Peptide: 18 AA.
XX
AC AA196249;
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group C enterotoxin disulfide loop.
XX
KW Enterotoxin; SEC1, SEC2, SEC3 FRI 913; SEC3 4446; SEC-Bovine;
XX SEC-Ovine; toxin; disulfide loop; protein engineering.
OS Staphylococcus aureus.
XX
PN W09927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25107.
XX
PR 02-DEC-1997; 97US-0067357.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Bohach GI;
XX
DR WPI, 1999-358008/30.
XX N-PSDB; AAX58884.
XX
PT Non-toxic modified staphylococcal enterotoxins
XX

PS Disclosure; Page 3; 25pp; English.
XX
CC This peptide corresponds to the disulfide loop, i.e. amino acids
CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,
CC SEC3, FRI 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AAY06251-53
CC and AAY06255-58). The invention relates to pyrogenic toxins, such as
CC staphylococcal enterotoxins, modified in the disulfide loop region.
CC Typically, the modification involves deletions within the disulfide
CC loop region of SEC (see AAY06261). The modified toxins retain useful
CC biological properties, such as the ability to induce cytokine
CC production, but have substantially reduced toxicity compared to the
CC corresponding unmodified native toxin. Emetic response inducing
CC activity and fever inducing activity are typically decreased by at
CC least about 100-fold, while LD50 (in Dutch Belted rabbits) is at
CC least 100-fold higher than the native toxin.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 102; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CYFSSKDNVGVKVTGKTC 18
1 CYFSSKDNVGVKVTGKTC 18
XXXXXXXXXXXXXXXXXXXX
DB 1 CYFSSKDNVGVKVTGKTC 18
XXXXXXXXXXXXXXXXXXXX
XX
RESULT 2
ABG71377 standard; Peptide; 18 AA.
XX
AC ABG71377;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin disulphide loop region.
XX
KM Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KM emetic response-inducing activity; staphylococcal enterotoxin;
KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KM SEC1; SEC2; SEC3-FRI913; SEC-4446; SEC-bovine.
XX
OS Staphylococcus aureus.
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11619.
XX
PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX
PT New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning -
XX
PS Disclosure; Fig 15; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC for vaccination against diseases such as toxic shock syndrome and

CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC disulphide loop region, occurring in several enterotoxins.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 102; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CYFSSKDNVGVKVTGKTC 18
1 CYFSSKDNVGVKVTGKTC 18
XXXXXXXXXXXXXXXXXXXX
DB 1 CYFSSKDNVGVKVTGKTC 18
XXXXXXXXXXXXXXXXXXXX
XX
RESULT 3
ABG71380 standard; Peptide; 18 AA.
XX
AC ABG71380;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin C1 (SEC1) protein fragment.
XX
KM Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KM emetic response-inducing activity; staphylococcal enterotoxin; SEC1;
KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
XX
OS Staphylococcus aureus.
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11619.
XX
PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX
DR N-FSDB; ABS56822.
XX
XX
PT New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning -
XX
PS Example 1; Fig 1; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC protein fragment.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 102; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 10CYFSSKDNVGVKVTGKTC 18
10CYFSSKDNVGVKVTGKTC 18
XXXXXXXXXXXXXXXXXXXX
DB 1 CYFSSKDNVGVKVTGKTC 18
XXXXXXXXXXXXXXXXXXXX

RESULT 4
AAR13208
ID AAR13208 standard; Protein; 238 AA.
XX
XX
AC AAR13208;
XX
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C3.
XX
XX
XX SEC3; cancer treatment; pyrogen; tumouricide.
XX
XX
OS Staphylococcus aureus.
XX
XX
PN WO9110680-A.
XX
XX
PD 25-JUL-1991.
XX
XX
PF 17-JAN-1991; 91MO-US00342.
XX
XX
PR 17-JAN-1990; 90US-0466577.
XX
XX
PA (TERM/) TERMAN D S.
XX
XX
PI Terman DS;
XX
XX
DR WPI; 1991-237984/32.
XX
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
XX
PS Disclosure; Fig 1; 74pp; English.
XX
XX
CC SEC3 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
CC polypeptides having structural homology to Staphylococcal
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
XX
XX
SQ See AAR13203-R13211.
XX
XX
SQ Sequence 238 AA;
XX
XX
Query Match 100.0%; Score 102; DB 12; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTGKTC 18
Db 92 CYFSSKDNVGVKVTGKTC 109
XX
XX
RESULT 5
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
XX
AC AAR45016;
XX
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
XX
DE Staphylococcal enterotoxin SEC3.
XX
XX
XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
XX auto-immune disease; toxicity; Protein A; perfusion system.
XX
XX
OS Staphylococcus aureus.
XX

PN WO9324136-A1.
XX
XX
PD 09-DEC-1993.
XX
XX
PF 01-JUN-1993; 93MO-US05213.
XX
XX
PR 01-JUN-1992; 92US-0891718.
XX
XX
PA (STON/) STONE J L.
PA (TERM/) TERMAN D S.
XX
XX
PI Stone JL, Terman DS;
XX
XX
DR WPI; 1993-405418/50.
XX
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
XX
PS Disclosure; Fig 1; 90pp; English.
XX
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and auto-immune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 238 AA;
XX
XX
Query Match 100.0%; Score 102; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTGKTC 18
Db 92 CYFSSKDNVGVKVTGKTC 109
XX
XX
RESULT 6
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
XX
AC AAB67343;
XX
XX
DT 23-APR-2001 (first entry)
XX
XX
DE Staphylococcus aureus enterotoxin C3 protein.
XX
XX
XX Tumour; cancer; immune; enterotoxin.
XX
XX
OS Staphylococcus aureus.
XX
XX
PN US6180097-B1.
XX
XX
PD 30-JAN-2001.
XX
XX
PF 30-OCT-1998; 98US-0183437.
XX
XX
PR 31-JAN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91MO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX
XX
XX (TERM/) TERMAN D S.
XX
XX
PI Terman DS;
XX

CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
CC See AAR13203-R13211.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGGKTC 110

RESULT 9
AAR45015
ID AAR45015 standard; protein; 239 AA.

XX AAR45015;

DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SECL.

KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KM auto-immune disease; toxicity; Protein A; perfusion system.

OS Staphylococcus aureus.

PN WO9324136-A1.

XX WO9324136-A1.

PD 09-DEC-1993.

PF 01-JUN-1993; 93WO-US05213.

PR 01-JUN-1992; 92US-0891718.

PA (STON/) STONE J L.

PI (TERM/) TERMAN D S.

PT Stone JL, Terman DS;

XX WPI; 1993-405418/50.

XX Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases

PS Disclosure; Fig 1; 90pp; English.

XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)

CC which may be used in the methods of the invention for treating cancer

CC in a patient. These SEs, and homologues of them, can be used as

CC tumouricidal agents for treating cancers and auto-immune disease.

CC They exhibit tumouricidal activity and toxicity identical to that

CC observed for the Protein A perfusion system. They may be administered

CC by i.v. injection.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGGKTC 110

RESULT 10

AAV06255 0
ID AAV06255 standard; Protein; 239 AA.

XX AAV06255;

AC AAV06255;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-MNCoPeland.

XX Enterotoxin; SEC-MNCoPeland; toxin; disulfide loop;

KW protein engineering.

OS Staphylococcus aureus.

PN WO9927889-A2.

PD 10-JUN-1999.

PF 01-DEC-1998; 98WO-US25107.

PR 02-DEC-1997; 97US-0067357.

PA (IDAH-) IDAHO RES FOUND INC.

PI Bohach GI;

PT WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C

CC enterotoxin SEC-MNCoPeland. The invention relates to pyrogenic

CC toxins, such as staphylococcal enterotoxins, modified in the

CC disulfide loop region. Typically, the modification involves

CC deletions within the disulfide loop region of SEC (see AAV06261).

CC The modified toxins retain useful biological properties, such as

CC the ability to induce cytokine production, but have substantially

CC reduced toxicity compared to the corresponding unmodified native

CC toxin. Emetic response inducing activity and fever inducing

CC activity are typically decreased by at least about 100-fold, while

CC LD50 (in Dutch Belted rabbits) is at least 100-fold higher than

CC the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGGKTC 110

RESULT 11
AAV06256
ID AAV06256 standard; Protein; 239 AA.

XX AAV06256;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-4446.

XX Enterotoxin; SEC-4446; toxin; disulfide loop;

KW protein engineering.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC-4446. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06251). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX belted rabbits) is at least 100-fold higher than the native toxin.
XX
SQ Sequence 239 AA;
Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGKVTGKTC 18
DB 93 CYFSSKDNVKGKVTGKTC 110
RESULT 12
AAY06251
ID AAY06251 standard; Protein; 239 AA.
XX
XX AAY06251;
XX
XX 23-AUG-1999 (first entry)
XX
XX Staphylococcal group C enterotoxin SEC1.
XX
XX Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX

XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC1. The invention relates to pyrogenic toxins, such
XX as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06251). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX belted rabbits) is at least 100-fold higher than the native toxin.
XX
SQ Sequence 239 AA;
Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGKVTGKTC 18
DB 93 CYFSSKDNVKGKVTGKTC 110
RESULT 13
AAY06252
ID AAY06252 standard; Protein; 239 AA.
XX
XX AAY06252;
XX
XX 23-AUG-1999 (first entry)
XX
XX Staphylococcal group C enterotoxin SEC2.
XX
XX Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 93..110
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX WPI; 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC2. The invention relates to pyrogenic toxins, such
XX as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAY06251). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX belted rabbits) is at least 100-fold higher than the native toxin.
XX

CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08; Mismatches 0; Indels 0; Gaps 0;

DB 1 CYPSSKDNVKGVTGKTC 18
93 CYPSSKDNVKGVTGKTC 110

RESULT 14
AAV06253 standard; Protein; 239 AA.

XX AAV06253;

XX 23-AUG-1999 (first entry)

XX Staphylococcal group C enterotoxin SEC3-FRI913.

XX Enterotoxin; SEC3-FRI913; toxin; disulfide loop;
XX protein engineering.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Disulfide-bond 93..110

XX MO9927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC3-FRI913. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAV06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while LD50 (in Dutch
XX Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08; Mismatches 0; Indels 0; Gaps 0;

DB 1 CYPSSKDNVKGVTGKTC 18
93 CYPSSKDNVKGVTGKTC 110

RESULT 15
AAB67342 standard; peptide; 239 AA.

XX AAB67342;

XX 23-APR-2001 (first entry)

XX Staphylococcus aureus enterotoxin C1 protein.

XX Tumour; cancer; immune; enterotoxin.

XX Staphylococcus aureus.

XX US6180097-B1.

XX 30-JAN-2001.

XX 30-OCT-1998; 98US-0183437.

XX 31-JAN-1994; 94US-0189424.

XX 19-JUN-1995; 95US-0491746.

XX 03-OCT-1989; 89US-0416530.

XX 17-JAN-1990; 90US-0466577.

XX 17-JAN-1991; 91WO-US00342.

XX 01-JUN-1992; 92US-0891718.

XX 02-MAR-1993; 93US-0025144.

XX (TERM/) THERMAN D S.

XX Terman DS;

XX WPI; 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro

XX or in vivo comprises exogenous nucleic acids encoding a superantigen

XX and a costimulatory molecule -

XX Disclosure; Fig 2; 16pp; English.

XX The present invention relates to a tumour cell capable of stimulating
XX antitumor immune reactivity in vitro or in vivo contains and
XX expresses an exogenous nucleic acid molecule encoding a superantigen
XX or its active fragment and an exogenous nucleic acid molecule
XX encoding a costimulatory molecule that activates T cells in
XX conjunction with an antigenic stimulus. The invention may be used
XX for cancer therapy by stimulating an anticancer immune response
XX in vivo or ex vivo.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 22; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08; Mismatches 0; Indels 0; Gaps 0;

DB 1 CYPSSKDNVKGVTGKTC 18
93 CYPSSKDNVKGVTGKTC 110

Search completed: October 15, 2003, 16:56:55
Job time : 49.3575 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:51:46 ; Search time 13.7964 Seconds
(without alignments)
55.202 Million cell updates/sec

Title: US-09-555-115A-13
Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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4: /cgm2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgm2_6/prodata/1/iaa/PCUTUS_COMB.pep:*
6: /cgm2_6/prodata/1/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	89	4	US-09-144-776B-21
2	102	100.0	89	4	US-09-144-776B-22
3	102	100.0	89	4	US-09-144-776B-23
4	102	100.0	238	3	US-08-896-933-28
5	102	100.0	238	4	US-09-114-235-28
6	102	100.0	239	3	US-08-896-933-27
7	102	100.0	269	4	US-09-114-235-27
8	102	100.0	269	4	US-09-144-776B-14
9	48	47.1	170	4	US-09-252-991A-29047
10	46	45.1	263	2	US-08-892-690-3
11	46	45.1	374	2	US-07-857-224B-82
12	46	45.1	374	2	US-07-857-224B-83
13	46	45.1	375	4	US-09-347-878-56
14	44	43.1	134	2	US-08-482-728A-14
15	44	43.1	176	1	US-08-145-595A-4
16	44	43.1	176	2	US-08-451-747-4
17	44	43.1	176	3	US-09-134-852-4
18	42	41.2	514	1	US-08-361-820-21
19	42	41.2	514	1	US-08-479-939-21
20	42	41.2	514	1	US-08-483-432-21
21	40.5	39.7	155	4	US-09-252-991A-19995
22	40	39.2	210	4	US-09-247-155-121
23	40	39.2	264	3	US-08-924-570A-2
24	40	39.2	320	3	US-09-092-437-2
25	40	39.2	374	2	US-07-857-224B-80
26	40	39.2	374	2	US-07-857-224B-81
27	40	39.2	374	2	US-07-857-224B-84

28	40	39.2	374	2	US-07-857-224B-85	Sequence 85, Appl
29	40	39.2	375	2	US-07-857-224B-86	Sequence 86, Appl
30	40	39.2	412	2	US-08-741-134-2	Sequence 2, Appl
31	40	39.2	690	4	US-09-252-991A-29429	Sequence 29429, A
32	40	39.2	1053	4	US-09-328-352-6788	Sequence 6788, Ap
33	39.5	38.7	765	4	US-09-252-991A-24791	Sequence 24791, A
34	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
35	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
36	39	38.2	94	4	US-08-938-085A-35	Sequence 35, Appl
37	39	38.2	94	4	US-08-938-085A-37	Sequence 37, Appl
38	39	38.2	94	4	US-10-072-844-35	Sequence 35, Appl
39	39	38.2	94	4	US-10-072-844-37	Sequence 37, Appl
40	39	38.2	95	4	US-09-107-532A-6140	Sequence 6140, Ap
41	39	38.2	228	1	US-08-278-091-7	Sequence 7, Appl
42	39	38.2	228	1	US-08-483-859-7	Sequence 7, Appl
43	39	38.2	228	1	US-08-472-173-7	Sequence 7, Appl
44	39	38.2	228	2	US-08-487-167-7	Sequence 7, Appl
45	39	38.2	228	2	US-08-482-816-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-144-776B-21
Sequence 21, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCNR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09144, 776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21
Query Match# 100.0%; Score 102; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKTC 18
Db 54 CYFSSKDNVKGKTC 71

RESULT 2

US-09-144-776B-22

; Sequence 22, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,

Mark A. Olson

Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen

Vaccines

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris

STREET: US Army MRC -504 Scott Street

MCMR-JA (Charles H. Harris-Patent

Atty)

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,776B

FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 89

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-144-776B-22

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKTC 18
Db 54 CYFSSKDNVKGKTC 71

RESULT 3

US-09-144-776B-23

; Sequence 23, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,

Mark A. Olson

Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen

Vaccines

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris

STREET: US Army MRC -504 Scott Street

MCMR-JA (Charles H. Harris-Patent

Atty)

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,776B

FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 89

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-144-776B-23

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKTC 18
Db 54 CYFSSKDNVKGKTC 71

RESULT 4

US-08-896-933-28

; Sequence 28, Application US/08896933
; Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: Tumor Killing Effects of Enterotoxins,

File Reference: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

CURRENT FILING DATE: 1997-07-18

EARLIER APPLICATION NUMBER: 08/252,978

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 28

LENGTH: 238

TYPE: PR

ORGANISM: *Staphylococcus aureus*

US-08-896-933-28

Query Match 100.0%; Score 102; DB 3; Length 238;

Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 92 CYFSSKDNVGVGTGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ. ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-28

Query Match 100.0%; Score 102; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 92 CYFSSKDNVGVGTGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ. ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

Query Match 100.0%; Score 102; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 93 CYFSSKDNVGVGTGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ. ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-27

Query Match 100.0%; Score 102; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGKTC 18
Db 93 CYFSSKDNVGVGTGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; City: Fort Detrick
; State: Maryland
; Country: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match      100.0%; Score 102; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKTC 18
Db      120 CYFSSKDNVKGKTC 137

RESULT 9
US-09-252-991A-29047
; Sequence 29047, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29047
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29047

Query Match      47.1%; Score 48; DB 4; Length 170;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKTC 14
Db      116 CSEFARDNAGRATG 129

RESULT 10
US-08-692-690-3
; Sequence 3, Application US/08692690
; Patent No. 5932420
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```

```

; STREET: 3174 Porter Drive
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,690
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0339 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624778
US-08-892-690-3

Query Match      45.1%; Score 46; DB 2; Length 263;
Best Local Similarity 43.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKTC 16
Db      90 CFFSDPVSIPGGE 105

RESULT 11
US-07-857-224B-82
; Sequence 82, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; City: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (international) 41 1 632 2830
; TELEFAX: (international) 41 1 262 2437
; TELEX: none

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; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE: Alcohol dehydrogenase, Table 3 Column 3
; PUBLICATION INFORMATION:
; AUTHORS:
; JOERNVALL, H.
; AUTHORS: Persson, M.
; AUTHORS: Jeffery, J.
; TITLE: Alcohol dehydrogenases
; JOURNAL: Proceedings of the National Academy of Sciences, USA
; VOLUME: 78
; PAGES: 4226-4230
; DATE: 1981
; US-07-857-224B-82

Query Match      45.1%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGYTGKTC 18
Db 174 CGFSTGYGSANVAVKTPGSTC 195

RESULT 12
US-07-857-224B-83
; Sequence 83, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (international) 41 1 632 2830
; TELEFAX: (international) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE: Alcohol dehydrogenase, Table 3 Column 4
; PUBLICATION INFORMATION:
; AUTHORS:
; JOERNVALL, H.
```

```

; AUTHORS: Persson, M.
; AUTHORS: Jeffery, J.
; TITLE: Alcohol dehydrogenases
; JOURNAL: Proceedings of the National Academy of Sciences, USA
; VOLUME: 78
; PAGES: 4226-4230
; DATE: 1981
; US-07-857-224B-83

Query Match      45.1%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGYTGKTC 18
Db 174 CGFSTGYGSANVAVKTPGSTC 195

RESULT 13
US-09-347-878-56
; Sequence 56, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-347-878-56

Query Match      45.1%; Score 46; DB 4; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGYTGKTC 18
Db 175 CGFSTGYGSANVAVKTPGSTC 196

RESULT 14
US-08-482-728A-14
; Sequence 14, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802e1 Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

NAME: Silva, Robin M.
 REGISTRATION NUMBER: 38,304
 REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-1249
 TELEEX: 910 277229
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 134 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-482-728A-14

Query Match 43.1%; Score 44; DB 2; Length 134;
 Best Local Similarity 44.4%; Pred. No. 14;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKTKC 18
 Db 21 CLCGEKGIGKTTGKKLC 38

RESULT 15

US-08-145-995A-4
 Sequence 4, Application US/08145995A
 Patent No. 5482850
 GENERAL INFORMATION:
 APPLICANT: CARLOW, CLOTTIDE K.S.
 TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ADDRESSEE: CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/145,995A
 FILING DATE: 29-OCT-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RESNICK, DAVID S.
 REGISTRATION NUMBER: 34235
 REFERENCE/DOCKET NUMBER: 43406
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-3400
 TELEFAX: (617) 523-6440
 TELEEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 176 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-145-995A-4

Query Match 43.1%; Score 44; DB 1; Length 176;
 Best Local Similarity 44.4%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKTKC 18
 Db 41 CLCGEKGIGKTTGKKLC 58

Search completed: October 15, 2003, 17:08:32
 Job time: 14.7964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 27.2695 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115A-13
Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgnt2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgnt2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
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13: /cgnt2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	89	15	US-10-002-784A-36
2	102	100.0	89	15	US-10-002-784A-37
3	102	100.0	89	15	US-10-002-784A-38
4	102	100.0	266	8	US-08-882-431-14
5	102	100.0	266	10	US-09-870-759-12
6	102	100.0	266	12	US-09-751-708A-12
7	102	100.0	266	15	US-10-002-784A-14
8	46	45.1	263	9	US-09-265-710-3
9	46	45.1	263	12	US-10-366-020-3
10	46	45.1	375	10	US-09-981-353-113
11	46	45.1	375	12	US-09-738-630-92
12	46	45.1	395	9	US-09-925-302-497
13	42	41.2	211	15	US-10-156-761-8802
14	42	41.2	332	15	US-10-021-811-54
15	41.5	40.7	993	15	US-10-128-714-3467

16	41.5	40.7	1105	15	US-10-128-714-8467	Sequence 8467, Ap
17	41	40.2	163	12	US-10-238-075-786	Sequence 786, Ap
18	41	40.2	137	11	US-09-764-891-4188	Sequence 4188, Ap
19	40.5	39.7	1139	15	US-10-156-761-10856	Sequence 10856, A
20	40	39.2	152	12	US-10-040-895-2	Sequence 2, Appli
21	40	39.2	210	12	US-09-903-190-121	Sequence 13, Appl
22	40	39.2	263	11	US-09-823-356-13	Sequence 13, Appl
23	40	39.2	263	9	US-09-946-374-43	Sequence 43, Appl
24	40	39.2	263	12	US-10-015-387A-43	Sequence 43, Appl
25	40	39.2	263	12	US-10-006-130A-43	Sequence 43, Appl
26	40	39.2	263	12	US-10-199-672-184	Sequence 184, Ap
27	40	39.2	263	12	US-10-006-172A-43	Sequence 43, Appl
28	40	39.2	263	12	US-10-187-749-184	Sequence 184, Ap
29	40	39.2	263	12	US-10-194-457-184	Sequence 184, Ap
30	40	39.2	263	12	US-10-184-642-184	Sequence 184, Ap
31	40	39.2	263	12	US-10-196-747-184	Sequence 184, Ap
32	40	39.2	263	12	US-10-015-382A-43	Sequence 43, Appl
33	40	39.2	263	12	US-10-017-253A-43	Sequence 43, Appl
34	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
35	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
36	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
37	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
38	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
39	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
40	40	39.2	263	12	US-10-173-659-184	Sequence 184, Ap
41	40	39.2	263	12	US-10-173-707-184	Sequence 184, Ap
42	40	39.2	263	12	US-10-174-569-184	Sequence 184, Ap
43	40	39.2	263	12	US-10-174-583-184	Sequence 184, Ap
44	40	39.2	263	12	US-10-174-587-184	Sequence 184, Ap
45	40	39.2	263	12	US-10-174-589-184	Sequence 184, Ap

ALIGNMENTS

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RESULT 1
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36
```

Query Match 100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CYFSSKDNVKGVTGKTC 18
Db 54 CYFSSKDNVKGVTGKTC 71
```

```
RESULT 2
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
```

```

; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-37

```

```

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CYFSSKDNVGVKVTGKTC 18
      |||||
Db      54 CYFSSKDNVGVKVTGKTC 71

```

```

RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US2003003644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-38

```

```

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CYFSSKDNVGVKVTGKTC 18
      |||||
Db      54 CYFSSKDNVGVKVTGKTC 71

```

```

RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John Moran
; STREET: US Army MRCW -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK

```

```

; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14

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```

Query Match      100.0%; Score 102; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CYFSSKDNVGVKVTGKTC 18
      |||||
Db      120 CYFSSKDNVGVKVTGKTC 137

```

```

RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-870-759-12

```

```

Query Match      100.0%; Score 102; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CYFSSKDNVGVKVTGKTC 18
      |||||
Db      120 CYFSSKDNVGVKVTGKTC 137

```

```

RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1

```

```

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
; US-09-751-708A-12

Query Match      100.0%; Score 102; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
DB      120  CYFSSKDNVGVKVTGKTC 137

RESULT 7
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US2003003644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PR1
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
; US-10-002-784A-14

Query Match      100.0%; Score 102; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGKTC 18
DB      120  CYFSSKDNVGVKVTGKTC 137

RESULT 8
US-09-265-710-3
; Sequence 3, Application US/09265710
; Patent No. US20020042126A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purni
; TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```

```

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/892,690
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0339 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 624778
; US-09-265-710-3

Query Match      45.1%; Score 46; DB 9; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTGK 16
DB      90  CFPSDSDPNSIPGGE 105

RESULT 9
US-10-366-020-3
; Sequence 3, Application US/10366020
; Publication No. US20030152989A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Goll, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/366,020
; FILING DATE: 11-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,161
; FILING DATE: 1998-12-07
; APPLICATION NUMBER: US/08/791,338
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

```
;
;   REGISTRATION NUMBER: 36, 749
;   REFERENCE/DOCKET NUMBER: PF-0208 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 263 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;       LIBRARY: GenBank
;       CLONE: 624778
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-366-020-3

Query Match      45.1%; Score 46; DB 12; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 CYFS---SKDNVKGVTGKTC 16
Db      90 CFFDSEDPVNSIPGGE 105

RESULT 10
US-09-981-353-113
; Sequence 113, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
;   APPLICANT: Laasek, Amy W.
;   TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;   FILE REFERENCE: PA-0038 US
;   CURRENT APPLICATION NUMBER: US/09/981,353
;   CURRENT FILING DATE: 2001-10-11
;   NUMBER OF SEQ ID NOS: 194
;   SOFTWARE: PERL Program
;   SEQ ID NO 113
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: Incyte ID No. US20020160382A1 2512879CD1
US-09-981-353-113

Query Match      45.1%; Score 46; DB 10; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1 CYFS---SKDNVKGVTGKTC 18
Db      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 11
US-09-738-630-92
; Sequence 92, Application US/09738630
; Publication No. US20030166213A1
; GENERAL INFORMATION:
;   APPLICANT: Greenspan, Ralph J.
;   APPLICANT: Shaw, Paul J.
;   TITLE OF INVENTION: Methods for Identifying Compounds That
;   TITLE OF INVENTION: Modulate Disorders Related to Nitric Oxide/cGMP-Dependent
;   TITLE OF INVENTION: Protein Kinase Signaling
;   FILE REFERENCE: P-NI 3906
;   CURRENT APPLICATION NUMBER: US/09/738,630
;   CURRENT FILING DATE: 2000-12-15
;   NUMBER OF SEQ ID NOS: 105
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 92
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;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-738-630-92

Query Match      45.1%; Score 46; DB 12; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1 CYFS---SKDNVKGVTGKTC 18
Db      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 12
US-09-925-302-497
; Sequence 497, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA104
;   CURRENT APPLICATION NUMBER: US/09/925,302
;   CURRENT FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: PCT/US00/05918
;   PRIOR FILING DATE: 2000-03-08
;   PRIOR APPLICATION NUMBER: 60/124,270
;   PRIOR FILING DATE: 1999-03-12
;   NUMBER OF SEQ ID NOS: 896
;   SOFTWARE: Patent In Ver. 2.0
;   SEQ ID NO 497
;   LENGTH: 395
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (164)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-497

Query Match      45.1%; Score 46; DB 9; Length 395;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1 CYFS---SKDNVKGVTGKTC 18
Db      195 CGFSTGYGSANVAKVTPGSTC 216

RESULT 13
US-10-156-761-8802
; Sequence 8802, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;   APPLICANT: OMURA, SATOSHI
;   APPLICANT: IKEDA, HARUO
;   APPLICANT: ISHIKAWA, JUN
;   APPLICANT: HORIKAWA, HIROSHI
;   APPLICANT: SHIBA, TADAYOSHI
;   APPLICANT: SAKAKI, YOSHIYUKI
;   APPLICANT: HATTORI, MASAHIRA
;   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;   FILE REFERENCE: 249-262
;   CURRENT APPLICATION NUMBER: US/10/156,761
;   CURRENT FILING DATE: 2002-05-29
;   PRIOR APPLICATION NUMBER: JP 2001-204089
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-272697
;   PRIOR FILING DATE: 2001-08-02
;   NUMBER OF SEQ ID NOS: 15109
;   SEQ ID NO 8802
;   LENGTH: 211
;   TYPE: PRT
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; ORGANISM: Streptomyces avermitilis
; US-10-156-761-8802

Query Match
Best Local Similarity 41.2%; Score 42; DB 15; Length 211;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YFSSKDNVGVKT 13
   :|||||:|
Db 58 HFSSKDNLTAKT 69

RESULT 14
US-10-021-811-54
; Sequence 54, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Canoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odeh, Joan
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BR1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 54
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-021-811-54

Query Match
Best Local Similarity 41.2%; Score 42; DB 15; Length 332;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKTG 15
   |||||:|
Db 197 CYASSADNIRMLKG 211

RESULT 15
US-10-128-714-3467
; Sequence 3467, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Weng
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3467
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; LENGTH: 993
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-3467

Query Match
Best Local Similarity 40.7%; Score 41.5; DB 15; Length 993;
Matches 9; Conservative 3; Mismatches 1; Indels 9; Gaps 1;

QY 5 SKDNV-----GKVTGKT 17
   :|||||:|
Db 102 TKDNICFQIDAEETITGKT 123

Search completed: October 15, 2003, 17:47:00
Job time : 27.2695 secs
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 13.6886 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115A-13

Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	266	1 ENSAC1	enterotoxin C-1 pr
2	102	100.0	266	2 A60114	enterotoxin C-2 pr
3	102	100.0	266	2 S11885	enterotoxin C3 - S
4	46	45.1	199	2 AG1583	weakly phosphoglyc
5	46	45.1	375	1 DEHUA	alcohol dehydrogen
6	46	45.1	375	1 DEHUA	alcohol dehydrogen
7	44	43.1	246	2 UQ1472	trypsin (EC 3.4.21
8	44	43.1	246	2 UQ1471	trypsin (EC 3.4.21
9	44	43.1	275	2 T32005	hypothetical prote
10	44	43.1	1403	1 A47328	natural killer cel
11	44	43.1	1507	2 B47328	natural killer cel
12	43	42.2	274	2 T13010	hypothetical prote
13	43	42.2	346	2 AE3434	lytB protein (impo
14	43	42.2	366	2 T26338	hypothetical prote
15	42	41.2	212	2 T05936	agglutinin isolat
16	42	41.2	235	2 E91097	hypothetical prote
17	42	41.2	235	2 A85943	hypothetical prote
18	42	41.2	260	2 B96944	2 deoxy-D-gluconat
19	42	41.2	358	2 T08477	inclusion membran
20	42	41.2	375	1 A38405	alcohol dehydrogen
21	42	41.2	378	2 AC1454	protein gp18 from
22	42	41.2	378	2 AD1090	protein gp18 from
23	42	41.2	430	2 A87634	peptidase, M20/M25
24	41	40.2	57	2 S70473	neurotoxin Ts-kapp
25	41	40.2	199	2 T08573	hypothetical prote
26	41	40.2	199	2 AD1230	phosphoglycerate m
27	41	40.2	269	2 B97113	protein serine/thr
28	41	40.2	368	1 DEHUA6	alcohol dehydrogen
29	41	40.2	375	1 A33909	alcohol dehydrogen

30	41	40.2	746	2 AD1622	probable integral
31	41	40.2	750	2 G81361	probable flagellin
32	41	40.2	1127	2 T03105	major single-stran
33	40.5	39.7	333	2 D83585	hypothetical prote
34	40.5	39.7	725	2 T17732	helicase-like prot
35	40.5	39.7	1102	2 A84480	probable retroelem
36	40	39.2	99	2 G84242	hypothetical prote
37	40	39.2	242	2 H69066	hypothetical prote
38	40	39.2	266	1 S18159	ribosomal protein
39	40	39.2	320	2 H95136	hypothetical prote
40	40	39.2	320	2 B99005	ribonucleoside-dip
41	40	39.2	348	2 D70195	hypothetical prote
42	40	39.2	374	2 DEHOAS	alcohol dehydrogen
43	40	39.2	375	1 I55359	alcohol dehydrogen
44	40	39.2	375	1 DEHUA6	alcohol dehydrogen
45	40	39.2	375	1 DEHOAL	alcohol dehydrogen

ALIGNMENTS

RESULT 1
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
C/Accession: S06356; A01816
R/Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A/Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to
A/Reference number: S06356; MUID:88038352; PMID:2823067
A/Accession: S06356
A/Molecule type: DNA
A/Residues: 1-266 <BOH>
A/Cross-References: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R/Schmidt, U.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-266/Product: enterotoxin C-1 #status experimental <MAT>
A/Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A/Reference number: A01816; MUID:83213327; PMID:6189824
A/Accession: A01816
A/Molecule type: protein
A/Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C/Genetics:
A/Genes: entC1
C/Superfamily: enterotoxin B
C/Keywords: enterotoxin
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-266/Product: enterotoxin C-1 #status experimental <MAT>
F/120-137/Diulfide bonds: #status experimental

Query Match 100.0%; Score 102; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
DB 120 CYFSSKDNVKGVTGGKTC 137

RESULT 2
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N/Alternate names: enterotoxin C-3 precursor
C/Species: Staphylococcus aureus
C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
C/Accession: A60114; B60114; A33866
R/Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A/Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A/Reference number: A60114; MUID:89277549; PMID:2543637
A/Accession: A60114
A/Status: not compared with conceptual translation
A/Molecule type: DNA

```
A;Residues: 1-266 <BOH>
A;Accession: B60114
A;Molecule type: Protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Beiley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match          100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGKTC 18
Db      120  CYFSSKDNVKGKVTGKTC 137

RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S11885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
A;Reference number: S11885; MUID:90220508; PMID:23255627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
A;Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B

Query Match          100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGKTC 18
Db      120  CYFSSKDNVKGKVTGKTC 137

RESULT 4
AG1583
weakly phosphoglycerate mutase 1 homolog lin1208 [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1583
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseguret, O.; Entian, K.D.; Fehli, H.
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madheno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96439.1; PID:g16413682; GSPDB:GN00178
```

```
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin1208

Query Match          45.1%; Score 46; DB 2; Length 199;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      2  YFSSKDNVKGKVTGKTC 18
Db      1510  YWERTSKIGKVTGLKNC 167

RESULT 5
DEHUA
alcohol dehydrogenase (EC 1.1.1.1) 1 - human
N;Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
C;Accession: S02265; A25428; A24408; I39398; I39397
R;Matsu, Y.; Yokoyama, S.
FEBS Lett. 243, 57-60, 1989
A;Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
A;Reference number: S02265; MUID:89153548; PMID:2920825
A;Accession: S02265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-375 <MATS>
R;Ikuta, T.; Szeto, S.; Yoshida, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
A;Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and exp
A;Reference number: A94120; MUID:86120995; PMID:2935875
A;Accession: A25428
A;Molecule type: mRNA
A;Residues: 1-375 <IKU>
A;Cross-references: GB:M12271; NID:g178091; PIDN:AA68131.1; PID:g178092
R;von Bahr-Lindstrom, H.; Hoog, J.O.; Heden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K.
Biochemistry 25, 2465-2470, 1986
A;Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
A;Reference number: A24408; MUID:86243367; PMID:3013304
A;Accession: A24408
A;Molecule type: mRNA
A;Residues: 1-375 <YON>
A;Cross-references: GB:M12963; NID:g178089; PIDN:AA51590.1; PID:g178090
R;Yasunami, M.; Kikuchi, I.; Sarapat, D.; Yoshida, A.
Genomics 7, 152-158, 1990
A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
A;Reference number: I39398; MUID:90269803; PMID:2347582
A;Accession: I39398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <YAS>
A;Cross-references: GB:M37066; NID:g178095; PIDN:AA51591.1; PID:g178096
R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
Gene 90, 271-279, 1990
A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
A;Reference number: I39397; MUID:90382676; PMID:2169444
A;Accession: I39397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <STS>
A;Cross-references: GB:M32656; NID:g178093; PIDN:AA52276.1; PID:g178094
C;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
C;Genetics:
A;Gene: GDB:ADH1
A;Cross-references: GDB:119650; OMIM:103700
A;Map position: 4q21-4q23
A;Intons: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: ethanol degradation
A;Note: human alcohol dehydrogenase 1 is expressed predominately in fetal and neonatal li
```

C:Superfamily: alcohol dehydrogenase, long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 P:2-315/Product: alcohol dehydrogenase 1 #status predicted <MAT>
 P:32-366/Domin: long-chain alcohol dehydrogenase homology <LAH>
 P:195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F:47/68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 45.1%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

1 CYS-----SKDNVGYTGKTC 18
 175 CCFSTGCGSAVNAAKVTPGSTC 196

RESULT 6
 DEHUB
 Alcohol dehydrogenase (EC 1.1.1.1) 2 [validated] - human
 N:Alternate names: alcohol dehydrogenase beta chain; class I alcohol dehydrogenase
 C:Species: Homo sapiens (man)
 C>Date: 25-Feb-1985, #sequence, revision 02-Aug-1994 #text change 15-Sep-2000
 C:Accession: A23607; A38916; I39399; A26281; I39402; I39401; S05202; S10621; I39400; A00
 R:Heden, L.O.; Hoog, J.O.; Larsson, K.; Lake, M.; Lagerholm, E.; Holmgren, A.; Vallee, B
 FEBS Lett. 194, 327-332, 1986
 A>Title: cDNA clones coding for the beta-subunit of human liver alcohol dehydrogenase ha
 A:Reference number: A23607; MUID:86082371; PMID:3000832
 A:Accession: A23607
 A:Molecule type: mRNA
 A:Residues: 1-375 <HEM>
 A:Cross-references: EMBL:X03350; NID:g28415; PIDN:CAA27056.1; PID:g28416
 R:Ikuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2703-2707, 1985
 A>Title: Molecular cloning of a full-length cDNA for human alcohol dehydrogenase.
 A:Reference number: A38916; MUID:85190565; PMID:2986130
 A:Accession: A38916
 A:Molecule type: mRNA
 A:Residues: 1-375 <IKU>
 A:Cross-references: GB:M24317; NID:g178097
 A>Note: this sequence has been revised in reference A38917
 R:Ikuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5578, 1985
 A:Reference number: A38917
 A:Contents: annotation; extram
 R:Yokoyama, S.; Yokoyama, R.; Rotwein, P.
 Jpn. J. Genet. 62, 241-256, 1987
 A>Title: Molecular characterization of cDNA clones encoding the human alcohol dehydrogen
 A:Reference number: I39399
 A:Accession: I39399
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-375 <YOK>
 A:Cross-references: GB:000137; NID:g219427; PIDN:BA00084.1; PID:g219428
 R:Buehler, G.; Smith, M.; Bilanchone, V.; Hatfield, G.W.
 J. Biol. Chem. 261, 2027-2033, 1986
 A>Title: Molecular analysis of the human class I alcohol dehydrogenase gene family and n
 A:Reference number: A26281; MUID:8611189; PMID:2935533
 A:Accession: A26281
 A:Molecule type: DNA
 A:Residues: 1-229, 'K', 231-375 <DNB>
 A:Cross-references: GB:M24317; GB:K01883; NID:g178097; PIDN:AA51884.1; PID:g178098
 A>Note: the authors translated the codon AAA for residue 230 as Phe
 R:Yasunuma, M.; Kikuchi, I.; Sarapat, D.; Yoshida, A.
 Genomics 7, 152-158, 1990
 A>Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly
 A:Reference number: I39398; MUID:90268803; PMID:2347582
 A:Accession: I39402
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-6 <YAS>
 A:Cross-references: GB:M37067; NID:g178114; PIDN:AA51593.1; PID:g178115

R:Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990
 A>Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: interc
 A:Reference number: I39397; MUID:90082676; PMID:2169444
 A:Accession: I39401
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <STE>
 A:Cross-references: GB:M32657; NID:g178112; PIDN:AA52277.1; PID:g178113
 R:Matsumoto, Y.; Yokoyama, R.; Yokoyama, S.
 Eur. J. Biochem. 183, 317-320, 1989
 A>Title: The genes for human alcohol dehydrogenases beta(1) and beta(2) differ by only o
 A:Reference number: S05202; MUID:89338401; PMID:2547609
 A:Accession: S05202
 A:Molecule type: DNA
 A:Residues: 1-47, 'H', 49-375 <MATS>
 A:Cross-references: EMBL:X15447; NID:g28385
 A>Note: allelic beta-2 variant found predominately in oriental populations
 A>Note: the sequence in GenBank entry HSADH221, release 103 (PID:e28260), has an incorr
 R:Brig, T.; von Wartburg, J.P.; Wermuth, B.
 FEBS Lett. 234, 53-55, 1988
 A>Title: cDNA sequence of the beta(2)-subunit of human liver alcohol dehydrogenase.
 A:Reference number: S10621; MUID:88271624; PMID:2968918
 A:Accession: S10621
 A:Molecule type: mRNA
 A:Residues: 1-47, 'H', 49-343 <EHR>
 A>Note: only a list of differences from various previously published sequences is shown
 R:Xu, Y.L.; Carr, L.G.; Boston, W.F.; Li, T.K.; Edenberg, H.J.
 Genomics 2, 209-214, 1988
 A>Title: Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci following I
 A:Reference number: I39400; MUID:88284699; PMID:3397059
 A:Accession: I39400
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7, 'W', 9-56, 'K', 58-165, 'K', 167-234, 'V', 236-375 <RE3>
 A:Cross-references: GB:M21692; NID:g178099; PIDN:AA51592.1; PID:g178100
 R:Hempel, J.; Buhler, R.; Kaiser, R.; Holmgren, B.; de Zeleneki, C.; von Wartburg, J.P.;
 Eur. J. Biochem. 145, 437-445, 1984
 A>Title: Human liver alcohol dehydrogenase. 1. The primary structure of the beta-1beta-1
 A:Reference number: A00335; MUID:85076637; PMID:6391920
 A:Accession: A00335
 A:Molecule type: protein
 A:Residues: 2-129, 131-375 <HEM>
 A>Note: allelic beta-1 variant found predominately in caucasian and negroid populations
 R:Buhler, R.; Hempel, J.; Kaiser, R.; von Wartburg, J.P.; Vallee, B.L.; Jornvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6320-6324, 1984
 A>Title: Human alcohol dehydrogenase: structural differences between the beta and gamma s
 ndants in livers of different mammals.
 A:Reference number: A05182; MUID:85038508; PMID:6387702
 A:Accession: A05182
 A:Molecule type: protein
 A:Residues: 12-34, 'V', 36-38, 41-85, 101-114, 131-160, 170-213, 273-313, 331-341-367 <BUH>
 R:Burnell, J.C.; Carr, L.G.; Dwyer, F.E.; Edenberg, H.J.; Li, T.K.; Boston, W.F.
 Biochem. Biophys. Res. Commun. 146, 1227-1233, 1987
 A>Title: The human beta-3 alcohol dehydrogenase subunit differs from beta-1 by a Cys for
 A:Reference number: A26826
 A:Accession: A26826
 A:Molecule type: protein
 A:Residues: 368-369, 'C', 371-375 <BUR>
 A>Note: allelic beta-3 variant found as a minor form occurring to a greater extent in neg
 R:Huxley, T.D.; Boston, W.F.; Hamilton, J.A.; Amel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8149-8153, 1991
 A>Title: Structure of human beta-1beta-1 alcohol dehydrogenase: catalytic effects of non
 A:Reference number: A40987; MUID:91376103; PMID:1896463
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms
 A>Note: structure of beta-1 variant dimer
 R:Huxley, T.D.; Boston, W.F.; Hamilton, J.A.; Amel, L.M.
 submitted to the Brookhaven Protein Data Bank, January 1993
 A:Reference number: A52127; PDB:3HND
 A:Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 2-375
 C:Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C:Genetics:
 A:Gene: GDB:ADH2

A:Cross-references: GDB:119651; OMIM:103720
 A:Map position: 4q22-4q22
 A:Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
 C:Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded b
 C:Function:
 A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
 A:Pathway: alcohol degradation
 A>Note: human alcohol dehydrogenase beta is expressed predominantly in fetal lung and ne
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
 F:2-375/Product: alcohol dehydrogenase 2 #status experimental <MAT>
 F:3-356/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F:195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
 F:47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
 F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match 45.1%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Oy 1 CYSFSGYGSAMVAKVPGSTC 196
 175 CYSFSGYGSAMVAKVPGSTC 196

RESULT 7
 J01472
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
 C:Accession: J01472
 R:Kang, J.; Wiegand, U.; Mueller-Hill, B.
 Gene 110, 181-187, 1992
 A:Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
 A:Reference number: J01471; MUID:92165057; PMID:1537555
 A:Accession: J01472
 A:Molecule type: mRNA
 A:Residues: 1-246 <KAN>
 A:Cross-references: EMBL:X59013; NID:957414; PIND:CAA41752.1; PID:957415
 A:Experimental source: pancreas
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; protein digestion; serine proteinase; zymogen
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-24/Domain: activation peptide #status predicted <ACT>
 F:25-246/Product: trypsin V, b-form #status predicted <MAT>
 F:25-239/Domain: trypsin homology <TRY>
 F:31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
 F:64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
 Best Local Similarity 43.8%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 FSSKDNVKGKVTGKTC 18
 16 FPTEDNDRIVGKTC 31

RESULT 8
 J01471
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
 C:Accession: J01471; S23784
 R:Kang, J.; Wiegand, U.; Mueller-Hill, B.
 Gene 110, 181-187, 1992
 A:Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
 A:Reference number: J01471; MUID:92165057; PMID:1537555
 A:Accession: J01471
 A:Molecule type: mRNA
 A:Residues: 1-246 <KAN>
 A:Cross-references: EMBL:X59012; NID:957412; PIND:CAA41751.1; PID:957413

A:Experimental source: pancreas
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; protein digestion; serine proteinase; zymogen
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-24/Domain: activation peptide #status predicted <ACT>
 F:25-246/Product: trypsin V, a-form #status predicted <MAT>
 F:25-239/Domain: trypsin homology <TRY>
 F:31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
 F:64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
 Best Local Similarity 43.8%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 FSSKDNVKGKVTGKTC 18
 16 FPTEDNDRIVGKTC 31

RESULT 9
 T32005
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32005
 R:Dante, M.; Kramer, J.; Twyman, B.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F36H9.
 A:Reference number: Z21110
 A:Accession: T32005
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-275 <DAN>
 A:Cross-references: EMBL:AF016668; PIND:AA866090.1; GSPDB:GNO0020; CESP:F36H9.2
 A:Experimental source: strain Bristol N2; clone F36H9
 C:Genetics:
 A:Gene: CESP:F36H9.2
 A:Map position: 2
 A:Introns: 26/2; 54/3; 80/1; 128/3; 152/1; 212/1

Query Match 43.1%; Score 44; DB 2; Length 275;
 Best Local Similarity 38.9%; Pred. No. 29;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CYSKDNVKGKVTGKTC 18
 193 CYSNSGKPEINPEMKYC 210

RESULT 10
 A47328
 A:Title: natural killer cell tumor-recognition protein - human
 N:Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
 C:Accession: A47328
 R:Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortolano, J.R.
 Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
 A:Title: A cyclophilin-related protein involved in the function of natural killer cells.
 A:Reference number: A47328; MUID:93133824; PMID:8421688
 A:Accession: A47328
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1403 <AND>
 A:Cross-references: GB:I04288; NID:g181251; PIND:AAA5734.1; PID:g181252
 A:Experimental source: NK killer cells from adult blood
 A>Note: sequence extracted from NCBI backbone (NCBIN:122798, NCBI:P.122800)
 C:Genetics:
 A:Gene: GDB:NKTR
 A:Cross-references: GDB:137171; OMIM:161565
 A:Map position: 3p23-3p21
 C:Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
 C:Keywords: alternative splicing; lymphocyte

Plant Physiol. 91, 124-129, 1989

A; Title: Cloning and characterization of root-specific barley lectin.

A;Reference number: Z15461

A;Accession: T05936

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-212 <LER>

A; Cross-references: EMBL:M29280; NID:g167070; PIDN:AAA32969.1; PID:g167071

C;Superfamily: wheat agglutinin; hevein chitin-binding domain homology

C.Keywords: lectin
E-1-36/Domatin: signal sequence #status predicted <SIG>

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E:27-212/Product: acclurin isolactin 1 #status predicted <MAT>
F;1-26/Domain: signal sequence #status predicted <SIG>
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F;27-69/Domain: hevein chitin-binding domain homology <HCB>

Query Match	41.28; Score 42; DB 2; Length 212;
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Best Local Similarity 50.0%; Pred. No. 46;

Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 CYSSKDNVGVTTGGKTC 18

Db 66 CYTSKR--CGTQAGGKTC 81

Search completed: October 15, 2003, 17:06:24
Job time : 14.6886 secs

Job time : 14.6886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 7.32934 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-13

Perfect score: 102
Sequence: 1 CYFSSKDNVGVKVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	266	1 ETC1 STAU	P01553 staphylococ
2	102	100.0	266	1 ETC2 STAU	P34071 staphylococ
3	102	100.0	266	1 ETC3 STAU	P23313 staphylococ
4	46	45.1	263	1 ITMA MOUSE	O61500 mus musculu
5	46	45.1	374	1 ADHA HUMAN	P07337 homo sapien
6	46	45.1	374	1 ADHB HUMAN	P00325 homo sapien
7	44	43.1	246	1 TRYA RAT	P32821 rattus norv
8	44	43.1	246	1 TRYB RAT	P32822 rattus norv
9	44	43.1	1453	1 NKCR MOUSE	P30415 mus musculu
10	44	43.1	1462	1 ISPH HUMAN	P04144 mus musculu
11	43	42.2	346	1 ISPH HUMAN	P04144 mus musculu
12	42	41.2	212	1 AGI HORVU	O8yfl1 bruceella me
13	42	41.2	358	1 INCI ECOLI	O52312 escherichia
14	42	41.2	375	1 ADHI RANPE	P22797 rana perez1
15	42	41.2	514	1 GUXC FUSOX	P46238 fusarium ox
16	41	40.2	35	1 SCKK TIRSE	P56219 cilius serr
17	41	40.2	336	1 OTCC STREPY	P16964 streptococ
18	41	40.2	368	1 ADH6 HUMAN	P28332 homo sapien
19	41	40.2	374	1 ADH7 PAPA	P14139 papio hamad
20	41	40.2	905	1 YD83 HUMAN	O9P244 homo sapien
21	40	39.2	127	1 ACPS THETN	O8R857 thermoanaer
22	40	39.2	242	1 RS4E MERTH	O26123 methanobact
23	40	39.2	263	1 ITMA HUMAN	O43376 homo sapien
24	40	39.2	265	1 RL7A CHICK	P32429 gallus gall
25	40	39.2	373	1 ADHS HORSE	P00338 equus cabal
26	40	39.2	374	1 ADHI RABIT	O03505 oryctolagus
27	40	39.2	374	1 ADHA PERMA	P00339 mus musculu
28	40	39.2	374	1 ADHA PERMA	P16680 peromyscus
29	40	39.2	374	1 ADHE HORSE	P00337 equus cabal
30	40	39.2	374	1 ADHG HUMAN	P00336 homo sapien
31	40	39.2	374	1 ADH1 MACMO	P28469 macaca mula
32	40	39.2	375	1 ADHA RAT	P06757 rattus norv
33	40	39.2	412	1 FK84 SPOFR	Q26486 spodoptera

34	40	39.2	523	1 TYD5 PABSO	P54771 papaver som
35	40	39.2	528	1 ACH2 CHICK	P09480 gallus gall
36	40	39.2	612	1 UN37 CAEEL	O02482 caenorhabdi
37	40	39.2	761	1 VPA BPP2	O06419 bacterioph
38	40	39.2	867	1 PH11 MOUSE	O54990 mus musculu
39	40	39.2	1170	1 TSPI1 MOUSE	P35441 mus musculu
40	40	39.2	1235	1 DNBI HCVMA	P17147 human cytom
41	39.5	38.7	664	1 SYM LISMO	O92E90 listeria in
42	39.5	38.7	664	1 SYM LISMO	O8yaf2 listeria mo
43	39	38.2	187	1 RECK YERPE	P37867 yersinia pe
44	39	38.2	256	1 Y0EC ECOLI	O46809 escherichia
45	39	38.2	259	1 KXK2 RAT	P00759 rattus norv

ALIGNMENTS

```
RESULT 1
ID ETC1 STAU STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN EMTCL.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20 (1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt U.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306 (1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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DR EMBL: X05815; CA29260.1; -
DR PIR: S06356; ENSACL.
DR HSSP: P34071; ISE2.
DR InterPro: IPR006177; Bctr1_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strep_tox_C1.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
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SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGKTKC 18
 DB 120 CYFSSKDNVKGKTKC 137
 RESULT 2
 ETC3_STAM STANDARD; PRT; 266 AA.
 ID ETC3_STAM
 AC P3407; 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN EMTX2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RX MEDLINE=89277549; Pubmed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 enterotoxins C1 and C2."
 RL Infect. Immun. 57:2249-2252 (1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; Pubmed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 Staphylococcus aureus reveals a zinc-binding site."
 RL Structure 3:769-779 (1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; Pubmed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins."
 RL Nat. Struct. Biol. 2:680-686 (1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; Pubmed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity."
 RL J. Mol. Biol. 269:270-280 (1997).
 CC -1- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 FAMILY.
 CC PIR; A60114; A60114.
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR PDB; 1COV; 19-SEP-01.
 DR PDB; 114Q; 19-SEP-01.
 DR PDB; 114Q; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR InterPro; IPR006127; Bctrl_tox.
 DR InterPro; IPR006123; Scap/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_DB.
 DR Pfam; PF02876; Staph_strep_tox_C1.1.

DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR002779; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; zinc;
 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT STRAND 48 48
 FT TURN 48 48
 FT HELIX 49 55
 FT STRAND 60 65
 FT STRAND 69 69
 FT TURN 73 73
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGKTKC 18
 DB 120 CYFSSKDNVKGKTKC 137
 RESULT 3
 ETC3_STAM STANDARD; PRT; 266 AA.
 ID ETC3_STAM
 AC P23313; 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN EMTX3 OR SAV2009 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 Staphylococcus aureus.

CC Bacteri: Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUS50 / ATCC 700699, and N315;
RX MEDLINE=20311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cai L., Oguchi A., Aoki K.-I., Nagai Y., Iian Y.-O., Ito T.,
RA Kanemori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake S.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9020508; PubMed=2325627;
RA Hoyde C.J., Hackett S.P., Bohach G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins.";
RL Mol. Gen. Genet. 220:329-333(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=97064178; PubMed=8906797;
RA Fields B.A., Malchiodi E.L., Li H., Yseem X., Stauffer C.V.,
RA Schlevert P.M., Karjalainen K., Mariuzza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen.";
RL Nature 384:188-192(1996).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.

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CC EMBL, AP003364; BAB58171.1; -;
CC DR EMBL, AP003135; BAB45097.1; -;
CC DR EMBL, X51661; CAA35972.1; -;
CC DR PIR, S11865; S11885.
CC PDB: 1JCK; 12-NOV-97.
CC PDB: 1JLG; 02-AUG-02.
CC PDB: 1KLU; 14-AUG-02.
CC InterPro: IPR006177; Bactrl tox.
CC InterPro: IPR006123; Staph/Strep toxin.
CC InterPro: IPR006126; Staph/Strep tox.
CC InterPro: IPR006173; Staph tox OB.
CC Pfam: PF02876; Staph_Strep_tox_C_1.
CC Pfam: PF0123; Staph_Strep_toxin_1.
CC PRINTS: PR00279; BACTRLTOXIN.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
CC Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FCA59 CRC64;
Query Match 100.0%; Score 102; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

OY      1  CYPSSKDNVGVKTGKTC 18
        |||||
DB      120 CYPSSKDNVGVKTGKTC 137

RESULT 4
ITMA_MOUSE
ID      ITMA_MOUSE          STANDARD;          PRT;          263 AA.
AC      Q61500;             Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Integrated membrane protein 2A (E25 protein).
GN      ITM2A OR ITM2 OR E25.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c; TISSUE=Mandible;
RX      MEDLINE=96325063; PubMed=8702837;
RA      Deleersnijder W., Hong G., Cortvriend R., Poitier C., Tytjanowski P.,
RA      Pitcois K., Vannacker E., Merregaert J.;
RT      "Isolation of markers for chondro-osteogenic differentiation using a
RT      cDNA library subtraction. Molecular cloning and characterization of a
RT      gene belonging to a novel multigene family of integral membrane
RT      proteins."
RL      J. Biol. Chem. 271:19475-19482(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RX      MEDLINE=99111395; PubMed=8992734;
RA      Pitcois K., Wauters J., Bossuyt P., Deleersnijder W., Merregaert J.;
RT      "Genomic organization and chromosomal localization of the Itm2a
RT      gene."
RL      Mamm. Genome 10:54-56(1999).
CC      -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC      -I- TISSUE SPECIFICITY: EXPRESSED IN MANDIBULAR CONDYLES, IN BONE AND
CC      IN HAIR FOLLICLES. STRONG EXPRESSION IN OSTEOGENIC TISSUES, SUCH
CC      AS NEONATAL CALVARIA, PAMS, TAIL AND SKIN.
CC      -I- SIMILARITY: BELONGS TO THE ITM2 FAMILY.
-----
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-----
DR      EMBL; L38971; AAC37700.1; -.
DR      EMBL; AF074020; AAC14549.1; -.
DR      MGD; MGI:107706; Itm2a.
KW      Pfam; PF04089; BRICHOS; 1.
KW      Transmembrane; Signal-anchor.
FT      TRANSMEM 54 74
FT      FT
SQ      CAROHND 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
          SEQUENCE 263 AA; 29705 MW; CF809834ABECD85A CXC64;

Query Match 45.1%; Score 46; DB 1; Length 263;
Best Local Similarity 43.8%; Pred. No. 4.1;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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AC P07327;
 DT 01-APR-1988 (Rel. 07, Last Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase alpha chain (BC 1.1.1.1).
 GN ADH1A OR ADH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=86243367; PubMed=3013304;
 RA von Bahr-Lindstrom H., Hoeoeg J.-O., Heden L.-O., Kaiser R.,
 Rietwood L., Larsson K., Lake M., Holmquist B., Holmgren A.,
 Hempel J., Vallee B.L., Joernvall H.;
 RT "CDNA and protein structure for the alpha subunit of human liver
 alcohol dehydrogenase.";
 RL Biochemistry 25:2465-2470(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89153548; PubMed=2920825;
 RA Matsuo Y., Yokoyama S.;
 RT "Molecular structure of the human alcohol dehydrogenase 1 gene.";
 RL FEBS Lett. 243:57-60(1989).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=90269803; PubMed=2347582;
 RA Ysuanumi M., Kikuchi I., Sarapata D., Yoshida A.;
 RT "The human class I alcohol dehydrogenase gene cluster: three genes
 are tandemly organized in an 80-kb-long segment of the genome.";
 RL Genomics 7:152-158(1990).
 CC -I- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -I- COFACTOR: Binds 2 zinc ions per subunit.
 CC -I- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC P1, ONE TO CLASS-III: CH1, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -I- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M12271; AAA68131.1; -;
 DR EMBL; M12963; AAA51590.1; -;
 DR EMBL; M37066; AAA51591.1; -;
 DR PIR; S02265; DEHUA.
 DR PDB; 1HSO; 27-APR-01.
 DR Genew; HGNC:249; ADH1A.
 DR GK; P07327; -;
 DR MIM; 103700; -;
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; NAS.
 DR GO; GO:0006066; P:alcohol metabolism; NAS.
 DR InterPro; IPR002328; ADH_zinc.

DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 FT Acetylation; 3D-structure.
 FT INIT MET 0
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 174 174 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 374 AA; 39727 MW; 5D2F5FE31C4962C CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 Oy 1 CYFS---SKDNVGYTGKTC 18
 Db 1740CGFTGYSANVAKVPGSTC 195
 RESULT 6
 ADHB_HUMAN STANDARD; PRT; 374 AA.
 AC P00325; Q13711; Q96KIT;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase beta chain (EC 1.1.1.1).
 GN ADH1B OR ADH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yokoyama S., Yokoyama R., Rotwein P.;
 RT "Molecular characterization of cDNA clones encoding the human alcohol
 RT dehydrogenase beta 1 and the evolutionary relationship to the other
 RT class I subunits alpha and gamma.";
 RL Jpn. J. Genet. 62:241-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=86082371; PubMed=3000832;
 RA Heden L.O., Hoeoeg J.-O., Larsson K., Lake M., Lagerholm B.,
 Rietwood L., Vallee B.L., Joernvall H., von Bahr-Lindstrom H.;
 RT "CDNA clones coding for the beta-subunit of human liver alcohol
 RT dehydrogenase have differently sized 3'-non-coding regions.";
 RL FEBS Lett. 194:327-332(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=86111889; PubMed=2935533;
 RA Diester G., Smith M., Blanchone V., Hatfield G.W.;
 RT "Molecular analysis of the human class I alcohol dehydrogenase gene
 RT family and nucleotide sequence of the gene encoding the beta
 RT subunit.";
 RL J. Biol. Chem. 261:2027-2033(1986).
 RN [5]
 RP SEQUENCE (BETA-1).
 RX MEDLINE=85076637; PubMed=6391920;
 RA Hempel J., Buhler R., Kaiser R., Holmquist B., de Zalsenski C.,
 von Wartburg J.-P., Vallee B.L., Joernvall H.;

RT "Human liver alcohol dehydrogenase. 1. The primary structure of the
 RT beta 1 beta 1 isoenzyme.";
 RL Eur. J. Biochem. 145:437-445(1984).
 RN [6]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=89338401; PubMed=2547609;
 RA Matsuo Y., Yokoyama R., Yokoyama S.;
 RT "The genes for human alcohol dehydrogenases beta 1 and beta 2 differ
 RT by only one nucleotide.";
 RL Eur. J. Biochem. 183:317-320(1989).
 RN [7]
 RP SEQUENCE FROM N.A. (BETA-3).
 RC TISSUE=Liver;
 RX MEDLINE=90024225; PubMed=2679216;
 RA Carr L.G., Xu Y., Ho W.H., Eidenberg H.J.;
 RT "Nucleotide sequence of the ADH2(3) gene encoding the human alcohol
 RT dehydrogenase beta 3 subunit.";
 RL Alcohol. Clin. Exp. Res. 13:594-596(1989).
 RN [8]
 RP SEQUENCE FROM N.A. (BETA-2).
 RC TISSUE=Liver;
 RA Polin L., Hey-Chi H.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88284699; PubMed=3397059;
 RA Xu Y.L., Carr L.G., Bosron W.F., Li T.K., Eidenberg H.J.;
 RT "Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci
 RT following DNA sequence amplification.";
 RL Genomics 2:209-214(1988).
 RN [10]
 RP SEQUENCE OF 40-85 FROM N.A.
 RA Oeier M., Speed W.C., Seaman M.T., Kidd K.K.;
 RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP VARIANT BETA-2.
 RX MEDLINE=84221897; PubMed=6374651;
 RA Joernvall H., Hempel J., Vallee B.L., Bosron W.F., Li T.-K.;
 RT "Human liver alcohol dehydrogenase: amino acid substitution in the
 RT beta 2 beta 2 Oriental isozyme explains functional properties,
 RT establishes an active site structure, and parallels mutational
 RT exchanges in the yeast enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3024-3028(1984).
 RN [12]
 RP VARIANT BETA-3.
 RX MEDLINE=87298549; PubMed=3619918;
 RA Burnell J.C., Carr L.G., Dwulet F.E., Eidenberg H.J., Li T.-K.,
 RT Bosron W.F.;
 RT "The human beta 3 alcohol dehydrogenase subunit differs from beta 1
 RT by a Cys for Arg-369 substitution which decreases NAD(H) binding.";
 RL Biochem. Biophys. Res. Commun. 146:1127-1133(1987).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=91376103; PubMed=1896463;
 RA Hurley T.D., Bosron W.F., Hamilton J.A., Amzel L.M.;
 RT "Structure of human beta 1 beta 1 alcohol dehydrogenase: catalytic
 RT effects of non-active-site substitutions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8149-8153(1991).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94260547; PubMed=8201622;
 RA Hurley T.D., Bosron W.F., Stone C.L., Amzel L.M.;
 RT "Structures of three human beta alcohol dehydrogenase variants.
 RT Correlations with their functional differences.";
 RL J. Mol. Biol. 239:415-429(1994).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=96291846; PubMed=8663387;
 RA Davis G.J., Bosron W.F., Stone C.L., Onusu-Dekyi K., Hurley T.D.;
 RT "X-ray structure of human betac2betac1 alcohol dehydrogenase. The
 RT contribution of ionic interactions to coenzyme binding.";
 RL J. Biol. Chem. 271:17057-17061(1996).
 CC -I- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +

CC NADH.
 CC -I- COPACITOR: Binds 2 zinc ions per subunit.
 CC -I- SUBUNIT: Dimer of identical or nonidentical chains of three types:
 CC alpha, beta and gamma.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
 CC MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
 CC ORIENTALS.
 CC -I- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMS IN HUMAN:
 CC PI, ONE TO CLASS-I: ALPHA, BETA, GAMMA, ONE TO CLASS-II:
 CC CLASS-V: ADH6.
 CC CLASS-IV: ADH7 AND ONE TO
 CC -I- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL; D00137; BAA00084.1; -;
 DR EMBL; X03350; CAA27056.1; -;
 DR EMBL; M24316; AAB59496.1; -;
 DR EMBL; M24308; AAB59496.1; JOINED.
 DR EMBL; M24309; AAB59496.1; JOINED.
 DR EMBL; M24310; AAB59496.1; JOINED.
 DR EMBL; M24311; AAB59496.1; JOINED.
 DR EMBL; M24312; AAB59496.1; JOINED.
 DR EMBL; M24313; AAB59496.1; JOINED.
 DR EMBL; M24314; AAB59496.1; JOINED.
 DR EMBL; M24317; AAB51884.1; -;
 DR EMBL; X15447; CAA33487.1; -;
 DR EMBL; X15448; CAA33487.1; JOINED.
 DR EMBL; X15449; CAA33487.1; JOINED.
 DR EMBL; X15450; CAA33487.1; JOINED.
 DR EMBL; X15451; CAA33487.1; JOINED.
 DR EMBL; X15452; CAA33487.1; JOINED.
 DR EMBL; X15453; CAA33487.1; JOINED.
 DR EMBL; X15454; CAA33487.1; JOINED.
 DR EMBL; X15455; CAA33487.1; JOINED.
 DR EMBL; X38290; AAB48003.1; -;
 DR EMBL; X38283; AAB48003.1; JOINED.
 DR EMBL; X38284; AAB48003.1; JOINED.
 DR EMBL; X38285; AAB48003.1; JOINED.
 DR EMBL; X38286; AAB48003.1; JOINED.
 DR EMBL; X38287; AAB48003.1; JOINED.
 DR EMBL; X38288; AAB48003.1; JOINED.
 DR EMBL; X38289; AAB48003.1; JOINED.
 DR EMBL; AF153821; AAD37446.1; -;
 DR EMBL; M21692; AAA51592.1; -;
 DR EMBL; AF040967; AAB96912.1; -;
 DR PIR; A23607; DEHUBA.
 DR PDB; 1HDY; 31-JAN-94.
 DR PDB; 1HDZ; 31-JAN-94.
 DR PDB; 3HUD; 31-JAN-94.
 DR PDB; 1DEH; 08-MAR-96.
 DR PDB; 1HTB; 07-DEC-95.
 DR PDB; 1HSZ; 27-APR-01.
 DR Genew; HGNC:250; ADH1B.
 DR GK; P00325; -;
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; TAS.
 DR GO; GO:0004889; F:electron transporter activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR GO; GO:0006059; P:ethanol oxidation; TAS.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; Adh_zinc_N; 1.
 DR PROSITE; PS00059; Adh_zinc; 1.

KM	Oxidoreductase; zinc; Metal-binding; NAD; Multigene family;
KW	Acetylation; Polymorphism; 3D-structure.
FT	INIT MET 0
FT	MOD RES 1 1 ACETYLATION.
FT	METAL 46 46 ZINC 1 (CATALYTIC).
FT	METAL 67 67 ZINC 1 (CATALYTIC).
FT	METAL 97 97 ZINC 2.
FT	METAL 100 100 ZINC 2.
Query Match:	45.1%; Score 46; DB 1; Length 374;
Best Local Similarity	54.5%; Pred. No. 5.8;
Matches	12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
OY	1 CYFS---SKDNVKGVTGKTC 18
DB	174 CGFSTGYGSAAVNAKVTGPGSTC 195
RESULT 7	
TRYA_RAT	STANDARD; PRT; 246 AA.
ID	TRYA_RAT
AC	P32821;
DT	01-OCT-1993 (Rel. 27, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Trypsin V-A precursor (BC 3.4.21.4).
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxId=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Pancreas;
RX	MEDLINE=92165057; PubMed=1537555;
RA	Kang J, Wiesand U, Mueller-Hill B;
RT	"Identification of cDNAs encoding two novel rat pancreatic serine
RT	proteases.";
RL	Gene 110:181-187(1992).
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Xaa, Lys- -Xaa.
CC	-1- SUBCELLULAR LOCATION: Extracellular.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC	-----
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CC	or send an email to license@isb-sdb.ch).
CC	-----
DR	EMBL; X59012; CAA41751.1; -.
DR	PIR; J01471; J01471.
DR	HSSP; P00763; IDPO.
DR	MEROPS; S01.092; -.
DR	InterPro; IPR001314; Chymotrypsin.
DR	InterPro; IPR001254; Ser.protease_Try.
DR	Pfam; PF00089; trypsin_1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	SMART; SM00020; Tryp_Spc; 1.
DR	PROSITE; PSS0240; TRYPsin_DOM; 1.
DR	PROSITE; PS00134; TRYPsin_HIS; 1.
DR	PROSITE; PS00135; TRYPsin_SER; FALSE NEG.
KW	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW	Multigene family.
FT	SIGNAL 1 15
FT	PROPEP 16 24
FT	CHAIN 25 246
FT	ACT SITE 64 64 TRYPSIN V-A.
FT	ACT SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID 31 160
FT	DISULFID 49 65
FT	DISULFID 133 233
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.

FT	DISULFID	140	206	BY SIMILARITY.
FT	DISULFID	171	185	BY SIMILARITY.
FT	DISULFID	196	220	BY SIMILARITY.
FT	SITE	194	194	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SO	SEQUENCE	246 AA;	26900 MM;	1EB59D8BBA1715 CRC64;
Query Match				
Best Local Similarity	43.1%;	Score 44;	DB 1;	Length 246;
Matches	7;	Conservative	4;	Mismatches
Oy	3	FSKDNVGVKVTGKTC	18	
Db	16	PFEDNDRIVGYYTC	31	
RESULT 8				
TRYB RAT				
ID_TRYB RAT	STANDARD;	PRT;	246 AA.	
AC	P32822;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Trypsin V-B precursor (EC 3.4.21.4).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Pancreas;			
RA	MEDLINE=92165057; PubMed=1537555;			
RA	Kang Y, Wiegand U, Mueller-Hill B;			
RT	"Identification of cDNAs encoding two novel rat pancreatic serine			
RT	proteases.";			
RL	Gene 110.181-187(1992).			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Xaa, Lys- -Xaa.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-----			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib.ch).			
CC	-----			
DR	EMBL; X59013; CA441752.1; -.			
DR	PIR; JQ1472; JQ1472.			
DR	HSSP; P00763; IDPO.			
DR	MEROPS; S01.093; -.			
DR	InterPro; IPR001254; Ser_protease_Try.			
DR	Pfam; PF00089; trypsin_1.			
DR	SMART; SM00020; Tryp_Spc; 1.			
DR	PROSITE; PS50240; TRYPsin DOM; 1.			
DR	PROSITE; PS00134; TRYPsin HIS; 1.			
DR	PROSITE; PS00135; TRYPsin SER; FALSE NEG.			
KM	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;			
KM	Multigene family.			
FT	SIGNAL	1	15	
FT	PROPEP	16	24	ACTIVATION PEPTIDE.
FT	CHAIN	25	246	TRYPSIN V-B.
FT	ACT_SITE	64	64	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	108	108	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	200	200	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	31	160	BY SIMILARITY.
FT	DISULFID	49	65	BY SIMILARITY.
FT	DISULFID	133	233	BY SIMILARITY.
FT	DISULFID	140	206	BY SIMILARITY.
FT	DISULFID	171	185	BY SIMILARITY.
FT	DISULFID	196	220	BY SIMILARITY.
FT	SITE	194	194	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SO	SEQUENCE	246 AA;	26819 MM;	1EB899CA1BA0025 CRC64;

Query Match 43.1%; Score 44; DB 1; Length 246;
 Best Local Similarity 43.8%; Pred. No. 8.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSKSDNVGKVTGKTC 18
 Db 16 PFTEDNDRIVGGYTC 31

RESULT 9

ID NCR MOUSE

ID NCR MOUSE STANDARD; PRT; 1453 AA.

AC P30415;

DT 01-APR-1993 (Rel. 25, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NK-tumor recognition protein (Natural-Killer cells cyclophilin-

related protein) (NK-TR protein).

GN NKTR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93133824; PubMed=8421688;

RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,

RT "A cyclophilin-related protein involved in the function of natural

killer cells."

RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).

RN [2]

RP REVISIONS TO C-TERMINUS.

RC STRAIN=BALB/c; TISSUE=Blood;

RA Anderson S.K.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.

CC INVOLVED IN THE FUNCTION OF NK CELLS.

CC -1- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.

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 CC -----

DR EMBL; L04289; AAA37500.2; ALT_INIT.

DR HSSP; Q27450; 1A33.

DR MGD; MGI:97346; NKTR.

DR InterPro; IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PROSITE; PS00170; CSA_PPIASE_1; 1.

DR PROSITE; PS50072; CSA_PPIASE_2; 1.

KW Cyclosporin; Isomerase; Rotamase; Repeat; Transmembrane.

FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.

FT DOMAIN 222 241 ARG/LYS-RICH (BASIC).

FT DOMAIN 422 459 ARG/LYS-RICH (BASIC).

FT DOMAIN 964 1003 ARG/LYS-RICH (BASIC).

FT DOMAIN 198 273 ARG/SER-RICH.

FT DOMAIN 468 565 ARG/SER-RICH.

FT DOMAIN 658 812 ARG/SER-RICH.

FT DOMAIN 1303 1453 ARG-SER TANDEM REPEAT-RICH.

SQ SEQUENCE 1453 AA; 163439 MW; DFL173FFB14B283B CRC64;

Query Match 43.1%; Score 44; DB 1; Length 1453;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
 Db 1 CYFSSKDNVKGKVTGKTC 18

Db 41 CLCSEKGLGKTTGKLC 58

RESULT 10

ID NCR HUMAN STANDARD; PRT; 1462 AA.

AC P30414;

DT 01-APR-1993 (Rel. 25, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NK-tumor recognition protein (Natural-Killer cells cyclophilin-

related protein) (NK-TR protein).

GN NKTR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=93133824; PubMed=8421688;

RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,

RT "A cyclophilin-related protein involved in the function of natural

killer cells."

RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).

RN [2]

RP REVISIONS.

RA Anderson S.K.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.

CC INVOLVED IN THE FUNCTION OF NK CELLS.

CC -1- SUBCELLULAR LOCATION: Membrane-anchored. Attached to the membrane

via its N-terminus.

CC -1- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.

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 CC -----

DR EMBL; L04288; AAA35734.2; -.

DR EMBL; AF184110; AAD56402.1; -.

DR HSSP; Q27450; 1A33.

DR Genew; HGNC:7833; NKTR.

DR GO; GO:0004600; F:cyclophilin; TAS.

DR InterPro; IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIASE_1; 1.

DR PROSITE; PS50072; CSA_PPIASE_2; 1.

KW Cyclosporin; Isomerase; Rotamase; Repeat; Membrane.

FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.

FT DOMAIN 219 240 ARG/LYS-RICH (BASIC).

FT DOMAIN 421 457 ARG/LYS-RICH (BASIC).

FT DOMAIN 970 1010 ARG/LYS-RICH (BASIC).

FT DOMAIN 194 244 ARG/SER-RICH.

FT DOMAIN 466 574 ARG/SER-RICH.

FT DOMAIN 664 814 ARG/SER-RICH.

FT DOMAIN 1311 1348 ARG-SER TANDEM REPEAT-RICH.

SQ SEQUENCE 1462 AA; 165676 MW; D98A1147763EF527 CRC64;

Query Match 43.1%; Score 44; DB 1; Length 1462;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKVTGKTC 18
 Db 41 CLCSEKGLGKTTGKLC 58

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RESULT 11
ISPH_BRUME STANDARD; PRT; 346 AA.
AC Q8YFRL;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ISPH protein.
GN ISPH OR LYTB OR BME11459.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MDLLINE=20020109; PubMed=11756689;
RA Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykdis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Coleman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Lelesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AE009582; AAL52640.1; -.
CC DR PIR; AE3434; AE3434.
CC DR HAMAP; MF 00191; -. 1.
CC DR InterPro; IPR003451; LytB.
CC DR Pfam; PF02401; LytB; 1.
CC DR TIGRFAMs; TIGR00216; isph_lytB; 1.
CC KW Isoprene biosynthesis; Complete proteome.
CC SQ SEQUENCE 346 AA; 37747 MW; EB9CID60EF73421B CRC64;
Query Match 42.2%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CYFSKDNVGVKT 13
Db 161 CHFDDEDNLGFT 173
RESULT 12
AGI_HORVU STANDARD; PRT; 212 AA.
AC P15312;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Root-specific lectin precursor.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;

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RN
RP SEQUENCE FROM N.A.
RA Lerner D.R., Raikhel N.V.;
RT Cloning and characterization of root-specific barley lectin."
RL Plant Physiol. 91:124-129(1989).
CC -1- FUNCTION: CARBOHYDRATE BINDING.
CC -1- SIMILARITY: Contains 4 chitin-binding domains.
CC
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CC -----
CC DR EMBL; M29280; AAA32969.1; -.
CC DR PIR; T05936; T05936.
CC DR HSP; P10969; 1WGT.
CC DR InterPro; IPR001002; Chitin binding_1.
CC DR Pfam; PF00187; Chitin bind_1; 4.
CC DR PRINTS; PR00451; CHITNBINDG.
CC DR SMART; SM00270; ChitBD1; 4.
CC DR PROSITE; PS00026; CHITIN BINDING; 4.
CC KW Lectin; Repeat; Chitin-binding; Glycoprotein; Signal;
CC Pyrolidone carboxylic acid.
CC SIGNL 1 26
CC FT CHAIN 27 212
CC FT DOMAIN 27 69
CC FT DOMAIN 70 112
CC FT DOMAIN 113 155
CC FT DOMAIN 156* 197
CC FT MOD RES 27 27
CC FT DISULFID 29 44
CC FT DISULFID 38 50
CC FT DISULFID 43 57
CC FT DISULFID 61 66
CC FT DISULFID 72 87
CC FT DISULFID 81 93
CC FT DISULFID 86 100
CC FT DISULFID 104 109
CC FT DISULFID 115 130
CC FT DISULFID 124 136
CC FT DISULFID 129 143
CC FT DISULFID 147 152
CC FT DISULFID 158 173
CC FT DISULFID 167 179
CC FT DISULFID 172 186
CC FT DISULFID 190 195
CC FT CARBOHYD 206
CC SQ SEQUENCE 212 AA; 21209 MW; 8D948245DB6825A5 CRC64;
Query Match 41.2%; Score 42; DB 1; Length 212;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;
QY 1 CYFSKDNVGVTKTC 18
Db 66 CYTSKR--CGTQAGKTC 81
RESULT 13
INCL_ECOLI STANDARD; PRT; 358 AA.
AC O52312; P71175; O52283;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein dncC.
GN INCC.
OS Escherichia coli.
OX Plasmid Incp-Beta R751.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Macartney D.P., Williams D.R., Stafford T., Foster A., Thomas C.M.;
RT "Evolution of the partitioning and global regulation functions of
the incp central control region."
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-109 FROM N.A.
RC STRAIN=K12 / C600;
RX MEDLINE=95291464; PubMed=7773415;
RA Thomas C.M., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;
RT "Evolution of the korA-oriV segment of promiscuous incp plasmids.";
RL Microbiology 141:1201-1210(1995).
CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS ENCODED BY THE TRF8 OPERON;
IT IS INVOLVED IN PLASMID MAINTENANCE AND REPLICATION (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY.
CC -----
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CC -----
CC
CC EMBL; U67194; AAC64421.1; -.
DR InterPro; IPR00707; ATPase_Para.
DR Pfam; PF00991; Para; 1.
KW plasmid; DNA replication.
SQ SEQUENCE 358 AA; 38246 MW; 44859F07844167BE CRC64;

Query Match 41.2%; Score 42; DB 1; Length 358;
Best Local Similarity 41.2%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CYFSKDNVGVGKGT 17
Db 45 CHFAGADGGGAGGCGS 61

RESULT 14
ADHI_RANGE STANDARD; PRT; 375 AA.
ID ADHI_RANGE
AC P22797;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alcohol dehydrogenase, major (EC 1.1.1.1).
OS Rana perezi (Perez's frog) (Western Mediterranean green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8403;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91175722; PubMed=2007119;
RA Cederslund E., Peralba J.M., Pares X., Joernvall H.;
RT "Amphibian alcohol dehydrogenase, the major frog liver enzyme.
Relationships to other forms and assessment of an early gene
duplication separating vertebrate class I and class III alcohol
dehydrogenases."
RL Biochemistry 30:2811-2816(1991).
RN [2]
RP SEQUENCE OF 1-5.
RX MEDLINE=90353571; PubMed=2387402;
RA Egeblad B., Betonius M., Danielsson O., Persson B., Cederslund E.,
RA Kaiser R., Holmquist B., Vallee B., Pares X., Jeffery J.,
RA Joernvall H.;
RT "Fast atom bombardment mass spectrometry and chemical analysis in

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RT determinations of acyl-blocked protein structures.";
RL FEBS Lett. 269:194-196(1990).
CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
NADH.
CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY. MORE CLOSELY RELATED TO CLASS I MAMMALIAN ENZYMES.
DR PIR; A38405; A38405.
DR HSSP; P00325; 1DEH.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR02085; Adh_zn_family.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PROSITE; PS00059; Adh_ZINC; 1.
KW Oxidoreductase; Zinc; Metal-binding; NAD; Acetylation.
FT MOD_RES 1
FT METAL 46 1 ACETYLATION (BY SIMILARITY).
FT METAL 46 46 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 68 68 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 98 98 ZINC 2 (BY SIMILARITY).
FT METAL 101 101 ZINC 2 (BY SIMILARITY).
FT METAL 104 104 ZINC 2 (BY SIMILARITY).
FT METAL 112 112 ZINC 2 (BY SIMILARITY).
FT METAL 175 175 ZINC 1 (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 375 AA; 40184 MW; 283E0A60E339195 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 375;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVGKGTGTC 18
Db 175 CGFSTGYGSAVNTGKVKPGSTC 196

RESULT 15
GUXC_FUSOX STANDARD; PRT; 514 AA.
ID GUXC_FUSOX
AC P46238;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative exoglucanase type C precursor (EC 3.2.1.91)
DE (Exocellobiohydrolase I) (1,4-beta-cellulohydrolase)
DE (Beta-glucanocellobiohydrolase).
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
NCBI_TaxID=5507;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047531; PubMed=7959045;
RA Shepard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
RA Hagen F.S., Upshall A., McKnight G.L., O'Hara P.J.;
RT "The use of conserved cellulase family-specific sequences to clone
RT cellulase homologue cDNAs from Fusarium oxysporum."
RL Gene 150:163-167(1994).
RN [2]
RP CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
in cellulose and cellobiose, releasing cellobiose from the non-
reducing ends of the chains.
CC -1- SIMILARITY: Contains 1 fungal-type cellulase-binding (CBD) domain.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
HYDROLASES).
CC -----
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CC -----
CC
CC EMBL; L29379; AAA65587.1; -.
DR HSSP; P00725; RCEL.

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DR InterPro: IPR000254; CBD_fungal.
 DR InterPro: IPR001722; Glyco_hydro_7.
 DR Pfam: PF00734; CBM_1; 1.
 DR Pfam: PF00840; Glyco_hydro_7; 1.
 DR ProDom: PD001821; CBD_fungal; 1.
 DR ProDom: PD16135; Glyco_hydro_7; 1.
 DR SMART: SM00236; fCBD; 1.
 DR PROSITE: PS00562; CBD_FUNGAL; 1.
 KM Cellulose degradation; Hydrolyase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 514 PUTATIVE EXOGLUCANASE TYPE C.
 FT DOMAIN 18 439 CATALYTIC.
 FT DOMAIN 440 482 LINKER.
 FT DOMAIN 483 514 CELLULOSE-BINDING (BY SIMILARITY).
 FT ACT_SITE 229 229 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 234 234 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 486 503 BY SIMILARITY.
 FT DISULFID 497 513 BY SIMILARITY.
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 514 AA; 54704 MM; 6A4617323A46E062 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 514;
 Best local Similarity 44.4%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKGKTC 18
 DB 66 CYTGKRWDTSTCTDGKTC 83

Search completed: October 15, 2003, 16:58:16
 Job time : 7.42934 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 : Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-13

Perfect score: 102
Sequence: 1 CYPSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	234	2	Q9R5X4
2	102	100.0	239	2	Q9R5X4
3	102	100.0	239	2	Q5157
4	102	100.0	239	2	Q51678
5	102	100.0	239	2	Q06532
6	102	100.0	239	2	Q06531
7	102	100.0	239	2	Q06533
8	102	100.0	266	16	Q8NXX6
9	96	94.1	239	2	Q9F0L6
10	93	91.2	239	2	Q06535
11	55	53.9	511	16	Q8R166
12	47	46.1	2108	5	Q815C7
13	46.5	45.6	505	2	Q50203
14	46	45.1	199	16	Q92CG4
15	46	45.1	233	11	Q9CRW4
16	46	45.1	263	11	Q8KH04

17	46	45.1	269	6	Q8MNN3	Q8MNN3 gorilla gor
18	45	44.1	276	4	Q9NBP0	Q9NBP0 homo sapien
19	44.5	43.6	107	4	Q9UL82	Q9UL82 homo sapien
20	44.5	43.6	457	12	Q9YQZ1	Q9YQZ1 randid herpe
21	44	43.1	275	5	Q16622	Q16622 caenorhabdi
22	44	43.1	299	10	Q8LAK6	Q8LAK6 arabidopsis
23	44	43.1	966	11	Q8CBP6	Q8CBP6 mus musculu
24	44	43.1	2301	5	Q95Z81	Q95Z81 oikopleura
25	43	42.2	126	5	Q95UQ5	Q95UQ5 branchiost
26	43	42.2	159	5	Q81XX7	Q81XX7 branchiost
27	43	42.2	274	10	Q9STR7	Q9STR7 arabidopsis
28	43	42.2	315	10	Q93VK9	Q93VK9 arabidopsis
29	43	42.2	368	5	Q9XXJ6	Q9XXJ6 caenorhabdi
30	43	42.2	372	16	Q8G257	Q8G257 bruceella su
31	43	42.2	765	5	Q26018	Q26018 plasmodium
32	43	42.2	765	5	Q8IKT6	Q8IKT6 plasmodium
33	43	42.2	1022	5	Q9W3E1	Q9W3E1 drosophila
34	42	41.2	148	16	Q8DRLX	Q8DRLX streptococ
35	42	41.2	161	17	Q8TLN3	Q8TLN3 methanosarc
36	42	41.2	224	8	Q9Z2S7	Q9Z2S7 ceratololen
37	42	41.2	235	16	Q8XET9	Q8XET9 escherichia
38	42	41.2	260	16	Q97M39	Q97M39 clostridium
39	42	41.2	278	2	Q51311	Q51311 nostoc punc
40	42	41.2	377	11	Q9QYV9	Q9QYV9 mus musculu
41	42	41.2	378	16	Q92FD6	Q92FD6 listeria in
42	42	41.2	378	16	Q8YAK1	Q8YAK1 listeria mo
43	42	41.2	430	16	Q9A3U5	Q9A3U5 caulobacter
44	42	41.2	1064	16	Q8KKI6	Q8KKI6 clostridium
45	41.5	40.7	731	16	Q8RG00	Q8RG00 fusobacteri

ALIGNMENTS

RESULT 1

ID	Q9R5X4	PRELIMINARY;	PRT;	234 AA.
AC	Q9R5X4;			
DT	01-MAY-2000 (T-REMBLrel. 13, Created)			
DT	01-MAY-2000 (T-REMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (T-REMBLrel. 23, Last annotation update)			
DE	ENTEROTOXIN=PYROGENIC toxin (Fragment).			
OS	Staphylococcus.			
OC	Bacteria; Firmicutes; Bacillales.			
OX	NCBI_TaxID=1279;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94325995; PubMed=8049778;			
RA	Van den Bussche R.A., Lyon J.D., Bohach G.A.;			
RL	Mol. Phylogenet. Evol. 2:281-292(1993).			
DR	HSPF, P34071; 1SE2.			
DR	InterPro: IPR006177; Bctr1 tox.			
DR	InterPro: IPR006123; Staph/Strep. toxin.			
DR	InterPro: IPR006126; Staph/Strep. tox.			
DR	InterPro: IPR006173; Staph tox OB.			
DR	Pfam: PF01123; Staph. Strep. toxin; 1.			
DR	Pfam: PF02876; Staph. Strep. tox_C; 1.			
DR	PRINTS; PR00279; BACTRIOTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
FT	NON_TER	1		
FT	NON_TER	234		
SO	SEQUENCE	234 AA;	234	
		MM;	D6A7B45FB9810052	CRC64;
Query Match		100.0%;	Score 102;	DB 2;
Best Local Similarity		100.0%;	Pred. No. 8.1e-09;	Length 234;
Matches	18;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 CYPSSKDNVKGVTGKTC 18
Db 88 CYPSSKDNVKGVTGKTC 105

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RESULT 2
005157 ID 005157 PRELIMINARY; PRT; 239 AA.
AC 005157;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
  Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
  Staphylococcus intermedius pyoderma isolates.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27536 MW; D660644660DB4191 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 93 CYFSSKDNVKGKVTGKTC 110

RESULT 3
053678 ID 053678 PRELIMINARY; PRT; 239 AA.
AC 053678;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13ETEB25C6989C2 CRC64;
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Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 93 CYFSSKDNVKGKVTGKTC 110

RESULT 4
006532 ID 006532 PRELIMINARY; PRT; 239 AA.
AC 006532;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18
Db 93 CYFSSKDNVKGKVTGKTC 110

RESULT 5
006531 ID 006531 PRELIMINARY; PRT; 239 AA.
AC 006531;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; 1SE2.
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DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 6
Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCoPeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR HMBL; L13378; AAA26622.1; -.
DR HSSP; P34071; 1STE.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 7
Q08XJ6 PRELIMINARY; PRT; 266 AA.
AC Q08XJ6;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).

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OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsuki K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KV Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 100.0%; Score 102; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 120 CYFSSKDNVGVKVTGKTC 137

RESULT 8
Q09F0L6 PRELIMINARY; PRT; 271 AA.
AC Q09F0L6;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70(2001).
DR EMBL; AF217235; AAG29599.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 9.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 125 CYFSSKDNVGVKVTGKTC 142

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RESULT 9
ID Q06535 PRELIMINARY; PRT; 239 AA.
AC Q06535;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR1 909;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13377; AAA26621.1; -.
DR HSP; P23113; IUCK.
DR InterPro; IPR061177; Bctr1_tox.
DR InterPro; IPR06123; Staph/Strep_toxin.
DR InterPro; IPR06126; Staph/Strep_tox.
DR InterPro; IPR06173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

Query Match 94.1%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 10
ID Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13379; AAA26623.1; -.
DR HSP; P34071; ISE2.
DR InterPro; IPR061177; Bctr1_tox.
DR InterPro; IPR06123; Staph/Strep_toxin.
DR InterPro; IPR06126; Staph/Strep_tox.
DR InterPro; IPR06173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

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FT NON TER 1 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 91.2%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 18
Db 93 CYFSSKDNVGVKVGKTC 110

RESULT 11
ID Q8R166 PRELIMINARY; PRT; 511 AA.
AC Q8R166;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cysteine permease.
GN FN1747.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
OX Fusobacterium.
OX NCBI_TaxId=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Malinas T., Pusch G., Haeflorn R.,
RA Fomseine M., Kyrides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018 (2002).
DR EMBL; AE010479; AAL93862.1; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR001463; Na/Ala_sympor1.
DR Pfam; PF01235; Na_Ala_symp; 1.
DR TIGRFAMs; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.
SQ SEQUENCE 511 AA; 56196 MW; 03D8A2859135EF3D CRC64;

Query Match 53.9%; Score 55; DB 16; Length 511;
Best Local Similarity 52.9%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVGKTC 17
Db 128 CYRSDKDTGRYFGGST 144

RESULT 12
ID Q8I5C7 PRELIMINARY; PRT; 2108 AA.
AC Q8I5C7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF1410C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=6329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berrian M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

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RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
 RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Selengue J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Piatibadi A.H., Fraumoltz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings I.M., Fraumoltz M.J., Roos D.S., Ralph S.A.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrett B.,
 RT "Genome sequence of the human malaria parasite *Plasmodium*
 RT *falciparum*.";
 RL Nature 419:98-511(2002).
 DR EMBL; AF014848; AAN36368.1; -;
 KW Hypochemical protein.
 SQ SEQUENCE 2108 AA; 248300 MW; 280464D22291B2D9 CRC64;
 QY Query Match 46.1%; Score 47; DB 5; Length 2108;
 Best Local Similarity 32.4%; Pred. No. 1.3e+02;
 Matches 12; Conservative 2; Mismatches 3; Indels 20; Gaps 1;
 Db 1 CYFSKDN-----VGKVTGKKT 17
 763 CYFSKKNDDYILKNINLTAKNSVVIILGNVSGKT 799
 RESULT 13
 ID 050203 PRELIMINARY; PRT; 505 AA.
 AC 050203;
 DT 01-JUN-1998 (T-EMBLrel. 06, Created)
 DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Chloroacetaldehyde dehydrogenase.
 GN ALDA.
 OS Xanthobacter autotrophicus.
 OG Plasmid linear plasmid pX401.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Xanthobacter.
 NC NCBI_TaxID=280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GU10;
 RX MEDLINE=98172729; PubMed=9511738;
 RA Bergeron H., Labbe D., Turmel C., Lau P.C.,
 RT "Cloning, sequence and expression of a linear plasmid-based and a
 RT chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
 RT in Xanthobacter autotrophicus G410.";
 RL Gene 207:9-18(1998).
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
 DR EMBL; AF029733; AAC13641.1; -;
 DR HSSP; P05091; ICM3.
 DR InterPro: IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldehyd.1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Oxidoreductase; Plasmid.
 SQ SEQUENCE 505 AA; 54945 MW; AD6A9EDB0297B804 CRC64;
 QY Query Match 45.6%; Score 46.5; DB 2; Length 505;
 Best Local Similarity 58.8%; Pred. No. 33;
 Matches 10; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
 Db 2 YFSKDNVGVGKVTGKTC 18
 34 YF---DNTSPVTGKTC 47
 RESULT 14
 ID 092CG4 PRELIMINARY; PRT; 199 AA.
 AC 092CG4;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Hypochemical protein lin1208.

GN LIN1208.
 OS *Listeria innocua*.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 NC NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX PubMed=11679669;
 RA Glaser P., Franke L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brant P., Chakraborty T.,
 RA Charbit A., Chatouan F., Couve E., de Darvar A., Denoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
 RA Entlin K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunz F., Kurapkac G.,
 RA Maduno E., Maitournon A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schueller T., Simoes N., Tietz A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.,
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:848-852(2001).
 DR EMBL; AL596168; CAC96439.1; -;
 DR ListerList; LIN01208;
 DR InterPro: IPR01345; PG/BPGM_mutase.
 DR Pfam; PF03000; PGAM; 1.
 DR PROSITE; PS00175; PG_MUTASE; 1.
 KW Hypochemical protein; Complete proteome.
 SQ SEQUENCE 199 AA; 22902 MW; E14DD962F4C6B85 CRC64;
 QY Query Match 45.1%; Score 46; DB 16; Length 199;
 Best Local Similarity 47.1%; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 Db 2 YFSKDNVGVGKVTGKTC 18
 151 YWEKTSKIGKVTGLKNC 167
 RESULT 15
 ID 09CRM4 PRELIMINARY; PRT; 233 AA.
 AC 09CRM4;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Integral membrane protein 2 (Fragment).
 GN ITM2A OR ITM2.
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Niimi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection.";
PI Nature 408:695-700(2001)

RL Nature 409:685-690 (2001).
DB EMBL: AY014024. PubMed 119

DR EMBL; AK014024; BAB29119.1; -..
DR MGD: MGI:107706. Ttm3a

DR	MGD; MGI:107706; Itcm2a.
ET	NON TER 1 1

FT	NON TER	1	1
SO	SEQUENCE	233	AA: 263

SEQUENCE	233 AA; 26321 MW; B073D1FD94DEF2E9 CRC64;
SD	

Query Match	Score	DB	Length
45.1%	46	11	233

Best Local Similarity 43.8%; Pred. No. 17;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKTGGK 16

Db 60 CFFDSEDPVNSIPGGE 75

Search completed: October 15, 2003, 17:04:12
Job time : 36.8623 secs

Job time : 36.8623 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-14
Perfect score: 100
Sequence: 1 CYFSSKDNVGVKTSKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	18	20	AAV06250
2	100	100.0	18	24	ABG71378
3	100	100.0	239	20	AAV06254
4	100	100.0	240	24	ABG71370
5	96	96.0	18	20	AAV06249
6	96	96.0	18	24	ABG71377
7	96	96.0	18	24	ABG71380
8	96	96.0	238	12	AA13208
9	96	96.0	238	14	AA145016

10	96	96.0	238	22	AA167343	Staphylococcus aur
11	96	96.0	238	12	AB176239	Staphylococcus aur
12	96	96.0	239	23	AA13207	Staphylococcus ent
13	96	96.0	239	14	AA145015	Staphylococcus ent
14	96	96.0	239	20	AAV06255	Staphylococcus gro
15	96	96.0	239	20	AAV06256	Staphylococcus gro
16	96	96.0	239	20	AAV06251	Staphylococcus gro
17	96	96.0	239	20	AAV06252	Staphylococcus gro
18	96	96.0	239	22	AAV06253	Staphylococcus gro
19	96	96.0	239	22	AAV06254	Staphylococcus aur
20	96	96.0	239	23	AAV06258	Staphylococcus aur
21	96	96.0	240	24	ABG71367	Staphylococcus ent
22	96	96.0	240	24	ABG71368	Staphylococcus ent
23	96	96.0	240	24	ABG71369	Staphylococcus ent
24	96	96.0	240	24	ABG71371	Staphylococcus ent
25	96	96.0	240	24	ABG71372	Staphylococcus ent
26	96	96.0	266	21	AAV70108	Staphylococcus ent
27	96	96.0	266	23	AAV79507	Staphylococcus SEC
28	90	90.0	239	20	AAV06257	Staphylococcus gro
29	90	90.0	240	24	ABG71373	Staphylococcus ent
30	87	87.0	18	24	ABG71379	Staphylococcus ent
31	81	81.0	239	20	AAV06258	Staphylococcus gro
32	81	81.0	240	24	ABG71374	Staphylococcus ent
33	66	66.0	14	20	AAV06259	Staphylococcus ent
34	66	66.0	14	24	ABG71381	Staphylococcus ent
35	47	47.0	374	20	AAV43983	Human alcohol dehy
36	47	47.0	374	20	AAV43984	Human alcohol dehy
37	47	47.0	375	23	ABG79657	Invertebrate forag
38	47	47.0	395	21	AAV58159	Lung cancer associ
39	46	46.0	299	21	AAV06436	Arabidopsis thalia
40	46	46.0	315	21	AAV06435	Arabidopsis thalia
41	46	46.0	340	21	AAV06434	Arabidopsis thalia
42	45	45.0	312	21	AAV52524	Arabidopsis thalia
43	45	45.0	319	21	AAV52530	Arabidopsis thalia
44	45	45.0	335	21	AAV52529	Arabidopsis thalia
45	45	45.0	342	21	AAV52523	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAV06250 standard; Peptide: 18 AA.
ID AAV06250;
XX
AC AAV06250;
XX
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group C enterotoxin disulfide loop.
XX
XX Enterotoxin; SEC3 FRI 909; toxin; disulfide loop;
KW protein engineering.
XX
XX Staphylococcus aureus.
OS
XX
XX WO9927889-A2.
XX
XX 10-JUN-1999.
XX
XX
PF 01-DEC-1998; 98WO-US25107.
XX
XX 02-DEC-1997; 97US-0067357.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Bohach GI;
XX
XX WPI, 1999-358008/30.
XX
XX Non-toxic modified staphylococcal enterotoxins
XX
XX
XX Disclosure; Page 3; 25pp; English.
PS

XX This peptide corresponds to the disulfide loop, i.e. amino acids
CC 96-106, of Staphylococcus aureus group C enterotoxin SEC FRI 909.
CC The invention relates to pyrogenic toxins, such as staphylococcal
CC enterotoxins, modified in the disulfide loop region. Typically,
CC the modification involves deletions within the disulfide loop
CC region (see AAY06261). The modified toxin retain useful biological
CC properties, such as the ability to induce cytokine production, but
CC have substantially reduced toxicity compared to the corresponding
CC unmodified native toxin. Emetic response inducing activity and
CC fever inducing activity are typically decreased by at least about
CC 100-fold, while LD50 (in Dutch Belted rabbits) is at least
CC 100-fold higher than the native toxin.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 100; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTSGKTC 18
DB 1 CYFSSKDNVGVKVTSGKTC 18
RESULT 2
ABG71378
ID ABG71378 standard; Peptide: 18 AA.
XX
AC ABG71378;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin SEC3-FRI909 disulfide loop region.
XX
XX Modified pyrogenic toxin; disulfide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin;
KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
XX SEC3-FRI909.
XX
OS Staphylococcus aureus.
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11619.
XX
PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX WPI; 2003-058608/05.
XX
DR WPI; 2003-058608/05.
XX
PT New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning -
XX
PS Disclosure; Fig 15; 67pp; English.
XX
XX The invention relates to a modified pyrogenic toxin derived from a native
CC disulfide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulfide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC disulfide loop region.

XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 100; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTSGKTC 18
DB 1 CYFSSKDNVGVKVTSGKTC 18
RESULT 3
AAY06254
ID AAY06254 standard; Protein: 239 AA.
XX
AC AAY06254;
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group C enterotoxin SEC3-FRI909.
XX
XX Enterotoxin; SEC3-FRI909; toxin; disulfide loop;
KW protein engineering.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 93..110
XX
XX WO927889-A2.
XX
PN WO927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25107.
XX
PR 02-DEC-1997; 97US-0067357.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Bohach GT;
XX
XX WPI; 1999-358008/30.
XX
DR WPI; 1999-358008/30.
XX
PT Non-toxic modified staphylococcal enterotoxins
XX
PS Disclosure; Page 17; 25pp; English.
XX
XX This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC3-FRI909. The invention relates to pyrogenic toxins,
CC such as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxin
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.
XX
SQ Sequence 239 AA;
Query Match 100.0%; Score 100; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTSGKTC 18
DB 93°CYFSSKDNVGVKVTSGKTC 110
RESULT 4
ABG71370

ID ABG71370 standard; Protein; 240 AA.
 XX
 AC ABG71370;
 XX
 XX 29-JAN-2003 (first entry)
 DT
 XX Staphylococcal enterotoxin SEC3-FRI909.
 DE
 XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KM emetic response-inducing activity; staphylococcal enterotoxin;
 KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KM SEC3-FRI909.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 FT /label= unknown
 PN
 XX WO200283169-A1.
 PD 24-OCT-2002.
 XX
 XX 11-APR-2002; 2002WO-US11619.
 PF
 XX 13-APR-2001; 2001US-283720P.
 PR
 XX (IDAH-) IDAHO RES FOUND INC.
 PA
 XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 PI
 XX WPI; 2003-058608/05.
 DR
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
 PT an immune function and as a vaccine against toxic shock syndrome or
 PT food poisoning
 XX
 XX
 PS Disclosure; Fig 15; 67pp; English.
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic
 CC response-inducing activity decreased by about 100-fold in comparison to a
 CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FRI909.
 XX
 SQ Sequence 240 AA;
 Query Match 100.0%; Score 100; DB 24; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYPSSKDNVGVKVTSGKTC 18
 DB 93 CYPSSKDNVGVKVTSGKTC 110
 RESULT 5
 ID AAY06249 standard; Peptide; 18 AA.
 XX
 AC AAY06249;
 XX
 XX 23-AUG-1999 (first entry)
 DT
 XX Staphylococcal group C enterotoxin disulfide loop.
 DE
 XX Enterotoxin; SEC1; SEC2; SEC3 FRI 913; SEC3 4446; SEC-Bovine;

KW SEC-Ovine; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9927889-A2.
 PD 10-JUN-1999.
 XX
 XX 01-DEC-1998; 98WO-US25107.
 PF
 XX 02-DEC-1997; 97US-0067357.
 PR
 XX (IDAH-) IDAHO RES FOUND INC.
 PA
 XX Bohach GI;
 PI
 XX WPI; 1999-358008/30.
 DR N-PSDB; AAX58884.
 XX
 PT Non-toxic modified staphylococcal enterotoxins
 XX
 PS Disclosure; Page 3; 25pp; English.
 CC This peptide corresponds to the disulfide loop, i.e. amino acids
 CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,
 CC SEC3 FRI 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AAY06251-53
 CC and AAY06255-58). The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide
 CC loop region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine
 CC production, but have substantially reduced toxicity compared to the
 CC corresponding unmodified native toxin. Emetic response induced by
 CC activity and fever inducing activity are typically decreased by at
 CC least about 100-fold, while LD50 (in Dutch belted rabbits) is at
 CC least 100-fold higher than the native toxin.
 XX
 SQ Sequence 18 AA;
 Query Match 96.0%; Score 96; DB 20; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2.8e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYPSSKDNVGVKVTSGKTC 18
 DB 1 CYPSSKDNVGVKVTSGKTC 18
 RESULT 6
 ID ABG71377 standard; Peptide; 18 AA.
 XX
 AC ABG71377;
 XX
 XX 29-JAN-2003 (first entry)
 DT
 XX Staphylococcal enterotoxin disulphide loop region.
 DE
 XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KM emetic response-inducing activity; staphylococcal enterotoxin;
 KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KM SEC1; SEC2; SEC3-FRI913; SEC-4446; SEC-bovine.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200283169-A1.
 PD 24-OCT-2002.
 XX
 XX 11-APR-2002; 2002WO-US11619.
 PF
 XX 13-APR-2001; 2001US-283720P.
 PR

PA (IDAH-) IDAHO RES FOUND INC.
 XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX WPI; 2003-058608/05.
 DR
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
 PT an immune function and as a vaccine against toxic shock syndrome or
 PT food poisoning -
 XX
 XX Disclosure; Fig 15; 67pp; English.
 XX
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic
 CC response-inducing activity decreased by about 100-fold in comparison to a
 CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents a staphylococcal enterotoxin
 CC disulphide loop region, occurring in several enterotoxins.
 CC
 SQ Sequence 18 AA;
 XX
 Query Match 96.0%; Score 96; DB 24; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2.8e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGKVTGKTC 18
 1 |||||
 Db 1 CYFSSKDNVKGKVTGKTC 18
 |||||
 RESULT 7
 ABG71380
 ID ABG71380 standard; Peptide; 18 AA.
 XX
 AC ABG71380;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin C1 (SEC1) protein fragment.
 XX
 KM Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin; SEC1;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US11619.
 XX
 PR 13-APR-2001; 2001US-283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX
 DR N-PSDB; ABS56822.
 XX
 PT New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
 PT an immune function and as a vaccine against toxic shock syndrome or
 PT food poisoning -
 XX
 PS Example 1; Fig 1; 67pp; English.
 XX

CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic
 CC response-inducing activity decreased by about 100-fold in comparison to a
 CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents a staphylococcal enterotoxin
 CC protein fragment.
 CC
 SQ Sequence 18 AA;
 XX
 Query Match 96.0%; Score 96; DB 24; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2.8e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGKVTGKTC 18
 1 |||||
 Db 1 CYFSSKDNVKGKVTGKTC 18
 |||||
 RESULT 8
 AAR13208
 ID AAR13208 standard; Protein; 238 AA.
 XX
 AC AAR13208;
 XX
 DT 15-OCT-1991 (first entry)
 XX
 DE Staphylococcal enterotoxin C3.
 XX
 KM SEC3; cancer treatment; pyrogen; tumouricide.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9110680-A.
 XX
 PD 25-JUL-1991.
 XX
 PF 17-JAN-1991; 91WO-US00342.
 XX
 PR 17-JAN-1990; 90US-0466577.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 1991-237984/32.
 XX
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC SEC3 was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydropathy profiles.
 CC See AAR13203-R13211.
 CC
 SQ Sequence 238 AA;
 XX
 Query Match 96.0%; Score 96; DB 12; Length 238;
 Best Local Similarity 94.4%; Pred. No. 4.6e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 0

```

QY      1 CYFSSKDNVGVKVTSGKTC 18
      |||||
      92 CYFSSKDNVGVKVTSGKTC 109

Db

RESULT 9
AAR45016 standard; protein; 238 AA.
XX
AC      AAR45016;
XX
DT      25-MAR-2003 (updated)
DT      08-JUN-1994 (first entry)
XX
DE      Staphylococcal enterotoxin SEC3.
XX
KW      Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW      autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS      Staphylococcus aureus.
XX
PN      MO9324136-A1.
XX
PD      09-DEC-1993.
XX
PF      01-JUN-1993; 93WO-US05213.
XX
PR      01-JUN-1992; 92US-0891718.
XX
PI      (STON/) STONE J L.
PA      (TERM/) TERMAN D S.
XX
PI      Stone JL, Terman DS;
XX
DR      WPI; 1993-405418/50.
XX
PT      Use of staphylococcal enterotoxin(s) and homologues - for
PT      treating cancer in a patient or for the treatment of auto-immune
PT      diseases
XX
PS      Disclosure; Fig 1; 90pp; English.
XX
CC      The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC      which may be used in the methods of the invention for treating cancer
CC      in a patient. These SEs, and homologues of them, can be used as
CC      tumouricidal agents for treating cancers and autoimmune disease.
CC      They exhibit tumouricidal activity and toxicity identical to that
CC      observed for the Protein A perfusion system. They may be administered
CC      by i.v. injection.
CC      (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 238 AA;

Query Match      96.0%; Score 96; DB 14; Length 238;
Best Local Similarity 94.4%; Pred. No. 4.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CYFSSKDNVGVKVTSGKTC 18
      |||||
      92 CYFSSKDNVGVKVTSGKTC 109

Db

RESULT 10
AAB67343
ID      AAB67343 standard; peptide; 238 AA.
XX
AC      AAB67343;
XX
DT      23-APR-2001 (first entry)
XX
DE      Staphylococcus aureus enterotoxin C3 protein.
XX
KW      Tumour; cancer; immune; enterotoxin.
XX

```

```

XX      Staphylococcus aureus.
OS
XX      US6180097-B1.
PN
XX      30-JAN-2001.
PD
XX      30-OCT-1998; 98US-0183437.
PF
XX      31-JAN-1994; 94US-0189424.
PR      19-JUN-1995; 95US-0491746.
PR      03-OCT-1989; 89US-0416530.
PR      17-JAN-1990; 90US-0466577.
PR      17-JAN-1991; 91US-0500342.
PR      01-JUN-1992; 92US-0891718.
PR      02-MAR-1993; 93US-0025144.
XX
PA      (TERM/) TERMAN D S.
XX
PI      Terman DS;
XX
DR      WPI; 2001-158657/16.
XX
PT      Tumor cell capable of stimulating antitumor immune reactivity in vitro
PT      or in vivo comprises exogenous nucleic acids encoding a superantigen
PT      and a costimulatory molecule -
XX
PS      Disclosure; Fig 2; 16pp; English.
XX
CC      The present invention relates to a tumour cell capable of stimulating
CC      antitumor immune reactivity in vitro or in vivo contains and
CC      expresses an exogenous nucleic acid molecule encoding a superantigen
CC      or its active fragment and an exogenous nucleic acid molecule
CC      encoding a costimulatory molecule that activates T cells in
CC      conjunction with an antigenic stimulus. The invention may be used
CC      for cancer therapy by stimulating an anticancer immune response
CC      in vivo or ex vivo.
XX
SQ      Sequence 238 AA;

Query Match      96.0%; Score 96; DB 22; Length 238;
Best Local Similarity 94.4%; Pred. No. 4.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CYFSSKDNVGVKVTSGKTC 18
      |||||
      92 CYFSSKDNVGVKVTSGKTC 109

Db

RESULT 11
AAB76239
ID      AAB76239 standard; Protein; 238 AA.
XX
AC      AAB76239;
XX
DT      09-AUG-2002 (first entry)
XX
DE      Staphylococcus aureus enterotoxin C3.
XX
KW      Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
KW      antitumour; therapy.
XX
OS      Staphylococcus aureus.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 208
FT      /note= "given as 'O' in the specification"
XX
PN      US2002051765-A1.
XX
PD      02-MAY-2002.
XX
PF      19-DEC-2000; 2000US-0741503.
XX

```

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XX 31-JAN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-046577.
PR 17-JAN-1991; 91WO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX (TERM/) TERMAN D S.
PA
XX Terman DS;
PI
XX WPI; 2002-415198/44.
DR
XX Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens -
XX
XX Disclosure; Fig 2; 17pp; English.
PS
XX The present sequence is the protein sequence of enterotoxin C3
CC (SEC3) of Staphylococcus aureus. Similarity is shown, in several
CC stretches of sequence, between staphylococcal enterotoxins,
CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative
CC toxin (see AB876234-44). In the present invention, synthetic
CC polypeptides useful in tumour therapy and in blocking or destroying
CC autoreactive T and B lymphocyte populations are characterized by
CC substantial structural homology to staphylococcal enterotoxin A and
CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
CC statistically significant sequence homology and similarity (Z value
CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
CC 6) to include alignment of cysteine residues and similar hydrophathy
CC profiles. These superantigens are used to treat solid tumours,
CC including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient
CC with one or more superantigens ex vivo to generate stimulated cells,
CC selecting a specific V beta subset of cells, and reintroducing
CC these cells into the patient to induce an in vivo therapeutic,
CC tumoricidal reaction.
XX
XX Sequence 238 AA;
SQ
XX
XX Query Match 96.0%; Score 96; DB 23; Length 238;
Best Local Similarity 94.4%; Pred. No. 4.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTSGKTC 18
Db |||||
92 CYFSSKDNVGVKVTSGKTC 109
XX
XX RESULT 12
XX AAR13207
ID AAR13207 standard; Protein; 239 AA.
XX
XX AAR13207;
AC
XX 15-OCT-1991 (first entry)
DT
XX Staphylococcal enterotoxin C1.
DE
XX
XX Staphylococcal enterotoxin C1.
DE
XX SEC1; cancer treatment; pyrogen; tumouricide.
KM
XX Staphylococcus aureus.
OS
XX
XX WO9110680-A.
PN
XX 25-JUL-1991.
PD
XX 17-JAN-1991; 91WO-US00342.
PF
XX
XX

```

```

PR 17-JAN-1990; 90US-0465577.
XX
XX (TERM/) TERMAN D S.
PA
XX Terman DS;
PI
XX WPI; 1991-237984/32.
DR
XX Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
XX Disclosure; Fig 1; 74pp; English.
PS
XX SEC1 was isolated and purified from S. aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC1. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydrophathy profiles.
CC See AAR13203-R13211.
XX
XX Sequence 239 AA;
SQ
XX
XX Query Match 96.0%; Score 96; DB 12; Length 239;
Best Local Similarity 94.4%; Pred. No. 4.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKVTSGKTC 18
Db |||||
93 CYFSSKDNVGVKVTSGKTC 110
XX
XX RESULT 13
XX AAR45015
ID AAR45015 standard; protein; 239 AA.
XX
XX AAR45015;
AC
XX 25-MAR-2003 (updated)
DT
XX 08-JUN-1994 (first entry)
DE
XX Staphylococcal enterotoxin SEC1.
DE
XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KM autoimmune disease; toxicity; Protein A; perfusion system.
KM
XX Staphylococcus aureus.
OS
XX
XX WO9324136-A1.
PN
XX
XX 09-DEC-1993.
PD
XX
XX 01-JUN-1993; 93WO-US05213.
PF
XX 01-JUN-1992; 92US-0891718.
PR
XX (STON/) STONE J L.
PA (TERM/) TERMAN D S.
XX
XX Stone JL, Terman DS;
PI
XX
XX WPI; 1993-405418/50.
DR
XX
XX Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
XX Disclosure; Fig 1; 90pp; English.
XX

```

CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 239 AA;

Query Match

Best Local Similarity 96.0%; Score 96; DB 14; Length 239;
 Pred. No. 4.6e-07;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFFSSKDNVKGKVTSGKTC 18
 |||
 DB 93 CFFSSKDNVKGKVTGKTC 110

RESULT 14

ID AAY06255 standard; Protein; 239 AA.

AC AAY06255;

XX 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-MNCopeland.

XX Enterotoxin; SEC-MNCopeland; toxin; disulfide loop;

KM protein engineering.

XX Staphylococcus aureus.

OS Key Location/Qualifiers

FN Disulfide-bond 93..110

XX MO9927889-A2.

PD 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

PR 02-DEC-1997; 97US-0067357.

PA (IDAH-) IDAHO RES FOUND INC.

PI Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 17; 25pp; English.

CC This protein represents the Staphylococcus aureus type C
 CC enterotoxin SEC-MNCopeland. The invention relates to pyrogenic
 CC toxins, such as staphylococcal enterotoxins, modified in the
 CC disulfide loop region. Typically, the modification involves
 CC deletions within the disulfide loop region of SEC (see AAY06261).
 CC The modified toxins retain useful biological properties, such as
 CC the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native
 CC toxin. Emetic response inducing activity and fever inducing
 CC activity are typically decreased by at least about 100-fold, while
 CC LD50 (in Dutch Belted rabbits) is at least 100-fold higher than
 CC the native toxin.

XX Sequence 239 AA;

Query Match

Best Local Similarity 96.0%; Score 96; DB 20; Length 239;
 Pred. No. 4.6e-07;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFFSSKDNVKGKVTSGKTC 18
 |||
 DB 93 CFFSSKDNVKGKVTGKTC 110

RESULT 15

ID AAY06256 standard; Protein; 239 AA.

AC AAY06256;

XX 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-4446.

XX Enterotoxin; SEC-4446; toxin; disulfide loop;

KM protein engineering.

XX Staphylococcus aureus.

OS Key Location/Qualifiers

FN Disulfide-bond 93..110

XX MO9927889-A2.

PD 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

PR 02-DEC-1997; 97US-0067357.

PA (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 17; 25pp; English.

CC This protein represents the Staphylococcus aureus type C
 CC enterotoxin SEC-4446. The invention relates to pyrogenic
 CC toxins, such as staphylococcal enterotoxins, modified in the disulfide loop
 CC region. Typically, the modification involves deletions within the
 CC disulfide loop region of SEC (see AAY06261). The modified toxins
 CC retain useful biological properties, such as the ability to induce
 CC cytokine production, but have substantially reduced toxicity
 CC compared to the corresponding unmodified native toxin. Emetic
 CC response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match

Best Local Similarity 96.0%; Score 96; DB 20; Length 239;
 Pred. No. 4.6e-07;

QY 1 CFFSSKDNVKGKVTSGKTC 18
 |||
 DB 93 CFFSSKDNVKGKVTGKTC 110

Search completed: October 15, 2003, 16:56:56
 Job time : 50.3575 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:51:46 ; Search time 13.7964 Seconds
(without alignments)
55.202 Million cell updates/sec

Title: US-09-555-115A-14

Perfect score: 100

Sequence: 1 CYPSSKDNVSKVTSKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A COMB .pep.*
2: /cgn2_6/ptodata/1/1aa/5B COMB .pep.*
3: /cgn2_6/ptodata/1/1aa/6A COMB .pep.*
4: /cgn2_6/ptodata/1/1aa/6B COMB .pep.*
5: /cgn2_6/ptodata/1/1aa/PCUS COMB .pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	96.0	89	4	US-09-144-776B-21
2	96	96.0	89	4	US-09-144-776B-22
3	96	96.0	89	4	US-09-144-776B-23
4	96	96.0	238	3	US-08-896-933-28
5	96	96.0	238	4	US-08-314-235-28
6	96	96.0	239	3	US-08-896-933-27
7	96	96.0	239	4	US-09-314-235-27
8	96	96.0	266	4	US-09-144-776B-14
9	47	47.0	374	2	US-07-857-224B-82
10	47	47.0	374	2	US-07-857-224B-83
11	47	47.0	375	4	US-09-347-878-56
12	43	43.0	94	2	US-07-728-215-35
13	43	43.0	94	2	US-07-728-215-37
14	43	43.0	94	4	US-08-938-085A-35
15	43	43.0	94	4	US-08-938-085A-37
16	43	43.0	94	4	US-10-072-844-35
17	43	43.0	94	4	US-10-072-844-37
18	43	43.0	514	1	US-08-361-920-21
19	43	43.0	514	1	US-08-479-939-21
20	43	43.0	514	1	US-08-483-432-21
21	43	43.0	798	2	US-07-728-215-30
22	43	43.0	798	2	US-08-938-085A-30
23	43	43.0	798	4	US-10-072-844-30
24	42	42.0	170	4	US-09-252-991A-29047
25	42	42.0	374	2	US-07-857-224B-80
26	42	42.0	374	2	US-07-857-224B-81
27	41.5	41.5	155	4	US-09-252-991A-19995

28	41.5	41.5	765	4	US-09-252-991A-24791	Sequence 24791, A
29	41	41.0	374	2	US-07-857-224B-84	Sequence 84, Appl
30	41	41.0	374	2	US-07-857-224B-85	Sequence 85, Appl
31	41	41.0	375	2	US-07-857-224B-86	Sequence 86, Appl
32	41	41.0	412	2	US-08-741-134-2	Sequence 2, Appl
33	41	41.0	1053	4	US-09-328-352-6788	Sequence 6788, Ap
34	40.5	40.5	1170	1	US-08-313-288B-20	Sequence 20, Appl
35	40.5	40.5	239	3	US-08-896-933-21	Sequence 21, Appl
36	40.5	40.5	239	4	US-09-314-235-21	Sequence 21, Appl
37	40	40.0	263	2	US-08-892-690-3	Sequence 3, Appl
38	40	40.0	731	2	US-08-313-185-51	Sequence 51, Appl
39	40	40.0	731	2	US-08-459-499-15	Sequence 15, Appl
40	40	40.0	731	3	US-09-082-614A-51	Sequence 51, Appl
41	39.5	39.5	1333	4	US-09-347-878-20	Sequence 20, Appl
42	39	39.0	278	2	US-08-569-168-2	Sequence 2, Appl
43	39	39.0	383	2	US-08-569-168-7	Sequence 7, Appl
44	38	38.0	134	2	US-08-482-728A-14	Sequence 14, Appl
45	38	38.0	176	1	US-08-145-995A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-144-776B-21
; Sequence 21, Application US/09144776B
; Patent No. 6399332
GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21
Query Match 96.0%; Score 96; DB 4; Length 89;

Best Local Similarity 94.4%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
Db 54 CYFSSKDNVGVKVTGKTC 71

RESULT 2

US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson

Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen
Vaccines

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street

MCMR-JA (Charles H. Harris-Patent
Atty)

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144, 776B

FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 89

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-144-776B-22

Query Match 96.0%; Score 96; DB 4; Length 89;

Best Local Similarity 94.4%; Pred. No. 6.4e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
Db 54 CYFSSKDNVGVKVTGKTC 71

US-09-144-776B-23
; Sequence 23, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson

Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris

STREET: US Army MRC -504 Scott Street

MCMR-JA (Charles H. Harris-Patent
Atty)

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144, 776B

FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 89

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-144-776B-23

Query Match 96.0%; Score 96; DB 4; Length 89;

Best Local Similarity 94.4%; Pred. No. 6.4e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
Db 54 CYFSSKDNVGVKVTGKTC 71

US-08-896-933-28

Sequence 28, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
AND RELATED COMPOUNDS

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

EARLIER FILING DATE: 1997-07-18

EARLIER APPLICATION NUMBER: 08/252,978

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 28

LENGTH: 238

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-08-896-933-28

Query Match 96.0%; Score 96; DB 3; Length 238;

Best Local Similarity 94.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTSGKTC 18
Db 92 CYFSSKDNVGVKVTGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-28

Query Match 96.0%; Score 96; DB 4; Length 238;
Best Local Similarity 94.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTSGKTC 18
Db 92 CYFSSKDNVGVKVTGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-27

Query Match 96.0%; Score 96; DB 3; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTSGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-27

Query Match 96.0%; Score 96; DB 4; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTSGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match          96.0%; Score 96; DB 4; Length 266;
Best Local Similarity 94.4%; Pred. No. 1,9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CYPSSKDNVGVKTSKTC 18
Db      120 CYPSSKDNVGVKTSKTC 137

RESULT 9
US-07-857-224B-82
; Sequence 82, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (international) 41 1 632 2830
; TELEFAX: (international) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE: Alcohol dehydrogenase, Table 3 Column 3
; PUBLICATION INFORMATION:
; AUTHORS: Joernvall, H.
; AUTHORS: Persson, M.

```

```

; AUTHORS: Jeffery, J.
; TITLE: Alcohol dehydrogenases
; JOURNAL: Proceedings of the National Academy of Sciences, USA
; VOLUME: 78
; PAGES: 4226-4230
; DATE: 1981
US-07-857-224B-82

Query Match          47.0%; Score 47; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYPSSKDNVGVKTSKTC 18
Db      174 CYPSSKDNVGVKTSKTC 195

RESULT 10
US-07-857-224B-83
; Sequence 83, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (international) 41 1 632 2830
; TELEFAX: (international) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE: Alcohol dehydrogenase, Table 4
; PUBLICATION INFORMATION:
; AUTHORS: Joernvall, H.
; AUTHORS: Persson, M.
; AUTHORS: Jeffery, J.
; TITLE: Alcohol dehydrogenases
; JOURNAL: Proceedings of the National Academy of Sciences, USA
; VOLUME: 78
; PAGES: 4226-4230
; DATE: 1981
US-07-857-224B-83

Query Match          47.0%; Score 47; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYPSSKDNVGVKTSKTC 18

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Db 174 CGFSTGYGSANVAKVTPGSTC 195

RESULT 11

US-09-347-878-56
; Sequence 56, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-878-56

Query Match 47.0%; Score 47; DB 4; Length 375;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SDNNGKXTSGKTC 18

Db 175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 12

US-07-728-215-35
; Sequence 35, Application US/07728215
; Patent No. 5962643
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pyrela, Robert
; TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,215
; FILING DATE: 19910711
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-728-215-35

US-07-728-215-35

Query Match 43.0%; Score 43; DB 2; Length 94;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKXTSGKTC 18

Db 1 CVCRKRDNTNIEYSGKFC 18

RESULT 13

US-07-728-215-37
; Sequence 37, Application US/07728215
; Patent No. 5962643
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pyrela, Robert
; TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,215
; FILING DATE: 19910711
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-728-215-37

Query Match 43.0%; Score 43; DB 2; Length 94;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKXTSGKTC 18

Db 1 CVCRKRDNTNIEYSGKFC 18

RESULT 14

US-08-938-085A-35
; Sequence 35, Application US/08938085A
; Patent No. 6339148
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pyrela, Robert
; TITLE OF INVENTION: A No. 6339148el Integrin Beta Subunit and Uses
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
US-08-938-085A-35

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A
FILING DATE: 26-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-938-085A-35

Query Match 43.0%; Score 43; DB 4; Length 94;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGVTSGKTC 18
Db 1 CVCRKRDNTNEIYSGKFC 18

RESULT 15
US-08-938-085A-37
Sequence 37, Application US/08938085A
Patent No. 6339148
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pyeola, Robert
TITLE OF INVENTION: A No. 6339148e1 Integrin Beta Subunit and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A
FILING DATE: 26-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.

REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-938-085A-37

Query Match 43.0%; Score 43; DB 4; Length 94;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGVTSGKTC 18
Db 1 CVCRKRDNTNEIYSGKFC 18

Search completed: October 15, 2003, 17:08:32
Job time: 13.7964 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 27.2695 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115a-14
Perfect score: 100
Sequence: 1 CYFSSKDNVKGVTSGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	96.0	89	15	US-10-002-784A-36
2	96	96.0	89	15	US-10-002-784A-37
3	96	96.0	89	15	US-10-002-784A-38
4	96	96.0	89	15	US-08-882-431-14
5	96	96.0	266	8	US-09-870-759-12
6	96	96.0	266	12	US-09-751-708A-12
7	96	96.0	266	15	US-10-002-784A-14
8	96	96.0	266	15	US-09-981-353-113
9	96	96.0	266	15	US-09-738-630-92
10	96	96.0	266	15	US-09-925-302-497
11	96	96.0	266	15	US-10-021-811-54
12	96	96.0	266	15	US-10-072-841-35
13	96	96.0	266	15	US-10-072-841-37
14	96	96.0	266	15	US-09-778-927A-67
15	96	96.0	266	15	US-09-925-301-1163

16	43	43.0	565	15	US-10-106-698-4557	Sequence 4557, Ap
17	43	43.0	798	14	US-10-100-912-6	Sequence 6, Appl
18	43	43.0	798	14	US-10-072-841-30	Sequence 30, Appl
19	43	43.0	798	14	US-10-117-295A-1	Sequence 1, Appl
20	42	42.0	152	12	US-10-040-895-2	Sequence 2, Appl
21	42	42.0	211	15	US-10-156-761-8802	Sequence 8802, Ap
22	42	42.0	219	10	US-09-909-370-377	Sequence 377, Ap
23	42	42.0	219	10	US-09-909-088B-377	Sequence 377, Ap
24	42	42.0	219	10	US-09-905-291A-377	Sequence 377, Ap
25	42	42.0	219	10	US-09-965-529-3	Sequence 3, Appl
26	42	42.0	219	10	US-09-902-853-377	Sequence 377, Ap
27	42	42.0	219	10	US-09-907-824-377	Sequence 377, Ap
28	42	42.0	219	10	US-09-907-841-377	Sequence 377, Ap
29	42	42.0	219	11	US-09-904-011-377	Sequence 377, Ap
30	42	42.0	219	11	US-09-906-742-377	Sequence 377, Ap
31	42	42.0	219	11	US-09-906-838-377	Sequence 377, Ap
32	42	42.0	219	11	US-09-907-613-377	Sequence 377, Ap
33	42	42.0	219	11	US-09-907-942-377	Sequence 377, Ap
34	42	42.0	219	11	US-09-904-859-377	Sequence 377, Ap
35	42	42.0	219	11	US-09-909-204-377	Sequence 377, Ap
36	42	42.0	219	11	US-09-904-820-377	Sequence 377, Ap
37	42	42.0	219	11	US-09-904-786-377	Sequence 377, Ap
38	42	42.0	219	11	US-09-906-646-377	Sequence 377, Ap
39	42	42.0	219	11	US-09-906-700-377	Sequence 377, Ap
40	42	42.0	219	11	US-09-903-786-377	Sequence 377, Ap
41	42	42.0	219	11	US-09-902-903-377	Sequence 377, Ap
42	42	42.0	219	11	US-09-903-749A-377	Sequence 377, Ap
43	42	42.0	219	11	US-09-904-119-377	Sequence 377, Ap
44	42	42.0	219	11	US-09-904-956-377	Sequence 377, Ap
45	42	42.0	219	11	US-09-902-736-377	Sequence 377, Ap

ALIGNMENTS

RESULT 1
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match 96.0%; Score 96; DB 15; Length 89;
Best Local Similarity 94.4%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTSGKTC 18
Db 54 CYFSSKDNVKGVTSGKTC 71

RESULT 2
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33

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; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-37
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Query Match          96.0%; Score 96; DB 15; Length 89;
Best Local Similarity 94.4%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1  CYFSSKDNVGVKVTSGKTC 18
        |||
Db       54  CYFSSKDNVGVKVTSGKTC 71
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RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US2003003644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-38
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Query Match          96.0%; Score 96; DB 15; Length 89;
Best Local Similarity 94.4%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1  CYFSSKDNVGVKVTSGKTC 18
        |||
Db       54  CYFSSKDNVGVKVTSGKTC 71
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RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John Moran
; STREET: US Army MRC - 504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
```

```
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14
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Query Match          96.0%; Score 96; DB 8; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1  CYFSSKDNVGVKVTSGKTC 18
        |||
Db      120  CYFSSKDNVGVKVTSGKTC 137
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RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-870-759-12
```

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Query Match          96.0%; Score 96; DB 10; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1  CYFSSKDNVGVKVTSGKTC 18
        |||
Db      120  CYFSSKDNVGVKVTSGKTC 137
```

```
RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
```



```

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match          96.0%; Score 96; DB 12; Length 266;
Best Local Similarity 94.4%; Pred. No. 1,7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTSGKTC 18
Db      120  CYFSSKDNVGVKVTSGKTC 137

RESULT 7
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US200303644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match          96.0%; Score 96; DB 15; Length 266;
Best Local Similarity 94.4%; Pred. No. 1,7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CYFSSKDNVGVKVTSGKTC 18
Db      120  CYFSSKDNVGVKVTSGKTC 137

RESULT 8
US-09-981-353-113
; Sequence 113, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laegek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 375
; TYPE: PRT
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```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 2512879CD1
US-09-981-353-113

Query Match          47.0%; Score 47; DB 10; Length 375;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYFS----SKDNVGVKVTSGKTC 18
Db      175  CGFSTGYGSAVNVAKVTPGSTC 196

RESULT 9
US-09-738-630-92
; Sequence 92, Application US/09738630
; Publication No. US20030166213A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods For Identifying Compounds That
; TITLE OF INVENTION: Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
; FILE REFERENCE: P-NI 3906
; CURRENT APPLICATION NUMBER: US/09/738,630
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-630-92

Query Match          47.0%; Score 47; DB 12; Length 375;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1  CYFS----SKDNVGVKVTSGKTC 18
Db      175  CGFSTGYGSAVNVAKVTPGSTC 196

RESULT 10
US-09-925-302-497
; Sequence 497, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 497
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-497

Query Match          47.0%; Score 47; DB 9; Length 395;
Best Local Similarity 54.5%; Pred. No. 19;
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Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYPSSKDNVKGKTSKTC 18
Db 195 CGFSTGYGSAVNAKVTGPGSTC 216

RESULT 11
US-10-021-811-54
; Sequence 54, Application US/10021811
; Publication No. US2003002407A1
; GENERAL INFORMATION:
; APPLICANT: Canoon, Rebecca E.
; APPLICANT: Fang, Yijuan
; APPLICANT: Odell, Joan
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: B1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 54
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Glycine max
US-10-021-811-54

Query Match 44.0%; Score 44; DB 15; Length 332;
Best Local Similarity 46.7%; Pred. No. 47;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGKTSKTC 18
Db 197 CYASSADNIARMLKG 211

RESULT 12
US-10-072-841-35
; Sequence 35, Application US/10072841
; Publication No. US20020164708A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Dean
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. US20020164708A1e1 Integrin Beta Subunit and Uses
; thereof
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,841
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,215
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-072-841-35

Query Match 43.0%; Score 43; DB 14; Length 94;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGKTSKTC 18
Db 1 CVCRRKDNTEIYSGKFC 18

RESULT 13
US-10-072-841-37
; Sequence 37, Application US/10072841
; Publication No. US20020164708A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. US20020164708A1e1 Integrin Beta Subunit and Uses
; thereof
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,841
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,215
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-072-841-37

Query Match 43.0%; Score 43; DB 14; Length 94;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGKTSKTC 18
Db 1 CVCRRKDNTEIYSGKFC 18

Db 1 CVCRKRDNTNEIYSGKFC 18

```

RESULT 14
US-09-778-927A-67
; Sequence 67, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(543)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-67

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Query Match 43.0%; Score 43; DB 9; Length 543;
 Best Local Similarity 38.9%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTSGKTC 18
 Db 281 CVCRKRDNTNEIYSGKFC 298

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RESULT 15
US-09-925-301-1163
; Sequence 1163, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1163
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1163

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Query Match 43.0%; Score 43; DB 9; Length 565;
 Best Local Similarity 38.9%; Pred. No. 1.2e+02;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTSGKTC 18
 Db 303 CVCRKRDNTNEIYSGKFC 320

Search completed: October 15, 2003, 17:47:01
 Job time : 28.2695 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 13.6886 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115a-14

Perfect score: 100

Sequence: 1 CYFSSKDNVGVKTSKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	96.0	266	1 ENSAC1	enterotoxin C-1 pr
2	96	96.0	266	2 A60114	enterotoxin C-2 pr
3	96	96.0	266	2 S11885	enterotoxin C3 - S
4	47	47.0	375	1 DEHUA	alcohol dehydrogen
5	47	47.0	375	1 DEHUA	alcohol dehydrogen
6	46	46.0	368	2 T26338	hypothetical prote
7	45	45.0	274	2 T13010	hypothetical prote
8	44.5	44.5	1102	2 A84480	probable retroelem
9	43	43.0	94	2 C37057	fibronectin recept
10	43	43.0	346	2 AE3434	lycB protein [lipo
11	43	43.0	375	1 A38405	alcohol dehydrogen
12	43	43.0	419	2 B90084	hypothetical prote
13	43	43.0	773	1 A45059	beta-1 integrin su
14	43	43.0	798	2 A28193	integrin beta-1 ch
15	43	43.0	798	2 B28193	integrin beta-1* c
16	43	43.0	798	2 B27079	fibronectin recept
17	43	43.0	798	2 S01659	integrin beta-1 ch
18	43	43.0	799	1 JTM5FB	fibronectin recept
19	42	42.0	368	1 DEHUA6	alcohol dehydrogen
20	42	42.0	374	1 DEHUA5	alcohol dehydrogen
21	42	42.0	375	1 A33909	alcohol dehydrogen
22	42	42.0	375	1 DEHUA1	alcohol dehydrogen
23	42	42.0	1170	2 A40588	thrombospondin 1 p
24	41.5	41.5	333	2 D83585	hypothetical prote
25	41.5	41.5	417	2 H83370	hydrogen cyanide s
26	41	41.0	142	2 AG0456	50S ribosomal prot
27	41	41.0	266	1 S18159	ribosomal protein
28	41	41.0	269	2 B97113	protein serine/thr
29	41	41.0	355	2 C90144	terminal oxidase,

30	41	41.0	375	1 I55359	alcohol dehydrogen
31	41	41.0	375	1 DEHUA6	alcohol dehydrogen
32	41	41.0	375	1 DEHUA5	alcohol dehydrogen
33	41	41.0	375	1 A49107	alcohol dehydrogen
34	41	41.0	375	1 S29343	alcohol dehydrogen
35	41	41.0	376	1 A26468	alcohol dehydrogen
36	41	41.0	412	2 A55320	immunophilin FKBP4
37	41	41.0	429	2 T21113	hypothetical prote
38	41	41.0	523	2 T09615	tyrosine decarboxy
39	41	41.0	746	2 AD1622	probable integrin
40	41	41.0	803	1 IJCH3	integrin, band 3 p
41	41	41.0	1170	1 TSHUP1	thrombospondin 1 p
42	41	41.0	1335	2 B84512	probable retroelem
43	41	41.0	2543	2 T31687	suface antigen - p
44	40.5	40.5	1677	2 T43021	vitellogenin precu
45	40	40.0	199	2 AG1583	weakly phosphoglyc

ALIGNMENTS

RESULT 1
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #ext_change 16-Jun-1999
C/Accession: S06356; A01816
R/Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A/Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to
A/Reference number: S06356; MUID:88038352; PMID:2823067
A/Accession: S06356
A/Molecule type: DNA
A/Residues: 1-266 <BOH>
A/Cross-references: EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567
R/Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A/Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A/Reference number: A01816; MUID:83213327; PMID:6189824
A/Accession: A01816
A/Molecule type: protein
A/Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C/Genes: entC1
C/Superfamily: enterotoxin B
C/Keywords: enterotoxin
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-266/Product: enterotoxin C-1 #status experimental <MAT>
F/120-137/Diulfide bonds: #status experimental

Query Match 96.0%; Score 96; DB 1; Length 266;
Best Local Similarity 94.4%; Pred. No. 9.4e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKTSKTC 18
Db 120 CYFSSKDNVGVKTSKTC 137

RESULT 2
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N/Alternate names: enterotoxin C-3 precursor
C/Species: Staphylococcus aureus
C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #ext_change 16-Jul-1999
C/Accession: A60114; B60114; A33866
R/Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A/Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A/Reference number: A60114; MUID:89277549; PMID:2543637
A/Accession: A60114
A/Status: not compared with conceptual translation
A/Molecule type: DNA

A/Residues: 1-266 <BOH>
 A/Accession: B60114
 A/Molecule type: protein
 A/Residues: 28-66 <BOH2>
 R/Couch, J.L.; Betley, M.J.
 J. Bacteriol. 171, 4507-4510, 1989
 A/Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
 A/Reference number: A33866; MUID:99327174; PMID:2473979
 A/Accession: A33866
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-266 <COU>
 A/Cross-references: GB:M28364; NID:G153003; PIDN:AAA26624.1; PID:G153004
 C/Genetics:
 A/Gene: entC2
 C/Superfamily: enterotoxin B
 F,1-27/Domain: signal sequence #status predicted <SIG>
 F,28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 96.0%; Score 96; DB 2; Length 266;
 Best Local Similarity 94.4%; Pred. No. 9.4e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSGKTC 18
 |||||
 Db 120 CYFSSKDNVGVKVTSGKTC 137

RESULT 3
 S11885
 enterotoxin C3 - Staphylococcus aureus
 C/Species: Staphylococcus aureus
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C/Accession: S11885
 R/Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
 Mol. Gen. Genet. 220, 329-333, 1990
 A/Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
 A/Reference number: S11885; MUID:90220508; PMID:2325627
 A/Accession: S11885
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-266 <HOV>
 A/Cross-references: GB:X51661; NID:G46570; PIDN:CAA35972.1; PID:G46571
 C/Superfamily: enterotoxin B

Query Match 96.0%; Score 96; DB 2; Length 266;
 Best Local Similarity 94.4%; Pred. No. 9.4e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTSGKTC 18
 |||||
 Db 120 CYFSSKDNVGVKVTSGKTC 137

RESULT 4
 DEHUA
 alcohol dehydrogenase (EC 1.1.1.1) 1 - human
 N/Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
 C/Species: Homo sapiens (man)
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
 C/Accession: S02265; A25428; A24408; I39398; I39397
 R/Matsu, Y.; Yokoyama, S.
 FEBS Lett. 243, 57-60, 1989
 A/Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
 A/Reference number: S02265; MUID:9153548; PMID:2925825
 A/Accession: S02265
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-375 <MATS>
 R/Ikura, T.; Szeto, S.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
 A/Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and ev
 A/Reference number: A94120; MUID:86120995; PMID:2935875

A/Accession: A25428
 A/Molecule type: mRNA
 A/Residues: 1-375 <IKU>
 A/Cross-references: GB:M12271; NID:G178091; PIDN:AAA68131.1; PID:G178092
 R/von Bahr-Lindstrom, H.; Hoog, J.O.; Heden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K.
 Biochemistry 25, 2465-2470, 1986
 A/Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
 A/Reference number: A24408; MUID:86243367; PMID:3013304
 A/Accession: A24408
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-375 <VON>
 A/Cross-references: GB:M12963; NID:G178089; PIDN:AAA51590.1; PID:G178090
 R/Yasunami, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
 Genomics 7, 152-158, 1990
 A/Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
 A/Reference number: I39398; MUID:90269803; PMID:2347582
 A/Accession: I39398
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-6 <YAS>
 A/Cross-references: GB:M37066; NID:G178095; PIDN:AAA51591.1; PID:G178096
 R/Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990
 A/Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: intere
 A/Reference number: I39397; MUID:90382676; PMID:2169444
 A/Accession: I39397
 A/Status: preliminary; translated from GB/EMBL/DDBT

A/Molecule type: DNA
 A/Residues: 1-6 <STE>
 A/Cross-references: GB:M32656; NID:G178093; PIDN:AAA52276.1; PID:G178094
 C/Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C/Genetics:
 A/Gene: GDB:ADH1
 A/Cross-references: GDB:119650; OMIM:103700
 A/Map position: 4q21-4q23
 A/Intons: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
 C/Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
 C/Function:

A/Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
 A/Pathway: ethanol degradation
 A/Note: human alcohol dehydrogenase 1 is expressed predominately in fetal and neonatal li
 C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C/Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidore
 F,2-375/Product: alcohol dehydrogenase 1 #status predicted <MAT>
 F,32-366/Domain: long-chain alcohol dehydrogenase homology <LIADH>
 F,195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F,2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F,47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F,98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 47.0%; Score 47; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 9.5;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS---SKDNVGVKVTSGKTC 18
 |||||
 Db 175 CGFSTGVSAVNVAKVTPGSTC 196

RESULT 5
 DEHUA
 alcohol dehydrogenase (EC 1.1.1.1) 2 [validated] - human
 N/Alternate names: alcohol dehydrogenase beta chain; class I alcohol dehydrogenase
 C/Species: Homo sapiens (man)
 C/Date: 25-Feb-1985 #sequence_revision 02-Aug-1994 #text_change 15-Sep-2000
 C/Accession: A23607; A38916; I39399; A26281; I39402; I39401; S05202; S10621; I39400; A00;
 R/Heden, L.O.; Hoog, J.O.; Larsson, K.; Lake, M.; Lagerholm, E.; Holmgren, A.; Vallee, B.
 FEBS Lett. 194, 327-332, 1986
 A/Title: cDNA clones coding for the beta-subunit of human liver alcohol dehydrogenase hav
 A/Reference number: A23607; MUID:86082371; PMID:3000832
 A/Accession: A23607
 A/Molecule type: mRNA
 A/Residues: 1-375 <HED>

A:Cross-references: EMBL:X03350; NID:g28415; PIDN:CAA27056.1; PID:g28416
 R:Kura, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2703-2707, 1985
 A>Title: Molecular cloning of a full-length cDNA for human alcohol dehydrogenase.
 A:Reference number: A38916; MUID:85190565; PMID:2986130
 A:Accession: A38916
 A:Molecule type: mRNA
 A:Residues: 1-375 <IKU>
 A:Cross-references: GB:M24317; NID:g178097
 A>Note: this sequence has been revised in reference A38917
 R:Kura, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5578, 1985
 A:Reference number: A38917
 A:Accession: A38917
 A:Contents: annotation; extratum
 R:Yokoyama, S.; Yokoyama, R.; Rotwein, P.
 Jpn. J. Genet. 62, 241-256, 1987
 A>Title: Molecular characterization of cDNA clones encoding the human alcohol dehydrogenase
 A:Reference number: I39399
 A:Accession: I39399
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1375 <OK>
 A:Cross-references: GB:000137; NID:g219427; PIDN:BA00084.1; PID:g219428
 R:Duester, G.; Smith, M.; Balanphone, V.; Hatfield, G.W.
 J. Biol. Chem. 261, 2027-2033, 1986
 A>Title: Molecular analysis of the human class I alcohol dehydrogenase gene family and r
 A:Reference number: A26281; MUID:86111889; PMID:2935533
 A:Accession: A26281
 A:Molecule type: DNA
 A:Residues: 1-229, 'K', 231-375 <DUE>
 A:Cross-references: GB:M24317; GB:K01883; NID:g178097; PIDN:AAA51884.1; PID:g178098
 A>Note: the authors translated the codon AAA for residue 230 as Phe
 R:Yasunami, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
 Genomics 7, 152-158, 1990
 A>Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly
 A:Reference number: I39398; MUID:90269803; PMID:2347582
 A:Accession: I39402
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-6 <YAS>
 A:Cross-references: GB:M37067; NID:g178114; PIDN:AAA51593.1; PID:g178115
 R:Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990
 A>Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
 A:Reference number: I39397; MUID:90382676; PMID:2169444
 A:Accession: I39401
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <STB>
 A:Cross-references: GB:M32657; NID:g178112; PIDN:AAA52277.1; PID:g178113
 R:Matsumoto, Y.; Yokoyama, R.; Yokoyama, S.
 Eur. J. Biochem. 183, 317-320, 1989
 A>Title: The genes for human alcohol dehydrogenase beta(1) and beta(2) differ by only c
 A:Reference number: S05202; MUID:99338401; PMID:2547609
 A:Accession: S05202
 A:Molecule type: DNA
 A:Residues: 1-47, 'H', 49-375 <MATS>
 A:Cross-references: EMBL:X15447; NID:g283185
 A>Note: allelic beta-2 variant found predominately in oriental populations
 A>Note: the sequence in GenBank entry HSDH221, release 103 (PID:e228260), has an incorr
 R:Erlich, T.; von Warburg, J.P.; Wermuth, B.
 FEBS Lett. 234, 53-55, 1988
 A>Title: cDNA sequence of the beta(2)-subunit of human liver alcohol dehydrogenase.
 A:Reference number: S10621; MUID:88271624; PMID:2968918
 A:Accession: S10621
 A:Molecule type: mRNA
 A:Residues: 1-47, 'H', 49-343 <EHR>
 A>Note: only a list of differences from various previously published sequences is shown
 R:Xu, Y.L.; Carr, L.G.; Boston, W.F.; Li, T.K.; Edenberg, H.J.
 Genomics 2, 209-214, 1988
 A>Title: Genotyping of human alcohol dehydrogenase at the ADH2 and ADH3 loci following
 A:Reference number: I39400; MUID:88284699; PMID:3397059
 A:Accession: I39400

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7, 'M', 9-56, 'K', 58-165, 'K', 167-234, 'V', 236-375 <RB3>
 A:Cross-references: GB:M2692; NID:g178099; PIDN:AAA51592.1; PID:g178100
 R:Hempel, J.; Buhler, R.; Kaiser, R.; Holmquist, B.; de Zelenek, C.; von Warburg, J.P.;
 Eur. J. Biochem. 145, 437-445, 1984
 A>Title: Human liver alcohol dehydrogenase. 1. The primary structure of the beta-1beta-1
 A:Reference number: A00335; MUID:85076637; PMID:6391920
 A:Accession: A00335
 A:Molecule type: protein
 A:Residues: 2-129, 131-375 <HEN>
 A>Note: allelic beta-1 variant found predominately in caucasian and negroid populations
 R:Buhler, R.; Hempel, J.; Kaiser, R.; von Warburg, J.P.; Vallee, B.L.; Jornvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6320-6324, 1984
 A>Title: Human alcohol dehydrogenase: structural differences between the beta and gamma i
 ndants in livers of different mammals.
 A:Reference number: A05182; MUID:85038508; PMID:6387702
 A:Accession: A05182
 A:Molecule type: protein
 A:Residues: 12-34, 'V', 36-38, 41-85, 101-114, 131-160, 170-213, 273-313, 317-331, 341-367 <BUH>
 R:Burnell, J.C.; Carr, L.G.; Dwyer, F.E.; Edenberg, H.J.; Li, T.K.; Boston, W.F.
 Biochem. Biophys. Res. Commun. 146, 1227-1233, 1987
 A>Title: The human beta-3 alcohol dehydrogenase subunit differs from beta-1 by a Cys for
 A:Accession: A26826
 A:Molecule type: protein
 A:Residues: 368-369, 'C', 371-375 <BUR>
 A>Note: allelic beta-3 variant found as a minor form occurring to a greater extent in neg
 R:Huxley, T.D.; Boston, W.F.; Hamilton, J.A.; Amzel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8149-8153, 1991
 A>Title: Structure of human beta-1beta-1 alcohol dehydrogenase: catalytic effects of non
 A:Reference number: A40987; MUID:91376103; PMID:1896463
 A:Accession: A40987
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms
 A>Note: structure of beta-1 variant dimer
 R:Huxley, T.D.; Boston, W.F.; Hamilton, J.A.; Amzel, L.M.
 submitted to the Brookhaven Protein Data Bank, January 1993
 A:Reference number: A52127; PID:3HND
 A:Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 2-375
 A:Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C:Genetics:
 A:Gene: GDB:ADH2
 A:Cross-references: GDB:119651; OMIM:103720
 A:Map position: 4q22-4q22
 A:Insertions: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
 C:Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
 C:Function:
 A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
 A:Pathway: alcohol degradation
 A>Note: human alcohol dehydrogenase beta 1s expressed predominately in fetal lung and nec
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidore
 F;2-375/Product: alcohol dehydrogenase 2 #status experimental <MATS>
 F;32-366/Domains: long-chain alcohol dehydrogenase homology <LADH>
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
 F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
 F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match 47.0%; Score 47; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 9.5;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVKGKTSKTC 18
 DB 175 CGSTGYGSAVNAVKVPGSTC 196

RESULT 6
 T26338
 hypothetical protein Y102A5B.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: Y26338

R:Gardner, A.
submitted to the EMBL Data Library, June 1998

A:Reference number: Z20203

A:Accession: T26338

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-368 <full>

A:Cross-references: EMBL:AL023821; PIDN:CA19437.1; CESP:Y102A5B.3

A:Experimental source: clone Y102A5B

C:Genetic:

A:Gene: CESP:Y102A5B.3

A:Introns: 61/3; 76/3; 136/3; 185/1; 245/1

Query Match 46.0%; Score 46; DB 2; Length 368;
Best Local Similarity 43.8%; Pred. No. 14;

Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FSSKDNVGVKVTSGKTC 18

Db 144 FASKNNTGNMTGLLC 159

RESULT 7

hypothetical protein T24C20.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999

C:Accession: T13010

R:Choine, N.; Robert, C.; Brottier, P.; Winkler, P.; Catolico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A:Reference number: Z17586

A:Accession: T13010

A:Molecule type: DNA

A:Residues: 1-274 <CHO>

A:Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.90

A:Experimental source: cultivar Columbia; BAC clone T24C20

C:Genetic:

A:Gene: ATSP:T24C20.90

A:Map position: 3

A:Introns: 62/1; 84/1; 133/1; 171/1; 201/1; 271/3

Query Match 45.0%; Score 45; DB 2; Length 274;
Best Local Similarity 75.0%; Pred. No. 15;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 SKDNVGVKVTSGK 16

Db 137 SKDNVGVKVTSGK 148

RESULT 8

AB4480

probable retroelement pol polypeptide (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: AB4480

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

et al.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487; PMID:10617197

A:Accession: AB4480

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1102 <STO>

A:Cross-references: GB:AB002093; NID:94063762; PIDN:AAC98469.1; GSPDB:GN00139

C:Genetic:

A:Gene: AT2G06840

A:Map position: 2

Query Match 44.5%; Score 44.5; DB 2; Length 1102;

Best Local Similarity 55.6%; Pred. No. 69;

Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CYFSSKDNVGVKVTSGKTC 18

Db 328 CHQSSKD-LGKIDSCDTC 344

RESULT 9

fibronectin receptor beta chain - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 23-Jul-1999

C:Accession: C37057

R:Shepard, D.; Rozzo, C.; Starr, L.; Quaranta, V.; Erle, D.J.; Pytela, R.

J. Biol. Chem. 265, 11502-11507, 1990

A:Title: Complete amino acid sequence of a novel integrin beta subunit (betac6) identified

A:Reference number: A37057; MUID:90307659; PMID:2365683

A:Accession: C37057

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-94 <SHF>

A:Cross-references: GB:J05522

C:Superfamily: Integrin beta chain; laminin-type EGF-like homology

C:Keywords: cell adhesion; duplication; heterodimer; membrane protein

Query Match 43.0%; Score 43; DB 2; Length 94;
Best Local Similarity 38.9%; Pred. No. 11;

Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTSGKTC 18

Db 1 CVCRKRDNTNEISGKFC 18

RESULT 10

AE3434

lyb protein (imported) - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AE3434

R:DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, I.

.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: J03252; PMID:11756688

A:Accession: AE3434

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 <KUR>

A:Cross-references: GB:AE008917; PIDN:AAL52640.1; PID:gt17983462; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetic:

A:Gene: BME11459

A:Map position: 1

C:Superfamily: penicillin tolerance protein

Query Match 43.0%; Score 43; DB 2; Length 346;
Best Local Similarity 53.8%; Pred. No. 39;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVT 13

Db 161 CHFDDEDNIGFVT 173

RESULT 11

A38405

alcohol dehydrogenase (EC 1.1.1.1) I - Perez's frog

C:Species: Rana perezi (Perez's frog)

C>Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 24-Apr-1998

C:Accession: A38405

R:Cederlund, E.; Peralba, J.M.; Pares, X.; Joernvall, H.

Biochemistry 30, 2811-2816, 1991

A>Title: Amphibian alcohol dehydrogenase, the major frog liver enzyme. Relationships to ydrogenases.
A/Reference number: A38405; MUID:91175722; PMID:2007119
A/Accession: A38405
A/Molecule type: protein
A/Residues: 1-375 <CD>
C/Comment: The class I alcohol dehydrogenases are pyrazole-sensitive and have a high act
C/Complex: homodimer
C/Function:
A/Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
A/Pathway: alcohol degradation
C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C/Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
F/31-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F/195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
F/1/Modified site: acetylated amino end (Ala) #status experimental
F/6,66,115/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
F/98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 43.0%; Score 43; DB 1; Length 375;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 CYFSKDNVGVKVTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 175 CGFSTGVGSAVMTGKVPSTC 196

RESULT 12
B90084
hypothetical protein orf419 (imported) - Guillardia theta nucleomorph
C/Species: nucleomorph Guillardia theta
A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C/Accession: B90084
R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A/Title: The highly reduced genome of an enslaved algal nucleus.
A/Reference number: A99082; MUID:11323671; PMID:11323671
A/Accession: B90084
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-419 <DOU>
A/Cross-references: GB:AF165818; NID:G13794430; PIDN:AAK39805.1; GSPDB:GN00150
C/Genetics:
A/Map position: 1
A/Genome: nucleomorph
C/Keywords: nucleomorph

Query Match 43.0%; Score 43; DB 2; Length 419;
Best Local Similarity 56.2%; Pred. No. 47;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSKDNVGVKVTSGKTC 16
| | | | | | | | | | | | | | | | | | | | | |
Db 402 CHFSKLVNGLSGSYK 417

RESULT 13
I46059
beta-1 integrin subunit - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C/Accession: I46059
R/Mactlaren, L.A.; Wildeman, A.G.
Biol. Reprod. 53, 153-165, 1995
A/Title: Fibronectin receptors in preimplantation development: cloning, expression, and
A/Reference number: I46059; MUID:55399478; PMID:7555439
A/Accession: I46059
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-773 <MAC>

A/Cross-references: EMBL:U10865; NID:G520520; PIDN:AAA80571.1; PID:G520521
C/Superfamily: integrin beta chain; laminin-type EGF-like homology

Query Match 43.0%; Score 43; DB 2; Length 773;
Best Local Similarity 38.9%; Pred. No. 85;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSKDNVGVKVTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 513 CYCRKRDNTNIEVSGKFC 530

RESULT 14
A28193
integrin beta-1 chain precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C/Accession: A28193
R/Desimone, D.W.; Hynes, R.O.
J. Biol. Chem. 263, 5333-5340, 1988
A/Title: Xenopus laevis integrins. Structural conservation and evolutionary divergence of
A/Reference number: A28193; MUID:88186829; PMID:2833505
A/Accession: A28193
A/Molecule type: mRNA
A/Residues: 1-798 <DES>
A/Cross-references: GB:M20140; NID:G214550; PIDN:AAA49889.1; PID:G214551; GB:J03736
C/Superfamily: integrin beta chain; laminin-type EGF-like homology
C/Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein

Query Match 43.0%; Score 43; DB 2; Length 798;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSKDNVGVKVTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 536 CYCKKRDNPNIEVSGKYC 553

RESULT 15
B28193
integrin beta-1* chain precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C/Accession: B28193
R/Desimone, D.W.; Hynes, R.O.
J. Biol. Chem. 263, 5333-5340, 1988
A/Title: Xenopus laevis integrins. Structural conservation and evolutionary divergence of
A/Reference number: A28193; MUID:88186829; PMID:2833505
A/Accession: B28193
A/Molecule type: mRNA
A/Residues: 1-798 <DES>
A/Cross-references: GB:M20180; NID:G214552; PIDN:AAA49890.1; PID:G214553; GB:J03736
C/Superfamily: integrin beta chain; laminin-type EGF-like homology
C/Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein

Query Match 43.0%; Score 43; DB 2; Length 798;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSKDNVGVKVTSGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 536 CYCKKRDNPNIEVSGKYC 553

Search completed: October 15, 2003, 17:06:25
Job time : 14.6886 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: October 15, 2003, 16:22:43 ; Search time 7,3294 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115a-14

Perfect score: 100

Sequence: 1 CYFSSKDNVGVKVTSGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	96.0	266	1 ETC1_STAUV	P01553 staphylococ
2	96	96.0	266	1 ETC2_STAUV	P34071 staphylococ
3	96	96.0	266	1 ETC3_STAUV	P23313 staphylococ
4	47	47.0	374	1 ADHA_HUMAN	P07327 homo sapien
5	47	47.0	374	1 ADHB_HUMAN	P00325 homo sapien
6	43	43.0	346	1 ISPH_BRUME	Q8Y1T1 bruceella me
7	43	43.0	375	1 ADH1_RANPE	P22797 rana perezi
8	43	43.0	514	1 GUXC_FUSOX	P46238 fusarium ox
9	43	43.0	773	1 ITB1_BOVIN	P53712 bos taurus
10	43	43.0	798	1 ITB0_XENLA	P53713 xenopus lae
11	43	43.0	798	1 ITB1_FELCA	P53713 felis silve
12	43	43.0	798	1 ITB1_HUMAN	P05356 homo sapien
13	43	43.0	798	1 ITB1_MOUSE	P09055 mus musculu
14	43	43.0	798	1 ITB1_XENLA	P12606 xenopus lae
15	42	42.0	368	1 ADHG_HUMAN	P28332 homo sapien
16	42	42.0	373	1 ADHS_HORSE	P00328 equus cabal
17	42	42.0	374	1 ADHE_HORSE	P00327 equus cabal
18	42	42.0	374	1 ADH_PAPPA	P14139 papio hamad
19	42	42.0	633	1 CLPX_HUMAN	O76031 homo sapien
20	42	42.0	905	1 YD83_HUMAN	O9P284 homo sapien
21	42	42.0	1170	1 TSP1_MOUSE	P35441 mus musculu
22	41	41.0	265	1 RL7A_CHICK	P32429 gallus gall
23	41	41.0	374	1 ADH1_RABIT	P00329 mus musculu
24	41	41.0	374	1 ADHA_MOUSE	P00329 mus musculu
25	41	41.0	374	1 ADHA_PERMA	P1660 peromyscus
26	41	41.0	374	1 ADHG_HUMAN	P00326 homo sapien
27	41	41.0	374	1 ADH_MACAU	P28459 macaca mula
28	41	41.0	375	1 ADHA_RAT	P28457 rattus norv
29	41	41.0	412	1 EK84_SPROF	Q26466 spodoptera
30	41	41.0	523	1 TYDS_PAPSO	P54771 papaver som
31	41	41.0	803	1 ITB1_CHICK	P07228 gallus gall
32	41	41.0	1170	1 TSP1_BOVIN	Q28178 bos taurus
33	41	41.0	1170	1 TSP1_HUMAN	P07996 homo sapien

34	40.5	40.5	1677	1 VIT_ACTIR	Q90243 acipenser t
35	40	40.0	263	1 ITWA_MOUSE	Q61500 mus musculu
36	40	40.0	350	1 SYWM_CABEL	P46579 caenorhabdi
37	40	40.0	378	1 ADHP_RABIT	O46649 cryctolagus
38	40	40.0	425	1 PYRC_FUSIN	O81988 fusobacteri
39	40	40.0	576	1 SYRM_YEAST	P32048 saccharomyc
40	40	40.0	599	1 MK67_YEAST	O99257 saccharomyc
41	40	40.0	966	1 VIL3_ARATH	O81645 arabidopsis
42	40	40.0	4660	1 LRP2_RAT	P98158 rattus norv
43	39.5	39.5	1332	1 XDH_HUMAN	P47989 homo sapien
44	39	39.0	213	1 Y864_RICPR	O92ca2 rickettsia
45	39	39.0	372	1 ADH4_RANPE	O57380 rana perezi

ALIGNMENTS

```

RESULT 1
ID ETC1_STAUV STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SBC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1] 0
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.V., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC
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CC
CC EMBL: X05815; CA29260.1; -
CC PIR: S06356; ENSACT.
CC HSSP: P34071; ISB2.
CC InterPro: IPR006177; Bcst1_tox.
CC InterPro: IPR006123; Staph/Strep_toxin.
CC InterPro: IPR006126; Staph/Strep_tox.
CC InterPro: IPR006173; Staph_tox_OB.
CC Pfam: PF02876; Staph_Strep_tox_OB.
CC Pfam: PF01123; Staph_Strep_tox_C1.
CC Pfam: PF00279; BACTR1TOXIN.
CC PRINTS: PS00279; STAPH_STREP_TOXIN_1; 1.
CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC PROSITE: PS00248; STAPH_STREP_TOXIN_2; 1.
CC Enterotoxin; Toxin; Signal; Superantigen.
CC SIGNAL
CC CHAIN 28 266 ENTEROTOXIN TYPE C-1.
CC DISULFID 120 137
CC FT 177 177
CC CONFLICT 177 177 D -> N (IN REF. 2).

```

SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;
 Query Match 96.0%; Score 96; DB 1; Length 266;
 Best Local Similarity 94.4%; Pred. No. 2.4e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 CYFSSKDNVKGVTSGKTC 18
 Db 120 CYFSSKDNVKGVTSGKTC 137
 RESULT 2
 ETC2 STAAU STANDARD; PRT; 266 AA.
 AC P3407; STAP
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN ENT2C.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 RT enterotoxins C1 and C2.";
 RL Infect. Immun. 57:2249-2252 (1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RT Staphylococcus aureus reveals a zinc-binding site.";
 RL Structure 3:769-779 (1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686 (1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=9734373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity.";
 RL J. Mol. Biol. 269:270-280 (1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC PIR; A60114; A60114.
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR PDB; 1COV; 19-SEP-01.
 DR PDB; 114Q; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph toxin OB.
 DR Pfam; PF02876; Staph_strep_tox_C1.1.

DR Pfam; PF01123; Staph Strep toxin; 1.
 DR PRINTS; PR00279; BACTR1TOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KM Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KM 3D-structure.
 FT STGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
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 FT TURN 48 48
 FT HELIX 49 55
 FT STRAND 60 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 113
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
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 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
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 Query Match 96.0%; Score 96; DB 1; Length 266;
 Best Local Similarity 94.4%; Pred. No. 2.4e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 CYFSSKDNVKGVTSGKTC 18
 Db 120 CYFSSKDNVKGVTSGKTC 137
 RESULT 3
 ETC3 STAAU STANDARD; PRT; 266 AA.
 AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN ENT3 OR SAV2009 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878, 158879, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=1418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunami H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kunata S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT sequence comparison of all three type C staphylococcal
 RT enterotoxins";
 RL Mol. Gen. Genet. 220:329-333(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=97064178; PubMed=8906797;
 RA Fields B.A., Malchodi E.L., Li H., Yeern X., Stauffer C.V.,
 RA Schlievert P.M., Karjalainen K., Martiuzza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen";
 RL Nature 384:188-192(1996).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC EMBL; AP003364; BAB58171.1; -;
 CC EMBL; AP003365; BAB43097.1; -;
 CC EMBL; X51661; CA35972.1; -;
 CC PIR; S11885; S11885.
 CC PDB; 1JCK; 12-NOV-97.
 CC PDB; 1KLG; 02-AUG-02.
 CC PDB; 1KLU; 14-AUG-02.
 CC InterPro: IPR006177; Bcst1 tox.
 CC InterPro: IPR006123; Staph/Strep toxin.
 CC InterPro: IPR006126; Staph/Strep tox.
 CC InterPro: IPR006173; Staph_tox_OB.
 CC Pfam: PF02876; Staph_Scrlp_tox_C; 1.
 CC Pfam: PF0123; Staph_Scrlp_toxin; 1.
 CC PRINTS; PR00279; BACTRTOXIN.
 CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 CC Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
 CC Complete proteome.
 CC Complete proteome.
 CC FT SIGNAL 27
 CC CHAIN 1
 CC DISUFID 120 137 ENTEROTOXIN TYPE C-3.
 CC SEQUENCE 266 AA; 30671 MW; SED8A32D1FFCA59 CRC64;
 Query Match 96.0%; Score 96; DB 1; Length 266;
 Best Local Similarity 94.4%; Prid. No. 2,4e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKVTSGKTC 18
 DB 120 CYFSSKDNVGVKVTSGKTC 137
 RESULT 4
 ID ADHA HUMAN STANDARD; PRT; 374 AA.
 AC P07327;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase alpha chain (EC 1.1.1.1).
 GN ADHA OR ADH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=86243367; PubMed=3013304;
 RA von Bahr-Lindstrom H., Hoeeg J.-O., Heden L.-O., Kaiser R.,
 RA Pleetwood L., Larsson K., Lake M., Holmquist B., Holmgren A.,
 RA Hempel J., Vallee B.L., Joernvall H.;
 RT "cDNA and protein structure for the alpha subunit of human liver
 RT alcohol dehydrogenase";
 RL Biochemistry 25:2465-2470(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120995; PubMed=2935875;
 RA Ikura T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89153548; PubMed=2920825;
 RA Matsuo Y., Yokoyama S.;
 RT "Molecular structure of the human alcohol dehydrogenase 1 gene";
 RL FEBS Lett. 243:57-60(1989).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=90269803; PubMed=2347582;
 RA Yasunari M., Kikuchi I., Sarapata D., Yoshida A.;
 RT "The human class I alcohol dehydrogenase gene cluster: three genes
 RT are tandemly organized in an 80-Kb-long segment of the genome";
 RL Genomics 7:152-158(1990).
 CC -I- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 CC NADH.
 CC -I- COFACTOR: Binds 2 zinc ions per subunit.
 CC -I- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -I- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 CC EMBL; M12271; AAA68131.1; -;
 CC EMBL; M12963; AAA51590.1; -;
 CC EMBL; M37066; AAA51591.1; -;
 CC PIR; S02265; DEHUA.

DR PDB; 1HSO; 27-APR-01.
 DR Genew; HGNC:249; ADH1A.
 DR GK; P07337; -.
 DR MIM; 103700; -.
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; NAS.
 DR GO; GO:0006066; P:alcohol metabolism; NAS.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 KM Acetylation; 3D-structure.
 FT INIT MET 0 0
 FT MOD RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 174 174 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 374 AA; 3927 MW; 5D2F5F631C4962C CRC64;
 Query Match 47.0%; Score 47; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 3.3;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CYS---SKDNVGRKTSKTC 18
 DB 174 CGESTGYGSAMVAKVTPGSTC 195
 RESULT 5
 ADHB_HUMAN STANDARD; PRT; 374 AA.
 ID ADHB_HUMAN
 AC P00325; Q13711; Q96K17;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase beta chain (EC 1.1.1.1).
 GN ADH1B OR ADH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: CDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yokoyama S., Yokoyama R., Rotwein P.;
 RT "Molecular characterization of CDNA clones encoding the human alcohol
 RT dehydrogenase beta 1 and the evolutionary relationship to the other
 RT class I subunits alpha and gamma.";
 RL Jpn. J. Genet. 62:241-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=8608371; PubMed=3000832;
 RA Heden L.O., Hoege J.-O., Larsson K., Lake M., Lagerholm E.;
 RA Holmgren A., Vallee B.L., Joernvall H., von Bahr-Lindstrom H.;
 RT "CDNA clones coding for the beta-subunit of human liver alcohol
 RT dehydrogenase have differentially sized 3'-non-coding regions.";
 RL FEBS Lett. 194:327-332(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=8611889; PubMed=2935533;
 RA Duester G., Smith W., Blanchone V., Hatfield G.W.;
 RT "Molecular analysis of the human class I alcohol dehydrogenase gene

RT family and nucleotide sequence of the gene encoding the beta
 RT subunit.";
 RL J. Biol. Chem. 261:2027-2033(1986).
 RN [5]
 RP SEQUENCE (BETA-1).
 RX MEDLINE=85076637; PubMed=6391920;
 RA Hempel J., Buhler R., Kaiser R., Holmquist B., de Zalenksi C.,
 RA von Wartburg J.-P., Vallee B.L., Joernvall H.;
 RT "Human liver alcohol dehydrogenase. 1. The primary structure of the
 RT beta 1 beta 1 isoenzyme.";
 RL Eur. J. Biochem. 145:437-445(1984).
 RN [6]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=89338401; PubMed=2547609;
 RA Matsuo Y., Yokoyama R., Yokoyama S.;
 RT "The genes for human alcohol dehydrogenases beta 1 and beta 2 differ
 RT by only one nucleotide.";
 RL Eur. J. Biochem. 183:317-320(1989).
 RN [7]
 RP SEQUENCE FROM N.A. (BETA-3).
 RC TISSUE=Liver;
 RX MEDLINE=90024225; PubMed=2679216;
 RA Carr L.G., Xu Y., Ho W.H., Edenberg H.J.;
 RT "Nucleotide sequence of the ADH2(3) gene encoding the human alcohol
 RT dehydrogenase beta 3 subunit.";
 RL Alcohol. Clin. Exp. Res. 13:594-596(1989).
 RN [8]
 RP SEQUENCE FROM N.A. (BETA-2).
 RC TISSUE=Liver;
 RA Polin L., Hey-Chi H.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88284699; PubMed=3397059;
 RA Xu Y.L., Carr L.G., Boston W.F., Li T.K., Edenberg H.J.;
 RT "Cloning of human alcohol dehydrogenases at the ADH2 and ADH3 loci
 RT following DNA sequence amplification.";
 RL Genomics 2:209-214(1988).
 RN [10]
 RP SEQUENCE OF 40-85 FROM N.A.
 RA Oster W., Speed W.C., Seaman M.I., Kidd K.K.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP VARIANT BETA-2.
 RX MEDLINE=84221897; PubMed=6374651;
 RA Joernvall H., Hempel J., Vallee B.L., Boston W.F., Li T.-K.;
 RT "Human liver alcohol dehydrogenase: amino acid substitution in the
 RT beta 2 beta 2 Oriental isoenzyme explains functional properties,
 RT establishes an active site structure, and parallels mutational
 RT exchanges in the yeast enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3024-3028(1984).
 RN [12]
 RP VARIANT BETA-3.
 RX MEDLINE=87298549; PubMed=3619918;
 RA Burnell G.C., Carr L.G., Dwyer F.E., Edenberg H.J., Li T.-K.,
 RA Boston W.F.;
 RT "The human beta 3 alcohol dehydrogenase subunit differs from beta 1
 RT by a Cys for Arg-369 substitution which decreases NAD(H) binding.";
 RL Biochem. Biophys. Res. Commun. 146:1127-1133(1987).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=91376103; PubMed=1896463;
 RA Hurley T.D., Boston W.F., Hamilton J.A., Amzel L.M.;
 RT "Structure of human beta 1 beta 1 alcohol dehydrogenase: catalytic
 RT effects of non-active-site substitutions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8149-8153(1991).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94260547; PubMed=8201622;
 RA Hurley T.D., Boston W.F., Stone C.L., Amzel L.M.;
 RT "Structures of three human beta alcohol dehydrogenase variants.
 RT Correlations with their functional differences.";
 RL J. Mol. Biol. 239:415-429(1994).

RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=96291846; PubMed=8663387;
 RA Davis G.J., Bosron W.F., Stone C.L., Onusu-Dekyi K., Hurley T.D.;
 RT "X-ray structure of human betabeta1 alcohol dehydrogenase. The
 RL contribution of ionic interactions to coenzyme binding.";
 RL J. Biol. Chem. 271:11057-11061(1996).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
 CC MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
 CC ORIENTALS.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC PI, ONE TO CLASS-III: CHL, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL: D00137; BAA00084.1; -;
 DR EMBL: X03350; CAA27056.1; -;
 DR EMBL: M24316; AAB59496.1; -;
 DR EMBL: M24308; AAB59496.1; JOINED.
 DR EMBL: M24310; AAB59496.1; JOINED.
 DR EMBL: M24311; AAB59496.1; JOINED.
 DR EMBL: M24312; AAB59496.1; JOINED.
 DR EMBL: M24313; AAB59496.1; JOINED.
 DR EMBL: M24314; AAB59496.1; JOINED.
 DR EMBL: M24317; AAB51884.1; -;
 DR EMBL: X15447; CAA33487.1; -;
 DR EMBL: X15448; CAA33487.1; JOINED.
 DR EMBL: X15449; CAA33487.1; JOINED.
 DR EMBL: X15451; CAA33487.1; JOINED.
 DR EMBL: X15452; CAA33487.1; JOINED.
 DR EMBL: X15453; CAA33487.1; JOINED.
 DR EMBL: X15454; CAA33487.1; JOINED.
 DR EMBL: X15455; CAA33487.1; JOINED.
 DR EMBL: L38290; AAB48003.1; -;
 DR EMBL: L38283; AAB48003.1; JOINED.
 DR EMBL: L38284; AAB48003.1; JOINED.
 DR EMBL: L38285; AAB48003.1; JOINED.
 DR EMBL: L38286; AAB48003.1; JOINED.
 DR EMBL: L38287; AAB48003.1; JOINED.
 DR EMBL: L38288; AAB48003.1; JOINED.
 DR EMBL: L38289; AAB48003.1; JOINED.
 DR EMBL: AP153621; AAD37446.1; -;
 DR EMBL: M21692; AAA51592.1; -;
 DR EMBL: AF040967; AAB96912.1; -;
 DR PIR: A23607; DEHUB.
 DR PDB: 1HDX; 31-JAN-94.
 DR PDB: 1HDY; 31-JAN-94.
 DR PDB: 1HDZ; 31-JAN-94.
 DR PDB: 3HJD; 31-JAN-94.
 DR PDB: 1DEH; 08-MAR-96.
 DR PDB: 1HTB; 07-DEC-95.
 DR PDB: 1HSZ; 27-APR-01.
 DR Genew; HGNC:250; ADH1B.
 DR GK; P00325; -;
 DR MIM; 103720; -;

DR GO: GO:0004024; F.alcohol dehydrogenase, zinc-dependent activity; TAS.
 DR GO: GO:0005489; F.electron transporter activity; TAS.
 DR GO: GO:0008270; F.zinc ion binding activity; TAS.
 DR GO: GO:0006069; P.ethanol oxidation; TAS.
 DR InterPro: IPR002328; ADH_zinc.
 DR InterPro: IPR002085; Adh_zn_family.
 DR Pfam: PF0107; ADH_ZINC_N; 1.
 DR PROSITE: PS00059; ADH_ZINC; 1.
 KW oxidoreductase; zinc; metal-binding; NAD; Multigene family;
 KW acetylation; polymorphism; 3d-structure.
 FT INIT MET 0 0
 FT MOD RES 1 46 ACETYLATION.
 FT METAL 46 1 ZINC 1 (CATALYTIC).
 FT METAL 64 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 Query Match 47.0%; Score 47; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 3.3;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CYFS----SKDNVGYKTSKTC 18
 DB 174 CGFSTGYGSANVAVKVPSTC 195
 RESULT 6
 ID ISPH_BRUME STANDARD; PRT; 346 AA.
 AC 08YFRL;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ISPH protein.
 GN ISPH OR LYTB OR EWEI1459.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxId=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=1175668;
 RA DelVecchio V.G., Kaputal V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Resnik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
 CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
 CC (DMAPP) (By similarity).
 CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
 CC (last) step.
 CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE009582; AAL52640.1; -;
 DR PIR: AB3434; AE3434.
 DR HAMAP: MF_00191; -; 1.
 DR InterPro: IPR003451; LytB.
 DR Pfam: PF02401; LYTB; 1.
 DR TIGRFAMs: TIGR00216; isph_lytB; 1.
 KW isoprene biosynthesis; Complete proteome.

SEQ SEQUENCE 346 AA; 37747 MW; BB9C1D60EF7421B CRC64;

Query Match 43.0%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVT 13
|:|:|:|:|
Db 161 CHFDEENLGFVT 173

RESULT 7

ADH1_RANPE STANDARD; PRT; 375 AA.
ID ADH1_RANPE
AC P22757;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alcohol dehydrogenase, major (EC 1.1.1.1).
OS Rana perezi (Perez's frog) (Western Mediterranean green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8403;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91175722; PubMed=2007119;
RA Cederlund E., Petralba J.M., Pares X., Joernvall H.;
RT "Amphibian alcohol dehydrogenase, the major frog liver enzyme.
RT Relationships to other forms and assessment of an early gene
RT duplication separating vertebrate class I and class III alcohol
RT dehydrogenases.";
RL Biochemistry 30:2811-2816(1991).
RN [2]
RP SEQUENCE OF 1-5.
RX MEDLINE=90353571; PubMed=2387402;
RA Egestad B., Estenius M., Danielsson O., Persson B., Cederlund E.,
RA Kaiser R., Holmquist B., Vallee B., Pares X., Jefferey J.,
RA Joernvall H.;
RT "Fast atom bombardment mass spectrometry and chemical analysis in
RT determinations of acyl-blocked protein structures.";
RL FEBS Lett. 269:194-196(1990).
CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
CC NADH.
CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY. MORE CLOSELY RELATED TO CLASS I MAMMALIAN ENZYMES.
DR PIR: A38405; A38405.
DR HSSP: P00325; IDEH.
DR InterPro: IPR002328; Adh_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR Pfam: PF00107; Adh_zinc_N; 1.
DR PROSITE: PS00059; Adh_ZINC; 1.
KW Oxidoreductase; Zinc; Metal-binding; NAD; Acetylation.

FT MOD_RES 1 ACETYLATION.
FT METAL 46 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 68 ZINC 2 (BY SIMILARITY).
FT METAL 98 ZINC 2 (BY SIMILARITY).
FT METAL 101 ZINC 2 (BY SIMILARITY).
FT METAL 104 ZINC 2 (BY SIMILARITY).
FT METAL 112 ZINC 2 (BY SIMILARITY).
FT METAL 175 ZINC 1 (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 375 AA; 40184 MW; 283E0A60B3339195 CRC64;

Query Match 43.0%; Score 43; DB 1; Length 375;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVKGVTSGKTC 18
|:|:|:|:|
Db 175 CGFSTGYGSANVTGKVRGSGTC 196

RESULT 8

GUXC_FUSOX STANDARD; PRT; 514 AA.
ID GUXC_FUSOX
AC P46238;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative exoglucanase type C precursor (EC 3.2.1.91)
DE (Exocelllobionhydrolyase I) (1,4-beta-celllobiohydrolase)
DE (beta-glucanocelllobiohydrolase).
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5507;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047531; PubMed=7959045;
RA Sheppard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
RA Hagen F.S., Uphall A., McKnight G.L., O'Hara P.J.;
RT "The use of conserved cellulase family-specific sequences to clone
RT cellulase homologue cDNAs from Fusarium oxysporum.";
RL Gene 150:163-167(1994).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellobiose, releasing cellobiose from the non-
CC reducing ends of the chains.
CC -1- SIMILARITY: Contains 1 fungal-type cellulose-binding (CBD) domain.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
CC HYDROLASES).

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DR EMBL: L29379; AAA5587.1; -.
DR HSSP: P00725; GCEL.
DR InterPro: IPR000254; CBD_fungal.
DR InterPro: IPR001722; Glyco_hydro_7.
DR Pfam: PF00734; CBM_1; 1.
DR Pfam: PF00840; Glyco_hydro_7; 1.
DR Prodom: PD001821; CBD_fungal; 1.
DR Prodom: PD186135; Glyco_hydro_7; 1.
DR SMART: SM00236; FCB; 1.
DR PROSITE: PS00562; CBD_FUNGAL; 1.
KW Cellulose degradation; Hydrolyase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 514
FT DOMAIN 18 439
FT DOMAIN 440 482
FT DOMAIN 483 514
FT ACT_SITE 229 229
FT ACT_SITE 234 234
FT DISULFID 486 503
FT DISULFID 497 513
FT CARBOHYD 287 287
FT CARBOHYD 490 490
SQ SEQUENCE 514 AA; 54704 MW; 6A4617323A46062 CRC64;

Query Match 43.0%; Score 43; DB 1; Length 514;
Best Local Similarity 44.4%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTSGKTC 18
|:|:|:|:|
Db 66 CYTGKMDPSICTDKTC 83

RESULT 9

ITB1_BOVIN

ID ITB1 BOVIN STANDARD; PRT; 773 AA.
AC P53712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin beta-1 (Fibronectin receptor beta subunit) (CD29)
DE (Integrin VLA-4 beta subunit) (Fragment).
GN ITGB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95399478; PubMed=7545439;
RA MacIaren L.A., Wildeman A.G.;
RT "Fibronectin receptors in preimplantation development: cloning,
RT expression, and localization of the alpha 5 and beta 1 integrin
RT subunits in bovine trophoblast";
RL Biol. Reprod. 53:153-165(1995).
CC -1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-
CC 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
CC SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
CC 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
CC FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
CC FOR VCAM1 AND RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN
CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND
CC OSTEOPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
CC CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLIGRIN
CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
CC WIDE ARRAY OF LIGANDS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
CC ALPHA-V.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOPFORM BETA-1B
CC DOES NOT LOCALIZE TO FOCAL ADHESIONS.
CC -1- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
CC BONDS.
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC -1- SIMILARITY: Contains 2 VFMA-like domains.
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CC -----
CC EMBL, UI0865; AAA80571.1; -.
CC PIR, I46059; I46059.
CC HSSP, P05106; IJV2.
CC InterPro: IPR006209; EGF like.
CC InterPro: IPR002368; Integrin_B.
CC InterPro: IPR001169; Integrin_beta_C.
CC InterPro: IPR003659; Plexin-like.
CC InterPro: IPR002035; VWF_A.
CC Pfam: PF00362; Integrin_B; 1.
CC PRINTS: PR01186; INTEGRINB.
CC ProDom: PD001811; Integrin_B; 1.
CC SMART: SM00187; INB; 1.
CC SMART: SM00423; PSI; 1.
CC SMART: SM00327; VMA; 1.
CC PROSITE, PS00243; INTEGRIN_BETA; 3.

DR PROSITE, PS0022; EGF 1; UNKNOWN 2.
KM Integrin: Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Repeat; Phosphorylation.
FT 1
FT NON_TER 1
FT DOMAIN <1 705
FT TRANSMEM 706 728
FT DOMAIN 729 >773
FT DOMAIN 117 355
FT DOMAIN 443 612
FT REPEAT 443 492
FT REPEAT 493 536
FT REPEAT 537 575
FT REPEAT 576 612
FT DISULFID 4 441
FT DISULFID 12 22
FT DISULFID 15 52
FT DISULFID 25 41
FT DISULFID 184 278
FT DISULFID 238 392
FT DISULFID 378 432
FT DISULFID 412 668
FT DISULFID 439 443
FT DISULFID 454 466
FT DISULFID 463 502
FT DISULFID 468 477
FT DISULFID 474 493
FT DISULFID 508 513
FT DISULFID 510 535
FT DISULFID 515 530
FT DISULFID 532 537
FT DISULFID 551 556
FT DISULFID 553 584
FT DISULFID 558 567
FT DISULFID 569 576
FT DISULFID 590 595
FT DISULFID 592 638
FT DISULFID 597 607
FT DISULFID 610 613
FT DISULFID 617 626
FT DISULFID 623 700
FT DISULFID 642 676
FT MOD RES 760 760
FT CARBOHYD 27 27
FT CARBOHYD 71 71
FT CARBOHYD 74 74
FT CARBOHYD 189 189
FT CARBOHYD 246 246
FT CARBOHYD 340 340
FT CARBOHYD 383 383
FT CARBOHYD 394 394
FT CARBOHYD 458 458
FT CARBOHYD 497 497
FT CARBOHYD 561 561
FT CARBOHYD 646 646
FT NON TER 773 773
SQ SEQUENCE 773 AA; 85322 MW; 54340886CE157195 CR664;
Query Match 43.0%; Score 43; DB 1; Length 773;
Best Local Similarity 38.9%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Db 1 CYPSSKDNVNGKVTSGKTC 18
519 CVCRKRDNTNLTYSGRFC 530
RESULT 10
ID ITB0 XENLA STANDARD; PRT; 798 AA.
AC P12607;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

Integrin beta-1* precursor.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodidae; Xenopus.
 NC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88186829; PubMed=2833505;
 RA Deslmones D.W., Hynes R.O.;
 RT "Xenopus laevis integrins. Structural conservation and evolutionary
 divergence of integrin beta subunits.";
 RL J. Biol. Chem. 263:5333-5340(1988).
 CC -1- FUNCTION: BETA INTEGRINS ASSOCIATE WITH ALPHA SUBUNITS TO FORM
 RECEPTOR COMPLEXES THAT RECOGNIZE THE SEQUENCE R-G-D IN A WIDE
 ARRAY OF LIGANDS (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND BETA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY. THE
 INTEGRINS BETA-1 AND BETA-1* OF XENOPUS ONLY DIFFER BY 19 AMINO
 ACIDS.
 CC -1- SIMILARITY: Contains 2 WMPA-like domains.
 CC -----
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 CC -----
 DR EMBL; M20180; AAA49890.1; -.
 DR PIR; B28193; B28193.
 DR HSSP; P05106; IUV2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002369; Integrin_B.
 DR InterPro; IPR001169; Integrin_beta_C.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002035; WMPA.
 DR Pfam; PF00362; Integrin_B; 1.
 DR PRINTS; PRO1186; INTEGRIN.
 DR ProDom; PD001811; Integrin_B; 1.
 DR SMART; SM00187; INB; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00327; VMA; 1.
 DR PROSITE; PS00243; INTEGRIN_BETA; 3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
 KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
 KW Repeat; Signal; Phosphorylation.
 FT SIGNAL 1 21
 FT CHAIN 22 798 INTEGRIN BETA-1*.
 FT DOMAIN 22 727 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 728 751 POTENTIAL.
 FT DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 139 377 WMPA-LIKE.
 FT DOMAIN 466 635 4 CYSTEINE-RICH TANDEM REPEATS.
 FT REPEAT 466 515 I.
 FT REPEAT 516 559 II.
 FT REPEAT 560 598 III.
 FT REPEAT 599 635 IV.
 FT DISULFID 28 464 BY SIMILARITY.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 39 76 BY SIMILARITY.
 FT DISULFID 206 212 BY SIMILARITY.
 FT DISULFID 260 300 BY SIMILARITY.
 FT DISULFID 400 414 BY SIMILARITY.
 FT DISULFID 434 691 BY SIMILARITY.
 FT DISULFID 462 466 BY SIMILARITY.
 FT DISULFID 477 489 BY SIMILARITY.
 FT DISULFID 486 525 BY SIMILARITY.
 FT DISULFID 491 500 BY SIMILARITY.
 FT DISULFID 502 516 BY SIMILARITY.

FT DISULFID 531 536 BY SIMILARITY.
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 FT DISULFID 555 560 BY SIMILARITY.
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 FT DISULFID 576 607 BY SIMILARITY.
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 FT DISULFID 592 599 BY SIMILARITY.
 FT DISULFID 613 618 BY SIMILARITY.
 FT DISULFID 615 661 BY SIMILARITY.
 FT DISULFID 620 630 BY SIMILARITY.
 FT DISULFID 633 636 BY SIMILARITY.
 FT DISULFID 640 649 BY SIMILARITY.
 FT DISULFID 646 723 BY SIMILARITY.
 FT DISULFID 665 699 BY SIMILARITY.
 FT MOD RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 798 AA; 88303 MW; 1AC45EA3711CFC7 CRC64;
 Query Match 43.0%; Score 43; DB 1; Length 798;
 Best local Similarity 44.4%; Pred. No. 31;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 CYSSKDNNGKVTSGKTC 18
 Db 536 CVCCKRDNPNEYSGKXC 553
 ID IDTBL_FELCA STANDARD; PRT; 798 AA.
 AC P53713;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integrin beta-1 precursor (fibronectin receptor beta subunit)
 DE (CD29) (Integrin VLA-4 beta subunit).
 GN ITGB1.
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 CC NCB1_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Williet B.J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-
 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
 SEQUENCE G-P-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
 FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
 THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
 CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
 ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
 ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
 FOR VCAM1 AND RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN
 ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND
 OSTEOPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-I IN
 CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLIGGIN
 AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
 VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A

CC WIDE ARRAY OF LIGANDS.
 CC -1 SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
 CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
 CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
 CC ALPHA-V.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 CC -1 SIMILARITY: Contains 2 VFMA-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U27351; AAC19407.1; -.
 CC HSSP; P05106; 1JY2.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR002369; Integrin_B.
 DR InterPro: IPR001169; Integrin_beta_C.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam; PF00362; Integrin_B; 1.
 DR PRINTS; PR01186; INTEGRINB.
 DR ProDom; PD001811; Integrin_B; 1.
 DR SMART; SM00187; INB; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00327; VMA; 1.
 DR PROSITE; PS00243; INTEGRIN BETA; 3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN 2.
 KM Integrin. Cell adhesion. Receptor; Transmembrane; Glycoprotein;
 KM Repeat; Signal; Phosphorylation.
 FT SIGNAL 1 20
 FT CHAIN 1 798
 FT DOMAIN 21 728
 FT TRANSMEM 729 751
 FT DOMAIN 752 798
 FT DOMAIN 140 378
 FT DOMAIN 466 635
 FT REPEAT 466 515
 FT REPEAT 516 559
 FT REPEAT 560 598
 FT REPEAT 599 635
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 FT DISULFID 35 45
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 FT DISULFID 48 64
 FT DISULFID 207 213
 FT DISULFID 261 301
 FT DISULFID 401 415
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 FT DISULFID 462 466
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 FT DISULFID 491 500
 FT DISULFID 502 516
 FT DISULFID 531 536
 FT DISULFID 533 568
 FT DISULFID 538 553
 FT DISULFID 555 560
 FT DISULFID 574 579
 FT DISULFID 576 607
 FT DISULFID 581 590
 FT DISULFID 592 599
 FT DISULFID 613 618
 FT DISULFID 615 661
 FT DISULFID 620 630
 FT DISULFID 633 636
 FT DISULFID 640 649
 FT DISULFID 646 723
 FT DISULFID 665 699

FT MOD RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 798 AA; 88092 MW; 2A1C38771046D838 CRC64;
 Query Match 43.0%; Score 43; DB 1; Length 798;
 Best Local Similarity 38.9%; Pred. No. 31;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Db 536 CVCRRKDNINIEYSGKFC 553
 QY 1 CYFSSKDNVKGVTSGKTC 18
 DB 536 CVCRRKDNINIEYSGKFC 553
 RESULT 12
 ITB1_HUMAN STANDARD; PRT; 798 AA.
 ID ITB1_HUMAN
 AC P05556; P78466; P78467; Q13089; Q13090; Q13091; Q13212; Q14622;
 AC Q14647;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Integrin beta-1 precursor (fibronectin receptor beta subunit)
 DE (CD29 antigen) (Integrin VLA-4 beta subunit).
 DE ITB1 OR FNRI.
 GN ITB1 OR FNRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA-1A).
 RC TISSUE=Placenta;
 RX MEDLINE=88007843; PubMed=2958481;
 RA Argaves W.S., Suzuki S., Arai H., Thompson K., Pierschbacher M.D.,
 RA Ruoslahti E.;
 RT "Amino acid sequence of the human fibronectin receptor.";
 RL J. Cell Biol. 105:1183-1190(1987).
 RN [2]
 RP SEQUENCE OF 717-757 FROM N.A., AND CHARACTERIZATION OF BETA-1B.
 RX MEDLINE=93209984; PubMed=7681433;
 RA Balzac F., Belkin A.M., Koteliensky V.E., Balabanov Y.V., Altruda F.,
 RA Silengo L., Tarone G.;
 RT "Expression and functional analysis of a cytoplasmic domain variant of
 RT the beta 1 integrin subunit.";
 RL J. Cell Biol. 121:171-178(1993).
 RN [3]
 RP SEQUENCE OF 717-757 FROM N.A., AND FUNCTION.
 RX MEDLINE=95014744; PubMed=7523423;
 RA Balzac F., Recta S.F., Albini A., Melchiorri A., Koteliensky V.E.,
 RA Geuna M., Silengo L., Tarone G.;
 RT "Expression of beta 1B integrin isoform in CHO cells results in a
 RT dominant negative effect on cell adhesion and motility.";
 RL J. Cell Biol. 127:557-565(1994).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A; BETA-1B; BETA-1C AND
 RP BETA-1D).
 RC TISSUE=skeletal muscle;
 RX MEDLINE=95398646; PubMed=7545396;
 RA Zhidkova N.I., Belkin A.M., Mayne R.;
 RT "Novel isoform of beta 1 integrin expressed in skeletal and cardiac
 RT muscle.";
 RL Biochem. Biophys. Res. Commun. 214:279-285(1995).
 RN [5]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1B).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=91065539; PubMed=22494978;
 RA Altrendo F., Cervella F., Tarone G., Botta C., Balzac F., Stefanuto G.,
 RA Siliengo L.;
 RA "A human integrin beta 1 subunit with a unique cytoplasmic domain
 RT generated by alternative mRNA processing";
 RL Gene 95:261-266(1990).
 RM [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1D).
 RC MEDLINE=95377431; PubMed=7544296;
 RA van der Flier A., Kuikman I., Bauduin C., van der Neut R.,
 RA Sonnenberg A.;
 RA "A novel beta 1 integrin isoform produced by alternative splicing:
 RT unique expression in cardiac and skeletal muscle";
 RL FEBS Lett. 369:340-344(1995).
 RM [7]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A AND BETA-1C).
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=92202279; PubMed=1551917;
 RA Languino L.R., Ruoslahti E.;
 RA "An alternative form of the integrin beta 1 subunit with a variant
 RT cytoplasmic domain";
 RL J. Biol. Chem. 267:7116-7120(1992).
 RM [8]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1C-2).
 RX MEDLINE=98161805; PubMed=944094;
 RA Svineng G., Faessler R., Johansson S.;
 RA "Identification of beta1C-2, a novel variant of the integrin beta1
 RT subunit generated by utilization of an alternative splice acceptor
 site in exon C";
 RL Biochem. J. 330:1255-1263(1998).
 RM [9]
 CC -1- FUNCTION: INTERINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-
 CC 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTERINS ALPHA
 CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
 CC SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTERINS ALPHA-2/BETA-1, ALPHA-
 CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
 CC 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
 CC FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
 CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
 CC INTERLIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
 CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
 CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
 CC FOR VCAM1. IT RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN
 CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOACTIN AND
 CC OSTEOPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
 CC CYTOACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLIGRIN
 CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
 CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
 CC WIDE ARRAY OF LIGANDS. ISOFORM BETA-1B INTERFERES WITH ISOFORM
 CC BETA-1A RESULTING IN A DOMINANT NEGATIVE EFFECT ON CELL ADHESION
 CC AND MIGRATION (IN VITRO).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
 CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
 CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
 CC ALPHA-V.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM BETA-1B
 CC DOES NOT LOCALIZE TO FOCAL ADHESIONS.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=Beta-1A;
 CC IsoId=P05556-1; Sequence=Displayed;
 CC Name=Beta-1B;
 CC IsoId=P05556-2; Sequence=VSP_002741;
 CC Name=Beta-1C;
 CC IsoId=P05556-3; Sequence=VSP_002742;
 CC Name=Beta-1C-2;
 CC IsoId=P05556-4; Sequence=VSP_002743;
 CC Name=Beta-1D;
 CC IsoId=P05556-5; Sequence=VSP_002744;
 CC -1- TISSUE SPECIFICITY: ISOFORM BETA-1A IS WIDELY EXPRESSED, OTHER
 CC ISOFORMS ARE GENERALLY COEXPRESSED WITH A MORE RESTRICTED
 CC DISTRIBUTION. ISOFORM BETA-1B IS EXPRESSED IN SKIN, LIVER,

CC	SKELETAL MUSCLE, CARDIAC MUSCLE, PLACENTA, UMBILICAL VEIN
CC	ENDOTHELIAL CELLS, NEUROBLASTOMA CELLS, LYMPHOMA CELLS, HEPATOMA
CC	CELLS AND ASTROCYTOMA CELLS. ISOFORMS BETA-1C AND BETA-1C-2 ARE
CC	EXPRESSED IN MUSCLE, KIDNEY, LIVER, PLACENTA, CERVICAL EPITHELIUM,
CC	UMBILICAL VEIN ENDOTHELIAL CELLS, FIBROBLAST CELLS, EMBRYONAL
CC	KIDNEY CELLS, PLATELETS AND SEVERAL BLOOD CELL LINES. ISOFORM
CC	BETA-C-2, RATHER THAN ISOFORM BETA-1C, IS SELECTIVELY EXPRESSED IN
CC	PRIMARY T-CELLS. ISOFORM BETA-1C IS EXPRESSED IN NONPROLIFERATING
CC	AND DIFFERENTIATED PROSTATE GLAND EPITHELIAL CELLS. ISOFORM BETA-
CC	1D IS EXPRESSED SPECIFICALLY IN STRATIFIED MUSCLE (SKELETAL AND
CC	CARDIAC MUSCLE).
CC	- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC	-1- SIMILARITY: Contains 2 WFWA-like domains.
CC	-1- DATABASE: NAME=PROV; NOTE=CD guide CD29 entry;
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd29.htm".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X07979; CAA30790.1; --
DR	EMBL; U33882; AAA79835.1; --
DR	EMBL; U33879; AAA79835.1; JOINED.
DR	EMBL; M84237; AAA74402.1; --
DR	EMBL; U33879; AAA79832.1; --
DR	EMBL; M34189; AAA59182.1; --
DR	EMBL; U33880; AAA79833.1; --
DR	EMBL; U33879; AAA79833.1; JOINED.
DR	EMBL; U28257; AAA81366.1; --
DR	EMBL; U33882; AAA79834.1; --
DR	EMBL; U33879; AAA79834.1; JOINED.
DR	EMBL; U33881; AAA79834.1; JOINED.
DR	EMBL; M84237; AAA74403.1; --
DR	PDB; 1K11; 20-MAR-02.
DR	GeneW; HGNC:6153; ITGB1.
DR	MIM; 135630; --
DR	GO; GO:0004895; F:cell adhesion receptor activity; TAS.
DR	GO; GO:0005515; F:protein binding activity; IPI.
DR	GO; GO:0006968; P:cellular defense response; TAS.
DR	GO:0007156; P:homophilic cell adhesion; TAS.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR002369; Integrin_B.
DR	InterPro; IPR001169; Integrin_beta_C.
DR	Pfam; PF00362; Integrin_B_1.
DR	PRINTS; PR01186; INTEGRINB.
DR	Prodont; PD001811; Integrin_B; 1.
DR	PROSITE; PS00243; INTEGRIN_BETA_3.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_2.
KM	Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW	Repeat; Signal; Phosphorylation; Alternative splicing; 3D-structure.
FT	SIGNAL 1 20
FT	CHAIN 21 798 INTEGRIN BETA-1.
FT	DOMAIN 21 728 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 729 751 POTENTIAL.
FT	DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 140 378 WFWA-LIKE.
FT	DOMAIN 466 635 4 Cysteine-rich tandem repeats.
FT	REPEAT 466 515 1.
FT	REPEAT 516 559 II.
FT	REPEAT 560 598 III.
FT	REPEAT 599 635 IV.
FT	DISELTD 27 464 BY SIMILARITY.
FT	DISELTD 35 45 BY SIMILARITY.
FT	DISELTD 38 75 BY SIMILARITY.
FT	DISELTD 48 64 BY SIMILARITY.
FT	DISELTD 207 213 BY SIMILARITY.
FT	DISELTD 301 301 BY SIMILARITY.
FT	DISELTD 401 415 BY SIMILARITY.
FT	DISELTD 435 691 BY SIMILARITY.

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FT DISULFID 462 466 BY SIMILARITY.
FT DISULFID 477 489 BY SIMILARITY.
FT DISULFID 486 525 BY SIMILARITY.
FT DISULFID 491 500 BY SIMILARITY.
FT DISULFID 502 516 BY SIMILARITY.
FT DISULFID 531 536 BY SIMILARITY.
FT DISULFID 533 568 BY SIMILARITY.

Query Match 43.0%; Score 43; DB 1; Length 798;
Best Local Similarity 38.9%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVGVTSKRTC 18
Db 536 CYCRKRDNTNEISGKFC 553

RESULT 13
ITBL MOUSE STANDARD; PRT; 798 AA.
ID ITBL MOUSE
AC P09055;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin beta-1 precursor (Fibronectin receptor beta subunit)
DE (CD29 antigen) (Integrin VLA-4 beta subunit).
GN ITGB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1] TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=89005707; PubMed=3262537;
RA Tomioka S.;
RT "Murine mRNA for the beta-subunit of integrin is increased in
RT BALB/c-3T3 cells entering the G1 phase from the G0 state.";
RL FEBS Lett. 238:315-319(1988).
RN [2]
RP SEQUENCE OF 2-798 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=89235580; PubMed=2523953;
RA Holers V.M., Ruff T.G., Parke D.L., McDonald J.A., Ballard L.L.,
RA Brown E.J.;
RT "Molecular cloning of a murine fibronectin receptor and its
RT expression during inflammation. Expression of VLA-5 is increased in
RT activated peritoneal macrophages in a manner discordant from major
RT histocompatibility complex class II.";
RL J. Exp. Med. 169:1589-1605(1989).
CC -1- FUNCTION: INTEGRIN ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-
CC 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRIN ALPHA-
CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
CC SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRIN ALPHA-2/BETA-1, ALPHA-
CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
CC 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
CC FIBONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBONECTIN.
CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
CC FOR VCAM1 AND RECOGNIZES THE SEQUENCE O-I-D-S IN VCAM1. INTEGRIN
CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOACTIN AND
CC OSTROPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
CC CYTOACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLIGRIN
CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
CC WIDE ARRAY OF LIGANDS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
CC ALPHA-V.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

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CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC -1- SIMILARITY: Contains 2 WFPA-like domains.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@sib-sib.ch).
-----
CC EMBL; Y00769; CAA68738.1; -.
DR EMBL; X15202; CAA33272.1; -.
DR PIR; P0104; IUMSPB.
DR PIR; S01659; S01659.
DR HSSP; P05106; 1U72.
DR WGI; WGI96610; Itgb1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00362; Integrin_B; 1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00243; INTEGRIN_BETA; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat; Signal; Phosphorylation.
FT CHAIN 1 20
FT DOMAIN 21 798 INTEGRIN BETA-1.
FT TRANSMEM 729 751 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 752 798 POTENTIAL.
FT DOMAIN 140 378 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 466 635 WFPA-LIKE.
FT REPEAT 466 515 4 CYSTEINE-RICH TANDEN REPEATS.
FT REPEAT 516 559 I.
FT REPEAT 560 598 II.
FT REPEAT 599 635 III.
FT DISULFID 27 464 BY SIMILARITY.
FT DISULFID 35 45 BY SIMILARITY.
FT DISULFID 38 75 BY SIMILARITY.
FT DISULFID 48 64 BY SIMILARITY.
FT DISULFID 204 213 BY SIMILARITY.
FT DISULFID 261 301 BY SIMILARITY.
FT DISULFID 401 415 BY SIMILARITY.
FT DISULFID 435 691 BY SIMILARITY.
FT DISULFID 462 466 BY SIMILARITY.
FT DISULFID 477 489 BY SIMILARITY.
FT DISULFID 486 525 BY SIMILARITY.
FT DISULFID 491 500 BY SIMILARITY.
FT DISULFID 502 516 BY SIMILARITY.
FT DISULFID 531 536 BY SIMILARITY.
FT DISULFID 533 568 BY SIMILARITY.
FT DISULFID 538 553 BY SIMILARITY.
FT DISULFID 555 560 BY SIMILARITY.
FT DISULFID 574 579 BY SIMILARITY.
FT DISULFID 576 607 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT DISULFID 592 599 BY SIMILARITY.
FT DISULFID 613 618 BY SIMILARITY.
FT DISULFID 615 661 BY SIMILARITY.
FT DISULFID 620 630 BY SIMILARITY.
FT DISULFID 633 636 BY SIMILARITY.
FT DISULFID 640 649 BY SIMILARITY.
FT DISULFID 646 723 BY SIMILARITY.
FT DISULFID 665 699 BY SIMILARITY.
FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
FT CARBOHYD 50 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 385 385 E -> P (IN REF. 2).
FT CONFLICT 392 392 G -> A (IN REF. 2).
FT CONFLICT 443 445 IKI -> HSKL (IN REF. 2).
SQ SEQUENCE 798 AA; 88231 MW; 26788F7F0A168B56 CRC64;

Query Match 43.0%; Score 43; DB 1; Length 798;
Best Local Similarity 38.9%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGYTSGKTC 18
Db 536 CVCKKRDNNEVYSGKTC 553

RESULT 14
ITBL_XENLA STANDARD; PRT; 798 AA.
AC P12606;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin beta-1 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=88186829; PubMed=2833505;
RA Desimone D.W., Hynes R.O.;
RT "Xenopus laevis integrins. Structural conservation and evolutionary
divergence of integrin beta subunits."
RL J. Biol. Chem. 263:5333-5340(1988).
CC -1- FUNCTION: BETA INTEGRINS ASSOCIATE WITH ALPHA SUBUNITS TO FORM
RECEPTOR COMPLEXES THAT RECOGNIZE THE SEQUENCE R-G-D IN A WIDE
ARRAY OF LIGANDS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND BETA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY. THE
INTEGRINS BETA-1 AND BETA-1* OF XENOPUS ONLY DIFFER BY 19 AMINO
ACIDS.
CC -1- SIMILARITY: Contains 2 WFPA-like domains.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M20140; AAA9889.1; -.
CC PIR: A28193; A28193.
CC HSSP: P05106; JUV2.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR002369; Integrin B.
DR InterPro: IPR001169; Integrin_beta_C.
DR InterPro: IPR003659; plexin-like.
DR InterPro: IPR002035; WVF A.
DR Pfam: PF00362; Integrin_B_1.
DR PRINTS: PRO1186; INTEGRINB.
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DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00243; INTEGRIN_BETA_3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
KW Integrin; Cell Adhesion; Receptor; Transmembrane; Glycoprotein;
FT CHAIN 1 21
FT SIGNAL 22 798
FT DOMAIN 22 727 INTEGRIN_BETA-1.
FT TRANSMEM 728 751 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 752 798 POTENTIAL.
FT DOMAIN 139 377 CYTOPLASMIC (POTENTIAL).
FT REPEAT 466 635 WFPA-LIKE.
FT REPEAT 466 515 4 CYSTEINE-RICH TANDEN REPEATS.
FT REPEAT 516 559 I.
FT REPEAT 560 598 II.
FT REPEAT 599 635 III.
FT DISULFID 28 464 IV.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 39 76 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 206 212 BY SIMILARITY.
FT DISULFID 260 300 BY SIMILARITY.
FT DISULFID 400 414 BY SIMILARITY.
FT DISULFID 434 691 BY SIMILARITY.
FT DISULFID 462 466 BY SIMILARITY.
FT DISULFID 477 489 BY SIMILARITY.
FT DISULFID 486 525 BY SIMILARITY.
FT DISULFID 491 500 BY SIMILARITY.
FT DISULFID 502 516 BY SIMILARITY.
FT DISULFID 531 536 BY SIMILARITY.
FT DISULFID 533 568 BY SIMILARITY.
FT DISULFID 538 553 BY SIMILARITY.
FT DISULFID 555 560 BY SIMILARITY.
FT DISULFID 574 579 BY SIMILARITY.
FT DISULFID 576 607 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT DISULFID 592 599 BY SIMILARITY.
FT DISULFID 613 618 BY SIMILARITY.
FT DISULFID 615 661 BY SIMILARITY.
FT DISULFID 620 630 BY SIMILARITY.
FT DISULFID 633 636 BY SIMILARITY.
FT DISULFID 640* 649 BY SIMILARITY.
FT DISULFID 646 723 BY SIMILARITY.
FT DISULFID 665 699 BY SIMILARITY.
FT MOD RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 416 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 798 AA; 88167 MW; 093522509298531 CRC64;

Query Match 43.0%; Score 43; DB 1; Length 798;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGYTSGKTC 18
Db 536 CVCKKRDNNEVYSGKTC 553

RESULT 15
ADH6_HUMAN STANDARD; PRT; 368 AA.
ID ADH6_HUMAN
```

Db 181 FGAINTAKVTGSGTC 196
Search completed: October 15, 2003, 16:58:17
Job time : 8.42934 secs

AC P28332;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alcohol dehydrogenase 6 (EC 1.1.1.1).
GN ADH6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91352038; PubMed=1881901;
RA Yasunami M., Chen C.-S., Yoshida A.;
RT "A human alcohol dehydrogenase gene (ADH6) encoding an additional
RT class of isozyme.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:7610-7614(1991).
CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
CC NADH.
CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: STOMACH AND LIVER.
CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
CC PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
CC CLASS-V: ADH6
CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
CC -----
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CC -----
DR EMBL: M84402; AAA35509.1; -;
DR EMBL: M84403; AAA35509.1; JOINED.
DR EMBL: M84404; AAA35509.1; JOINED.
DR EMBL: M84405; AAA35509.1; JOINED.
DR EMBL: M84406; AAA35509.1; JOINED.
DR EMBL: M84407; AAA35509.1; JOINED.
DR EMBL: M84408; AAA35509.1; JOINED.
DR EMBL: M84409; AAA35509.1; JOINED.
DR PIR: A41274; DEHUA6.
DR HSSP: P00327; 2OHX.
DR GeneW; HGNC:255; ADH6.
DR GK; P28332; -;
DR MTM; 103735; -;
DR GO; GO:0005489; F:electron transporter activity; TAS.
DR GO; GO:0006069; P:ethanol oxidation; TAS.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family.
FT METAL 47
FT METAL 47
FT METAL 69
FT METAL 69
FT METAL 99
FT METAL 99
FT METAL 102
FT METAL 102
FT METAL 105
FT METAL 105
FT METAL 113
FT METAL 113
FT METAL 175
FT METAL 175
SQ SEQUENCE 368 AA; 39072 MW; EC8E81E9571E6241 CRC64;
Query Match 42.0%; Score 42; DB 1; Length 368;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGSGTC 18
| : | | | | |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-14
Perfect score: 100
Sequence: 1 CYFSSKDNVGVKTSKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	239	2	006535	006535 staphylococ
2	96	96.0	234	2 09R5X4	09R5X4 staphylococ
3	96	96.0	239	2 005157	005157 staphylococ
4	96	96.0	239	2 053678	053678 staphylococ
5	96	96.0	239	2 006532	006532 staphylococ
6	96	96.0	239	2 006531	006531 staphylococ
7	96	96.0	239	2 006533	006533 staphylococ
8	96	96.0	266	16 08NXJ6	08NXJ6 staphylococ
9	96	96.0	271	2 09FOL6	09FOL6 staphylococ
10	87	87.0	239	2 006534	006534 staphylococ
11	51	51.0	2108	5 0815C7	0815C7 plasmodium
12	49	49.0	511	16 08RI66	08RI66 fusobacteri
13	47	47.0	269	6 08MNS3	08MNS3 gorilla gor
14	46	46.0	299	10 08LAK6	08LAK6 arabidopsis
15	46	46.0	368	5 09XXJ6	09XXJ6 caenorhabdi
16	46	46.0	2301	5 095281	095281 cikopleura

17	45.5	45.5	457	12 09YQ21	09YQ21 ranid herpe
18	45	45.0	375	10 09STR7	09STR7 arabidopsis
19	45	45.0	214	10 093VK9	093VK9 arabidopsis
20	44.5	44.5	217	5 08SUN0	08SUN0 encephalico
21	44.5	44.5	1102	10 09ZVE4	09ZVE4 arabidopsis
22	44	44.0	217	5 09V7M7	09V7M7 dirosophila
23	44	44.0	765	5 026018	026018 plasmodium
24	44	44.0	765	5 08IXT6	08IXT6 plasmodium
25	43	43.0	1022	5 09W3E1	09W3E1 dirosophila
26	43	43.0	161	17 08TLN3	08TLN3 methanobarc
27	43	43.0	372	16 08G2S7	08G2S7 bruceella su
28	43	43.0	377	11 09QY79	09QY79 mus musculu
29	43	43.0	419	10 09BR25	09BR25 guillardia
30	43	43.0	504	11 08BVU1	08BVU1 mus musculu
31	43	43.0	648	10 08S5G6	08S5G6 oryza sativ
32	43	43.0	798	4 08WUM6	08WUM6 homo sapien
33	43	43.0	798	6 09GLP0	09GLP0 bos taurus
34	43	43.0	798	6 08SQC0	08SQC0 bos taurus
35	43	43.0	798	11 08BTU0	08BTU0 mus musculu
36	43	43.0	822	16 08EUA6	08EUA6 mycoplasma
37	43	43.0	1064	16 08XK16	08XK16 clostridium
38	42.5	42.5	142	16 08SES9	08SES9 oceanobacil
39	42	42.0	148	16 08DRX5	08DRX5 streptococc
40	42	42.0	219	4 09ULY5	09ULY5 homo sapien
41	42	42.0	224	8 09Z2S7	09Z2S7 ceratocolen
42	42	42.0	295	4 08IUN7	08IUN7 homo sapien
43	42	42.0	533	4 09H072	09H072 homo sapien
44	42	42.0	588	13 08JG67	08JG67 xenopus lae
45	42	42.0	1171	11 08CGB2	08CGB2 mus musculu

ALIGNMENTS

RESULT 1	006535	PRELIMINARY:	PRT;	239 AA.
ID	006535			
AC	006535			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Enterotoxin (Fragment).			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FRI 909;			
RX	MEDLINE=94011313; PubMed=8406814;			
RA	Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;			
RT	"Characterization of novel type C staphylococcal enterotoxins:			
RT	biological and evolutionary implications.";			
RL	Infect. Immun. 61:4254-4262(1993).			
DR	EMBL; L13377; AAA26621.1; -.			
DR	HSSP; P23313; JUCK.			
DR	InterPro: IPR006177; Bctr1 tox.			
DR	InterPro: IPR006123; Staph/Strep_toxin.			
DR	InterPro: IPR006126; Staph/Strep_tox.			
DR	Pfam; PF01123; Staph_strep_toxin; 1.			
DR	Pfam; PF02876; Staph_strep_tox C; 1.			
DR	PRINTS; PR00279; BACTRTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
FT	NON_TER			
SQ	SEQUENCE	239 AA;	27648 MW;	CC3CB3B04E4119E0 CRC64;
Query Match		100.0%;	Score 100;	DB 2; Length 239;
Best Local Similarity		100.0%;	Pred. No. 2.7e-08;	
Matches	18;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
Qy	1	CYFSSKDNVGVKTSKTC 18		

```
Db          93  CYFSSKDNVGVKVTGKTC 110

RESULT 2
Q9RSX4      PRELIMINARY;      PRT;      234 AA.
ID  Q9RSX4
AC  Q9RSX4;
DT  01-MAY-2000 (TREMblrel. 13, Created)
DT  01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS  Staphylococcus.
OC  Bacteria; Firmicutes; Bacillales.
OX  NCBI_TaxID=1279;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=94325995; Pubmed=8049778;
RA  Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL  Mol. Phylogenet. Evol. 2:281-292(1993).
DR  HSP: P34071; ISE2.
DR  InterPro: IPR006177; Bactrl_tox.
DR  InterPro: IPR006123; Staph/Strep_toxin.
DR  InterPro: IPR006126; Staph/Strep_tox.
DR  InterPro: IPR006173; Staph_tox_OB.
DR  Pfam: PF01123; Staph_Strep_toxin; 1.
DR  PRINTS: PR00279; BACTRLTOXIN.
DR  PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR  PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT  NON_TER 1
SQ  SEQUENCE 234 AA; 27122 MW; D6A7B45FB981052 CRC64;

Query Match          96.0%; Score 96; DB 2; Length 234;
Best Local Similarity 94.4%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  CYFSSKDNVGVKVTGKTC 18
Db          88  CYFSSKDNVGVKVTGKTC 105

RESULT 3
Q005157     PRELIMINARY;      PRT;      239 AA.
ID  Q005157
AC  Q005157;
DT  01-JUL-1997 (TREMblrel. 04, Created)
DT  01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  Type C enterotoxin (Fragment).
OS  Staphylococcus intermedius.
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=1285;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=95-011195;
RA  Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA  Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
RT  "Characterization of the type C enterotoxin (SEC-canine) produced by
RT  Staphylococcus intermedius pyoderma isolates."
RL  Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
DR  EMBL: U91526; AAB50248.1; -.
DR  HSP: P23313; IYCK.
DR  InterPro: IPR006177; Bactrl_tox.
DR  InterPro: IPR006123; Staph/Strep_toxin.
DR  InterPro: IPR006126; Staph/Strep_tox.
DR  InterPro: IPR006173; Staph_tox_OB.
DR  Pfam: PF01123; Staph_Strep_toxin; 1.
DR  Pfam: PF02876; Staph_Strep_tox_C; 1.
DR  PRINTS: PR00279; BACTRLTOXIN.
DR  PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR  PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT  NON_TER 1
SQ  SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;
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SQ  SEQUENCE 239 AA; 27536 MW; D66064460DE4191 CRC64;

Query Match          96.0%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  CYFSSKDNVGVKVTGKTC 18
Db          93  CYFSSKDNVGVKVTGKTC 110

RESULT 4
Q053678     PRELIMINARY;      PRT;      239 AA.
ID  Q053678
AC  Q053678;
DT  01-NOV-1996 (TREMblrel. 01, Created)
DT  01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  Enterotoxin (Fragment).
OS  Staphylococcus aureus.
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=1280;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=94011313; Pubmed=8406814;
RA  Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT  "Characterization of novel type C staphylococcal enterotoxins:
RT  biological and evolutionary implications."
RL  Infect. Immun. 61:4254-4262(1993).
DR  EMBL: L13376; AAA26620.1; -.
DR  HSP: P34071; ISE2.
DR  InterPro: IPR006177; Bactrl_tox.
DR  InterPro: IPR006123; Staph/Strep_toxin.
DR  InterPro: IPR006126; Staph/Strep_tox.
DR  InterPro: IPR006173; Staph_tox_OB.
DR  Pfam: PF01123; Staph_Strep_toxin; 1.
DR  Pfam: PF02876; Staph_Strep_tox_C; 1.
DR  PRINTS: PR00279; BACTRLTOXIN.
DR  PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR  PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT  NON_TER 1
SQ  SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match          96.0%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  CYFSSKDNVGVKVTGKTC 18
Db          93  CYFSSKDNVGVKVTGKTC 110

RESULT 5
Q06532      PRELIMINARY;      PRT;      239 AA.
ID  Q06532
AC  Q06532;
DT  01-NOV-1996 (TREMblrel. 01, Created)
DT  01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  Enterotoxin (Fragment).
OS  Staphylococcus aureus.
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=1280;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=740N;
RX  MEDLINE=94011313; Pubmed=8406814;
RA  Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT  "Characterization of novel type C staphylococcal enterotoxins:
RT  biological and evolutionary implications."
RL  Infect. Immun. 61:4254-4262(1993).
DR  EMBL: L13375; AAA26619.1; -.
DR  HSP: P34071; ISE2.
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DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 96.0%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 6
Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Mair J.C., Lyon J.D., Roberson J.R., Lupter M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL: L13374; AAA26618.1; -.
DR HSSP: P34071; 1STE2.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 96.0%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 7
Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
```

```
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCPoland;
RX MEDLINE=94011313; PubMed=8406814;
RA Mair J.C., Lyon J.D., Roberson J.R., Lupter M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL: L13378; AAA26622.1; -.
DR HSSP: P34071; 1STE.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386A8B825 CRC64;

Query Match 96.0%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 8
Q08XJ6 PRELIMINARY; PRT; 266 AA.
AC Q08XJ6;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94624.1; -.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 96.0%; Score 96; DB 16; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 120 CYFSSKDNVGVKVTGKTC 137
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RESULT 9
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AC Q9F0L6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DE Staphylococcus aureus enterotoxin C-bovine.
GN Sec-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens";
RU J. Bacteriol. 183:63-70 (2001).
DR EMBL; AF217235; AAC29599.1; -.
DR HSP; P34071; ISE2.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 3167 MW; 3493F628B042F10 CRC64;

Query Match 96.0%; Score 96; DB 2; Length 271;
Best Local Similarity 94.4%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYPSSKDNVGVKVTSGKTC 18
DB 125 CYPSSKDNVGVKVTSGKTC 142

RESULT 10
Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Mart J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RU Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13379; AAA26623.1; -.
DR HSP; P34071; ISE2.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

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FT NON TER 1 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 87.0%; Score 87; DB 2; Length 239;
Best Local Similarity 88.9%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYPSSKDNVGVKVTSGKTC 18
DB 93 CYPSSKDNVGVKVTSGKTC 110

RESULT 11
Q8I5C7 PRELIMINARY; PRT; 2108 AA.
AC Q8I5C7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DE Hypothetical protein.
GN Pfl1410C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3D7;
RX MEDLINE=2225705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angioli S.,
RA Barta M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlair L.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RU Nature 419:498-511 (2002).
DR EMBL; AE014848; AAN36368.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2108 AA; 248300 MW; 2B0464D22291B2D9 CRC64;

Query Match 51.0%; Score 51; DB 5; Length 2108;
Best Local Similarity 35.1%; Pred. No. 28;
Matches 13; Conservative 2; Mismatches 2; Indels 20; Gaps 1;

QY 1 CYPSSKDNVGVKVTSGKTC 17
DB 763 CYPSSKNDYILKINILTKNNKSVIILGNVSGKTC 799

RESULT 12
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AC Q8R166;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
DE Cysteine permease.
GN Fnl1747.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_Taxid=76856;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,

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RA Larsen N., D'Souza M., Malunas T., Pusch G., Haselkorn R.,
 RA Fongseim M., Kyriades N., Overbeek R., analysis of the oral bacterium Fusobacterium
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AE010479; AAL93862.1; -
 DR InterPro: IPR002293; AA/rel_permeaseL.
 DR InterPro: IPR001463; Na/Ala_symport.
 DR Pfam; PF01235; Na_Ala_sym; 1.
 DR TIGRPFAM; TIGR00835; agcs; 1.
 DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
 DR Complete proteome.
 SQ SEQUENCE 511 AA; 56196 MW; 03DBA2859135EF3D CRC64;
 QY
 DB 128 CYRSDKDNVGVTSKGT 17
 128 CYRSDKDNVGVTSKGT 144
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 AC 08MNN3;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Alcohol dehydrogenase 1 (Fragment).
 GN ADH1
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stautler R.L., Walker A., Ryder O., Lyons-Weiler M., Hedges S.B.;
 RT "Human and ape molecular clocks and constraints on paleontological
 hypotheses.";
 RL J. Hered. 92:0-0(2001).
 CC -1- COFACTOR: ZINC (BY SIMILARITY).
 DR EMBL; AF354624; AAL56229.1; -
 DR InterPro: IPR002328; ADH_zinc.
 DR InterPro: IPR002085; Adh_zn_family.
 DR Pfam; PF00107; adh_zinc; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KM Metal-binding; Oxidoreductase; Zinc.
 FT NON_TER 1
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 DB 169 GCFSTGYGSANVAKVTPGSTC 190
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 AC 08LAK6;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein.
 DE Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldman K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldman K.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087754; AAM65290.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 299 AA; 33821 MW; CED6107F70C3D76F CRC64;
 QY
 DB 120 TSKDNVGVTSKGT 16
 120 TSKDNVGVTSKGT 132
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 AC 09XXJ6;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Y102A5B.3 protein.
 GN Y102A5B.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gardner A.B.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; AL023821; CAA19437.1; -
 DR WormPep; Y102A5B.3; CE19286.
 DR InterPro: IPR001304; LECTIN_C.
 DR Pfam; PR00059; LECTIN_C; 2.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds
(without alignments)
58.003 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

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4	102	100.0	238	12	AA13208
5	102	100.0	238	14	AA145016
6	102	100.0	238	22	AA167343
7	102	100.0	238	23	AB176239
8	102	100.0	239	12	AA13207
9	102	100.0	239	14	AA145015

10	102	100.0	239	20	AAV06255	Staphylococcal gro
11	102	100.0	239	20	AAV06256	Staphylococcal gro
12	102	100.0	239	20	AAV06251	Staphylococcal gro
13	102	100.0	239	20	AAV06252	Staphylococcal gro
14	102	100.0	239	20	AAV06253	Staphylococcal gro
15	102	100.0	239	22	AA167342	Staphylococcus aur
16	102	100.0	239	22	AB176238	Staphylococcus aur
17	102	100.0	240	24	AB176237	Staphylococcal ent
18	102	100.0	240	24	AB176236	Staphylococcal ent
19	102	100.0	240	24	AB176235	Staphylococcal ent
20	102	100.0	240	24	AB176234	Staphylococcal ent
21	102	100.0	240	24	AB176233	Staphylococcal ent
22	102	100.0	266	21	AAV70108	Staphylococcal ent
23	102	100.0	266	23	AB176232	Staphylococcal ent
24	102	100.0	266	23	AB176231	Staphylococcal ent
25	96	94.1	18	24	AB176230	Staphylococcal ent
26	96	94.1	239	20	AAV06254	Staphylococcal gro
27	96	94.1	239	20	AAV06257	Staphylococcal gro
28	96	94.1	240	24	AB176229	Staphylococcal ent
29	96	94.1	240	24	AB176228	Staphylococcal ent
30	93	91.2	18	24	AAV06258	Staphylococcal ent
31	87	85.3	239	20	AAV06259	Staphylococcal gro
32	87	85.3	240	24	AB176227	Staphylococcal ent
33	66	64.7	14	20	AAV06256	Staphylococcal ent
34	66	64.7	14	24	AB176225	Staphylococcal ent
35	47	46.1	77	21	AAV06255	Staphylococcal ent
36	47	46.1	103	21	AAV06254	Staphylococcal ent
37	46	45.1	374	20	AAV06253	Staphylococcal ent
38	46	45.1	374	20	AAV06252	Staphylococcal ent
39	46	45.1	375	23	AB176224	Staphylococcal ent
40	46	45.1	395	21	AAV06251	Staphylococcal ent
41	45	44.1	277	23	AB176220	Staphylococcal ent
42	45	44.1	513	22	AAV06250	Staphylococcal ent
43	44	43.1	299	21	AAV06249	Staphylococcal ent
44	44	43.1	315	21	AAV06248	Staphylococcal ent
45	44	43.1	340	21	AAV06247	Staphylococcal ent

ALIGNMENTS

RESULT 1
AAV06249 standard; Peptide: 18 AA.
ID AAV06249;
XX AAV06249;
XX 23-AUG-1999 (first entry)
DT 23-AUG-1999 (first entry)
XX Staphylococcal group C enterotoxin disulfide loop.
DE Staphylococcal group C enterotoxin disulfide loop.
XX Enterotoxin; SEC1, SEC2, SEC3 FRI 913; SEC3 4446; SEC-Bovine;
KW SEC-Ovine; toxin; disulfide loop; protein engineering.
XX Staphylococcus aureus.
OS Staphylococcus aureus.
XX MO9927889-A2.
PN 10-JUN-1999.
XX 01-DEC-1998; 98WO-US25107.
PF 02-DEC-1997; 97US-0067357.
XX (IDAH-) IDAH RES FOUND INC.
PA Bohach GI;
XX WPI: 1999-358008/30.
DR N-PSDB; AAX58884.
XX Non-toxic modified staphylococcal enterotoxins
PT

PS Disclosure; Page 3; 25pp; English.

XX This peptide corresponds to the disulfide loop, i.e. amino acids
CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,
CC SEC3 FR1 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AAY06251-53
CC and AAY06255-58). The invention relates to pyrogenic toxins, such as
CC staphylococcal enterotoxins, modified in the disulfide loop region.
CC Typically, the modification involves deletions within the disulfide
CC loop region of SEC (see AAY06261). The modified toxins retain useful
CC biological properties, such as the ability to induce cytokine
CC production, but have substantially reduced toxicity compared to the
CC corresponding unmodified native toxin. Emetic response inducing
CC activity and fever inducing activity are typically decreased by at
CC least about 100-fold, while LD50 (in Dutch Belted rabbits) is at
CC least 100-fold higher than the native toxin.

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 102, DB 20, Length 18,
Best Local Similarity 100.0%; Pred. No. 2, 9e-09;
Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0

OY 1 CYFSSKDNVGVKGTKC 18
||| ||| ||| ||| ||| ||| |||
Db 1 CYFSSKDNVGVKGTKC 18

RESULT 2
ABG71377
ID ABG71377 standard; Peptide; 18 AA.

XX ABG71377;
DT 29-JAN-2003 (first entry)

XX Staphylococcal enterotoxin disulphide loop region.

DE Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin;
KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
RW SEC1; SEC2; SEC3-FR1913; SEC 4446; SEC-bovine.

XX Staphylococcus aureus.

OS WO200283169-A1.
PN
XX 24-OCT-2002.
PD
XX 11-APR-2002; 2002WO-US11619.
PF
XX 13-APR-2001; 2001US-283720P.
PR
XX (IDAH-) IDAHO RES FOUND INC.
PA
XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
PI WPI; 2003-056608/05.
DR
XX New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning -
XX
XX Disclosure; Fig 15; 67pp; English.

XX The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and

```

CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC disulphide loop region, occurring in several enterotoxins.
XX
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 102; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 CYFSSKDNVGVKVTGKTC 18
   |||||
Db 1 CYFSSKDNVGVKVTGKTC 18
   |||||

RESULT 3
ABG71380 0 *
ID ABG71380 standard; Peptide: 18 AA.
XX
XX ABG71380;
XX AC
XX DT
XX 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin C1 (SEC1) protein fragment.
XX
KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin; SEC1;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
XX
XX Staphylococcus aureus.
XX OS
XX WO200283169-A1.
XX EN
XX PD 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-US11619.
XX PE
XX 13-APR-2001; 2001US-283720P.
XX PR
XX (IDAH-) IDAHO RES FOUND INC.
XX PA
XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX PI
XX WI: 2003-058608/05.
XX DR
XX N-PSDB; ABS56822.
XX DR
XX
XX New modified staphylococcal enterotoxin derived from a native disulphide
XX loop-containing pyrogenic toxin, useful for non-specifically enhancing
XX an immune function and as a vaccine against toxic shock syndrome or
XX food poisoning -
XX
XX Example 1; Fig 1; 67pp; English.
XX
XX The invention relates to a modified pyrogenic toxin derived from a native
XX disulphide loop-containing pyrogenic toxin where the modified toxin
XX comprises a disulphide loop having no more than 10 amino acids. The
XX modified toxin has a fever-inducing activity or an emetic
XX response-inducing activity decreased by about 100-fold in comparison to a
XX native toxin. The modified pyrogenic toxin, that is a staphylococcal
XX enterotoxin, is useful for non-specifically enhancing an immune function
XX and for vaccination against diseases such as toxic shock syndrome and
XX food poisoning. This sequence represents a staphylococcal enterotoxin
XX protein fragment.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 102; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 CYFSSKDNVGVKVTGKTC 18
   |||||
Db 1 CYFSSKDNVGVKVTGKTC 18
   |||||

```



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RESULT 4
AAR13208
ID AAR13208 standard; Protein; 238 AA.
XX
AC AAR13208;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C3.
XX
KM SEC3; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1991; 91MO-US00342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SEC3 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
CC polypeptides having structural homology to Staphylococcal
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
CC See AAR13203-R13211.
XX
SQ Sequence 238 AA;
XX
Query Match 100.0%; Score 102; DB 12; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVGVKTKGKTC 18
Db 92 CYFSSKDNVGVKTKGKTC 109
XX
RESULT 5
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
AC AAR45016;
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEC3.
XX
KM Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KM auto-immune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX

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PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93MO-US05213.
XX
PR 01-JUN-1992; 92US-0891718.
XX
PA (STON/) STONE L.
PA (TERM/) TERMAN D S.
XX
PI Stone JL, Terman DS;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and auto-immune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 238 AA;
XX
Query Match 100.0%; Score 102; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVGVKTKGKTC 18
Db 92 CYFSSKDNVGVKTKGKTC 109
XX
RESULT 6
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
AC AAB67343;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin C3 protein.
XX
KM Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-0183437.
XX
PR 31-JUN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91MO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX

```

DR WPI; 2001-158657/16.
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro
PT or in vivo comprises exogenous nucleic acids encoding a superantigen
PT and a costimulatory molecule -
XX
XX Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and
CC expresses an exogenous nucleic acid molecule encoding a superantigen
CC or its active fragment and an exogenous nucleic acid molecule
CC encoding a costimulatory molecule that activates T cells in
CC conjunction with an antigenic stimulus. The invention may be used
CC for cancer therapy by stimulating an anticancer immune response
CC in vivo or ex vivo.
XX
SQ Sequence 238 AA;
QY
Query Match 100.0%; Score 102; DB 22; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 92 CYFSSKDNVGVKVTGKTC 109
1 CYFSSKDNVGVKVTGKTC 18
|||||
ABBT6239
ID ABB76239 standard; Protein; 238 AA.
XX
AC ABB76239;
XX
DT 09-AUG-2002 (first entry)
XX
DE Staphylococcus aureus enterotoxin C3.
XX
XX
XX Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
KM antitumour; therapy.
XX
XX Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 208 /note= "given as 'O' in the specification"
FT
XX
XX US2002051765-A1.
XX
XX 02-MAY-2002.
XX
XX 19-DEC-2000; 2000US-0741503.
XX
XX 31-JAN-1994; 94US-0189424.
XX 19-JUN-1995; 95US-0491746.
XX 03-OCT-1989; 89US-0416530.
XX 17-JAN-1990; 90US-0466577.
XX 17-JAN-1991; 91MO-US00342.
XX 01-JUN-1992; 92US-0891718.
XX 02-MAR-1993; 93US-0025144.
XX
XX (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 2002-415198/44.
XX
XX Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumour and stimulated with superantigens -
XX
XX Disclosure; Fig 2; 17pp; English.
XX

CC The present sequence is the protein sequence of enterotoxin C3
CC (SEC3) of Staphylococcus aureus. Similarity is shown, in several
CC stretches of sequence, between staphylococcal enterotoxins,
CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative
CC toxins (see ABB76234-44). In the present invention, synthetic
CC polypeptides useful in tumour therapy and in blocking or destroying
CC autoreactive T and B lymphocyte populations are characterised by
CC substantial structural homology to staphylococcal enterotoxin A and
CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
CC statistically significant sequence homology and similarity (Z value
CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
CC 6) to include alignment of cysteine residues and similar hydrophathy
CC profiles. These superantigens are used to treat solid tumours,
CC including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient
CC with one or more superantigens ex vivo to generate stimulated cells,
CC selecting a specific V beta subset of cells, and reintroducing
CC these cells into the patient to induce an in vivo therapeutic,
CC tumoricidal reaction.
XX
SQ Sequence 238 AA;
QY
Query Match 100.0%; Score 102; DB 23; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 92 CYFSSKDNVGVKVTGKTC 109
1 CYFSSKDNVGVKVTGKTC 18
|||||
AAR13207
ID AAR13207 standard; Protein; 239 AA.
XX
XX AAR13207;
XX
XX 15-OCT-1991 (first entry)
XX
XX Staphylococcal enterotoxin C1.
XX
XX
XX SEC1; cancer treatment; pyrogen; tumouricide.
XX
XX Staphylococcus aureus.
XX
XX WO9110680-A.
XX
XX 25-JUL-1991.
XX
XX 17-JAN-1991; 91MO-US00342.
XX
XX 17-JAN-1990; 90US-0466577.
XX
XX (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 1991-237984/32.
XX
XX Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX SEC1 was isolated and purified from S. aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC1. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically

CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
CC See AAR3203-R13211.

SQ Sequence 239 AA;

Query Match 100.0%; Score 102; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 9

AAR45015
ID AAR45015 standard; protein; 239 AA.

AC AAR45015;

DT 25-MAR-2003 (updated)

DT 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SEC1.

KM Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.

OS Staphylococcus aureus.

PN WO9324136-A1.

PD 09-DEC-1993.

PF 01-JUN-1993; 93WO-US05213.

PR 01-JUN-1992; 92US-0891718.

PA (STON/) STONE J L.

PA (TERM/) TERMAN D S.

PI Stone JL, Terman DS;

DR WPI; 1993-405418/50.

PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases

PS Disclosure; Fig 1; 90pp; English.

CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 239 AA;

Query Match 100.0%; Score 102; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 10

AAV06255
ID AAV06255 standard; Protein; 239 AA.

AC AAV06255;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-MNCoPeland.

KM Enterotoxin; SEC-MNCoPeland; toxin; disulfide loop;
KW protein engineering.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT Disulfide-bond 93..110

PN WO927889-A2.

PD 10-JUN-1999.

PF 01-DEC-1998; 98WO-US25107.

PR 02-DEC-1997; 97US-0067357.

PA (IDAH-) IDAHO RES FOUND INC.

PI Bohach GI;

DR WPI; 1999-358008/30.

PT Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 17; 25pp; English.

CC This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC-MNCoPeland. The invention relates to pyrogenic
CC toxins, such as staphylococcal enterotoxins, modified in the
CC disulfide loop region. Typically, the modification involves
CC deletions within the disulfide loop region of SEC (see AAV06261).
CC The modified toxins retain useful biological properties, such as
CC the ability to induce cytokine production, but have substantially
CC reduced toxicity compared to the corresponding unmodified native
CC toxin. Emetic response inducing activity and fever inducing
CC activity are typically decreased by at least about 100-fold, while
CC LD50 (in Dutch belted rabbits) is at least 100-fold higher than
CC the native toxin.

SQ Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 11

AAV06256
ID AAV06256 standard; Protein; 239 AA.

AC AAV06256;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-4446.

KM Enterotoxin; SEC-4446; toxin; disulfide loop;
KW protein engineering.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
 FH Disulfide-bond 93..110
 XX
 XX WO927889-A2.
 XX
 XX 10-JUN-1999.
 XX
 XX 01-DEC-1998; 98WO-US25107.
 XX
 XX 02-DEC-1997; 97US-0067357.
 XX
 XX (IDAH-) IDAHO RES FOUND INC.
 XX
 XX Bohach GI;
 XX
 XX WPI; 1999-358008/30.
 XX
 XX Non-toxic modified staphylococcal enterotoxins
 XX
 XX Disclosure; Page 17; 25pp; English.
 XX
 XX This protein represents the Staphylococcus aureus type C
 CC enterotoxin SEC-4446. The invention relates to pyrogenic toxins,
 CC such as staphylococcal enterotoxins, modified in the disulfide loop
 CC region. Typically, the modification involves deletions within the
 CC disulfide loop region of SEC (see AAY06261). The modified toxins
 CC retain useful biological properties, such as the ability to induce
 CC cytokine production, but have substantially reduced toxicity
 CC compared to the corresponding unmodified native toxin. Emetic
 CC response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin.
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 102; DB 20; Length 239;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVGVKVTGGKTC 18
 DB 93 CYFSSKDNVGVKVTGGKTC 110
 RESULT 12
 ID AAY06251 standard; Protein; 239 AA.
 XX
 XX AAY06251;
 XX
 XX 23-AUG-1999 (first entry)
 XX
 XX Staphylococcal group C enterotoxin SEC1.
 XX
 XX Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.
 XX
 XX Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 93..110
 XX
 XX WO927889-A2.
 XX
 XX 10-JUN-1999.
 XX
 XX 01-DEC-1998; 98WO-US25107.
 XX
 XX 02-DEC-1997; 97US-0067357.
 XX
 XX (IDAH-) IDAHO RES FOUND INC.
 XX
 XX Bohach GI;
 XX

XX WPI; 1999-358008/30.
 XX
 XX Non-toxic modified staphylococcal enterotoxins
 XX
 XX Disclosure; Page 17; 25pp; English.
 XX
 XX This protein represents the Staphylococcus aureus type C
 CC enterotoxin SEC1. The invention relates to pyrogenic toxins, such
 CC as staphylococcal enterotoxins, modified in the disulfide loop
 CC region. Typically, the modification involves deletions within the
 CC disulfide loop region of SEC (see AAY06261). The modified toxins
 CC retain useful biological properties, such as the ability to induce
 CC cytokine production, but have substantially reduced toxicity
 CC compared to the corresponding unmodified native toxin. Emetic
 CC response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin.
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 102; DB 20; Length 239;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVGVKVTGGKTC 18
 DB 93 CYFSSKDNVGVKVTGGKTC 110
 RESULT 13
 ID AAY06252 standard; Protein; 239 AA.
 XX
 XX AAY06252;
 XX
 XX 23-AUG-1999 (first entry)
 XX
 XX Staphylococcal group C enterotoxin SEC2.
 XX
 XX Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
 XX
 XX Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 93..110
 XX
 XX WO927889-A2.
 XX
 XX 10-JUN-1999.
 XX
 XX 01-DEC-1998; 98WO-US25107.
 XX
 XX 02-DEC-1997; 97US-0067357.
 XX
 XX (IDAH-) IDAHO RES FOUND INC.
 XX
 XX Bohach GI;
 XX
 XX WPI; 1999-358008/30.
 XX
 XX Non-toxic modified staphylococcal enterotoxins
 XX
 XX Disclosure; Page 17; 25pp; English.
 XX
 XX This protein represents the Staphylococcus aureus type C
 CC enterotoxin SEC2. The invention relates to pyrogenic toxins, such
 CC as staphylococcal enterotoxins, modified in the disulfide loop
 CC region. Typically, the modification involves deletions within the
 CC disulfide loop region of SEC (see AAY06261). The modified toxins
 CC retain useful biological properties, such as the ability to induce
 CC cytokine production, but have substantially reduced toxicity
 CC compared to the corresponding unmodified native toxin. Emetic

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:51:46 : Search time 13.7964 Seconds
(without alignments)
55.202 Million cell updates/sec

Title: US-09-555-115A-15
Perfect score: 102
Sequence: 1 CWFSSKDNVGVKTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqe, 42310858 residues
Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A COMB pep:*
2: /cgn2_6/prodata/1/1aa/5B COMB pep:*
3: /cgn2_6/prodata/1/1aa/6A COMB pep:*
4: /cgn2_6/prodata/1/1aa/6B COMB pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB pep:*
6: /cgn2_6/prodata/1/1aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	102	100.0	89	4	US-09-144-776B-21	Sequence 21, Appl
2	102	100.0	89	4	US-09-144-776B-22	Sequence 22, Appl
3	102	100.0	89	4	US-09-144-776B-23	Sequence 23, Appl
4	102	100.0	238	3	US-08-896-933-28	Sequence 28, Appl
5	102	100.0	238	4	US-09-314-235-28	Sequence 28, Appl
6	102	100.0	239	3	US-08-896-933-27	Sequence 27, Appl
7	102	100.0	239	4	US-09-314-235-27	Sequence 27, Appl
8	102	100.0	266	4	US-09-144-776B-14	Sequence 14, Appl
9	48	47.1	170	4	US-09-252-991A-29047	Sequence 29047, A
10	46	45.1	263	2	US-08-892-690-3	Sequence 3, Appl
11	46	45.1	374	2	US-07-857-224B-82	Sequence 82, Appl
12	46	45.1	374	2	US-07-857-224B-83	Sequence 83, Appl
13	46	45.1	375	4	US-09-347-878-56	Sequence 56, Appl
14	44	43.1	134	2	US-08-482-928A-14	Sequence 14, Appl
15	44	43.1	176	1	US-08-145-995A-4	Sequence 4, Appl
16	44	43.1	176	2	US-08-451-747-4	Sequence 4, Appl
17	44	43.1	176	3	US-09-134-852-4	Sequence 4, Appl
18	42	41.2	514	1	US-08-361-920-21	Sequence 21, Appl
19	42	41.2	514	1	US-08-479-939-21	Sequence 21, Appl
20	42	41.2	514	1	US-08-483-432-21	Sequence 21, Appl
21	40.5	39.7	155	4	US-09-252-991A-19995	Sequence 19995, A
22	40	39.2	210	4	US-09-247-155-121	Sequence 121, App
23	40	39.2	264	3	US-08-924-570A-2	Sequence 2, Appl
24	40	39.2	320	3	US-09-092-437-2	Sequence 2, Appl
25	40	39.2	374	2	US-07-857-224B-80	Sequence 80, Appl
26	40	39.2	374	2	US-07-857-224B-81	Sequence 81, Appl
27	40	39.2	374	2	US-07-857-224B-84	Sequence 84, Appl

28	40	39.2	374	2	US-07-857-224B-85	Sequence 85, Appl
29	40	39.2	375	2	US-07-857-224B-86	Sequence 86, Appl
30	40	39.2	412	2	US-08-741-134-2	Sequence 2, Appl
31	40	39.2	690	4	US-09-252-991A-29429	Sequence 29429, A
32	40	39.2	1053	4	US-09-328-352-6788	Sequence 6788, Ap
33	39.5	38.7	765	4	US-09-252-991A-29429	Sequence 29429, A
34	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
35	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
36	39	38.2	94	4	US-08-938-085A-35	Sequence 35, Appl
37	39	38.2	94	4	US-08-938-085A-37	Sequence 37, Appl
38	39	38.2	94	4	US-10-072-844-35	Sequence 35, Appl
39	39	38.2	94	4	US-10-072-844-37	Sequence 37, Appl
40	39	38.2	95	4	US-09-107-532A-6140	Sequence 6140, Ap
41	39	38.2	228	1	US-08-278-891-7	Sequence 7, Appl
42	39	38.2	228	1	US-08-483-859-7	Sequence 7, Appl
43	39	38.2	228	1	US-08-472-173-7	Sequence 7, Appl
44	39	38.2	228	2	US-08-487-167-7	Sequence 7, Appl
45	39	38.2	228	2	US-08-482-816-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-144-776B-21
Sequence 21, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21
Query Match 100.0%; Score 102; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
Db 54 CYFSSKDNVGVKVTGKTC 71

RESULT 2

US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-144-776B-22

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
Db 54 CYFSSKDNVGVKVTGKTC 71

RESULT 3

US-09-144-776B-23
; Sequence 23, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson

Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-144-776B-23

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
Db 54 CYFSSKDNVGVKVTGKTC 71

RESULT 4

US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 28
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28

Query Match 100.0%; Score 102; DB 3; Length 218;

Best Local Similarity 100.0%; Pred. No. 3,4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKGTGKTC 18
Db 92 CYFSSKDNVGVKGTGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-28

Query Match 100.0%; Score 102; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 3,4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKGTGKTC 18
Db 92 CYFSSKDNVGVKGTGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-27

Query Match 100.0%; Score 102; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3,4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKGTGKTC 18
Db 93 CYFSSKDNVGVKGTGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-27

Query Match 100.0%; Score 102; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 3,4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKGTGKTC 18
Db 93 CYFSSKDNVGVKGTGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2055
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match 100.0%; Score 102; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 3; 8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 18
Db 120 CYFSSKDNVKGKTC 137

RESULT 9
US-09-252-991A-29047
Sequence 29047, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29047
LENGTH: 170
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29047

Query Match 47.1%; Score 48; DB 4; Length 170;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 14
Db 116 CSFARDNAGRATG 129

RESULT 10
US-08-892-690-3
Sequence 3, Application US/08892690
Patent No. 5932420
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,690
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0339 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 624778
US-08-892-690-3

Query Match 45.1%; Score 46; DB 2; Length 263;
Best Local Similarity 43.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKTC 16
Db 90 CFFSDDPVNSIPGE 105

RESULT 11
US-07-857-224B-82
Sequence 82, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TELEX: none

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1 INFORMATION FOR SEQ ID NO: 82:
2 SEQUENCE CHARACTERISTICS:
3     LENGTH: 374
4     TYPE: amino acid
5     TOPOLOGY: linear
6 MOLECULE TYPE:
7     DESCRIPTION: protein
8     ORIGINAL SOURCE:
9         ORGANISM: human
10    FEATURE: Alcohol dehydrogenase, Table 3 Column 3
11    PUBLICATION INFORMATION:
12    AUTHORS:
13    AUTHORS: Joernvall, H.
14    AUTHORS: Persson, M.
15    AUTHORS: Jeffery, J.
16    TITLE: Alcohol dehydrogenases
17    JOURNAL: Proceedings of the National Academy of Sciences, USA
18    VOLUME: 78
19    PAGES: 4226-4230
20    DATE: 1981
21    US-07-857-224B-82
22
23 Query Match 45.1%; Score 46; DB 2; Length 374;
24 Best Local Similarity 54.5%; Pred. No. 19;
25 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 11
26
27 QY 1 CYFS---SKDNVGRVGRKTC 18
28 ||| ||| ||| ||| |||
29 Db 174 CGFSTGYGSAVNVAKVTPGSTC 195
30
31 RESULT 12
32 US-07-857-224B-83
33 Sequence 83, Application US/07857224B
34 Patent No. 5958784
35 GENERAL INFORMATION:
36 APPLICANT: Benner, Steven A.
37 TITLE OF INVENTION: Predicting Folded Structures of Proteins
38 NUMBER OF SEQUENCES: 114
39 CORRESPONDENCE ADDRESS:
40 ADDRESSEE: Steven A. Benner
41 STREET: Hadlaubstrasse 151
42 CITY: Zurich
43 STATE: none
44 COUNTRY: Switzerland
45 ZIP: (note: this is an international post code) CH-8092
46 COMPUTER READABLE FORM:
47 MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
48 COMPUTER: Apple Macintosh
49 OPERATING SYSTEM: Macintosh 7.0
50 SOFTWARE: Microsoft Word
51 CURRENT APPLICATION DATA:
52 APPLICATION NUMBER: US/07/857,224B
53 FILING DATE: 03/25/92
54 CLASSIFICATION: 436
55 PRIOR APPLICATION DATA: none
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (International) 41 1 632 2830
58 TELEFAX: (International) 41 1 262 2437
59
60 TELEX: none
61 INFORMATION FOR SEQ ID NO: 83:
62 SEQUENCE CHARACTERISTICS:
63     LENGTH: 374
64     TYPE: amino acid
65     TOPOLOGY: linear
66 MOLECULE TYPE:
67     DESCRIPTION: protein
68     ORIGINAL SOURCE:
69         ORGANISM: human
70    FEATURE: Alcohol dehydrogenase, Table 3 Column 4
71    PUBLICATION INFORMATION:
72    AUTHORS:
73    AUTHORS: Joernvall, H.

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AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-83

Query Match          45.1%   Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy      1 CYFS----SKDNVGKVTGKTC 18
        ||| ||||| |||
Db       174 CGFSTGYGSANVNAAKTPGSTC 195

RESULT 13           0
US-09-347-878-56
Sequence 56, Application US/09347878C
Patent No. 6376210
GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT FILING DATE: US/09347,878C
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-878-56

Query Match          45.1%   Score 46; DB 4; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Cy      1 CYFS----SKDNVGKVTGKTC 18
        ||| ||||| |||
Db       175 CGFSTGYGSANVNAAKTPGSTC 196

RESULT 14
US-08-482-728A-14
Sequence 14, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Pavan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Elehr, Hohbach, Teest, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
```

NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277229
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-14

Query Match 43.1%; Score 44; DB 2; Length 134;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
| : : : : :
Db 21 CLCSGKGLGKTKKLC 38

RESULT 15
US-08-145-995A-4
Sequence 4, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTTIDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-4

Query Match 43.1%; Score 44; DB 1; Length 176;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
| : : : : :
Db 41 CLCSGKGLGKTKKLC 58

Search completed: October 15, 2003, 17:08:32
Job time: 13.7964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 27.2695 Seconds
(Without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115A-15

Perfect score: 102

Sequence: 1 CYFSSKDNVGVKVTGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*

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12: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	89	15	US-10-002-784A-36
2	102	100.0	89	15	US-10-002-784A-37
3	102	100.0	89	15	US-10-002-784A-38
4	102	100.0	266	8	US-08-882-431-14
5	102	100.0	266	10	US-09-870-759-12
6	102	100.0	266	12	US-09-751-708A-12
7	102	100.0	266	15	US-10-002-784A-14
8	46	45.1	263	9	US-09-265-710-3
9	46	45.1	263	12	US-10-366-020-3
10	46	45.1	375	12	US-09-981-320-3
11	46	45.1	375	12	US-09-738-630-92
12	46	45.1	395	5	US-09-925-302-497
13	42	41.2	211	5	US-10-156-761-8802
14	42	41.2	332	15	US-10-021-811-54
15	41.5	40.7	993	15	US-10-128-714-3467

16	41.5	40.7	1105	15	US-10-128-714-8467	Sequence 8467, Ap
17	41	40.2	163	12	US-10-238-075-786	Sequence 786, Ap
18	41	40.2	307	11	US-09-764-891-4188	Sequence 4188, Ap
19	40.5	39.7	1139	15	US-10-156-761-10856	Sequence 10856, A
20	40	39.2	152	12	US-10-040-895-2	Sequence 2, Appl1
21	40	39.2	210	12	US-09-903-190-121	Sequence 121, App
22	40	39.2	263	9	US-09-823-356-13	Sequence 43, Appl
23	40	39.2	263	12	US-09-946-374-43	Sequence 43, Appl
24	40	39.2	263	12	US-10-015-3872A-43	Sequence 43, Appl
25	40	39.2	263	12	US-10-006-130A-43	Sequence 184, App
26	40	39.2	263	12	US-10-199-672-184	Sequence 184, App
27	40	39.2	263	12	US-10-006-172A-43	Sequence 43, Appl
28	40	39.2	263	12	US-10-187-749-184	Sequence 184, App
29	40	39.2	263	12	US-10-194-457-184	Sequence 184, App
30	40	39.2	263	12	US-10-184-642-184	Sequence 184, App
31	40	39.2	263	12	US-10-196-747-184	Sequence 184, App
32	40	39.2	263	12	US-10-015-392A-43	Sequence 43, Appl
33	40	39.2	263	12	US-10-017-253A-43	Sequence 43, Appl
34	40	39.2	263	12	US-10-173-689-184	Sequence 184, App
35	40	39.2	263	12	US-10-173-689-184	Sequence 184, App
36	40	39.2	263	12	US-10-173-689-184	Sequence 184, App
37	40	39.2	263	12	US-10-173-682-184	Sequence 184, App
38	40	39.2	263	12	US-10-173-682-184	Sequence 184, App
39	40	39.2	263	12	US-10-173-682-184	Sequence 184, App
40	40	39.2	263	12	US-10-173-682-184	Sequence 184, App
41	40	39.2	263	12	US-10-173-707-184	Sequence 184, App
42	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
43	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
44	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
45	40	39.2	263	12	US-10-174-569-184	Sequence 184, App

ALIGNMENTS

RESULT 1

US-10-002-784A-36

Sequence 36, Application US/10002784A

Publication No. US20030036644A1

GENERAL INFORMATION:

/33

APPLICANT: Ulrich, Robert G.

TITLE OF INVENTION: Bacterial Superantigen Vaccines

FILE REFERENCE: 003/233/SAP

CURRENT APPLICATION NUMBER: US/10/002,784A

PRIOR FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: 08/882,431, 09/144,776

PRIOR FILING DATE: 97-06-25; 98-09-01

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Apple Macintosh Microsoft Word 6.0

SEQ ID NO 36

LENGTH: 89

TYPE: PRP

ORGANISM: staphylococcal enterotoxin C1

FEATURE:

OTHER INFORMATION: partial sequence as shown in Figure 3

US-10-002-784A-36

Query Match 100.0%; Score 102; DB 15; Length 89;

Best Local Similarity 100.0%; Pred. No. 6.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18

DB 54 CYFSSKDNVGVKVTGKTC 71

RESULT 2

US-10-002-784A-37

Sequence 37, Application US/10002784A

Publication No. US20030036644A1

GENERAL INFORMATION:

/33

```

; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-37

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6,6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYSSKDNVGVKVTGGKTC 18
        |||
        54  CYSSKDNVGVKVTGGKTC 71

RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US2003003644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
; US-10-002-784A-38

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6,6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYSSKDNVGVKVTGGKTC 18
        |||
        54  CYSSKDNVGVKVTGGKTC 71

Db      54  CYSSKDNVGVKVTGGKTC 71

RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
```

```

; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-2065
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14

Query Match      100.0%; Score 102; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYSSKDNVGVKVTGGKTC 18
        |||
        120  CYSSKDNVGVKVTGGKTC 137

Db      120  CYSSKDNVGVKVTGGKTC 137

RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-870-759-12

Query Match      100.0%; Score 102; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYSSKDNVGVKVTGGKTC 18
        |||
        120  CYSSKDNVGVKVTGGKTC 137

Db      120  CYSSKDNVGVKVTGGKTC 137

RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
```

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/ GENERAL INFORMATION:
/ APPLICANT: TERMAN, David S
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
/ FILE REFERENCE: 751708
/ CURRENT APPLICATION NUMBER: US/09/751,708A
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: US 60/133,371
/ PRIOR FILING DATE: 1999-12-28
/ NUMBER OF SEQ ID NOS: 166
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 12
/ LENGTH: 266
/ TYPE: PR
/ ORGANISM: Staphylococcus aureus
/ US-09-751-708A-12

Query Match      100.0%; Score 102; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 2,2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYPSSKDNVGVGTGKTC 18
Db      120 CYPSSKDNVGVGTGKTC 137

RESULT 7
US-10-002-784A-14
/ Sequence 14, Application US/10002784A
/ Publication No. US200303644A1
/ GENERAL INFORMATION:
/ /33
/ APPLICANT: Ulrich, Robert G.
/ TITLE OF INVENTION: Bacterial Superantigen Vaccines
/ FILE REFERENCE: 003/233/SAP
/ CURRENT APPLICATION NUMBER: US/10/002,784A
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
/ PRIOR FILING DATE: 97-06-25; 98-09-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Apple Macintosh Microsoft Word 6.0
/ SEQ ID NO: 14
/ LENGTH: 266
/ TYPE: PR
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
/ US-10-002-784A-14

Query Match      100.0%; Score 102; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2,2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYPSSKDNVGVGTGKTC 18
Db      120 CYPSSKDNVGVGTGKTC 137

RESULT 8
US-09-265-710-3
/ Sequence 3, Application US/09265710
/ Patent No. US20020042126A1
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Lal, Preeti
/ APPLICANT: Shah, Puri V
/ TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
```

```
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/265,710
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/892,690
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 263 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 624778
/ US-09-265-710-3

Query Match      45.1%; Score 46; DB 9; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYPSSKDNVGVGTGK 16
Db      90 CFPDSEDVNSIPGGE 105

RESULT 9
US-10-366-020-3
/ Sequence 3, Application US/10366020
/ Publication No. US20030152989A1
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE
/ PROTEIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/366,020
/ FILING DATE: 11-Feb-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/207,161
/ FILING DATE: 1998-12-07
/ APPLICATION NUMBER: US/08/791,338
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
```

```

; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0208 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 624778
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-366-020-3

Query Match          45.1%; Score 46; DB 12; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 CYFS---SKDNVKGVTGKTC 16
Db      90 CFFDSEDPVMSIPGGE 105

RESULT 10
US-09-981-353-113
; Sequence 113, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 2512879CD1
US-09-981-353-113

Query Match          45.1%; Score 46; DB 10; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1 CYFS---SKDNVKGVTGKTC 18
Db      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 11
US-09-738-630-92
; Sequence 92, Application US/09738630
; Publication No. US20030166213A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; APPLICANT: Shaw, Paul J.
; TITLE OF INVENTION: Methods For Identifying Compounds That
; TITLE OF INVENTION: Metabolic Disorders Related To Nitric Oxide/cGMP-Dependent
; FILE REFERENCE: P-NI 3906
; CURRENT APPLICATION NUMBER: US/09/738,630
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
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; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-630-92

Query Match          45.1%; Score 46; DB 12; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1 CYFS---SKDNVKGVTGKTC 18
Db      175 CGFSTGYGSANVAKVTPGSTC 196

RESULT 12
US-09-925-302-497
; Sequence 497, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 497
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 0 SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-497

Query Match          45.1%; Score 46; DB 9; Length 395;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY      1 CYFS---SKDNVKGVTGKTC 18
Db      195 CGFSTGYGSANVAKVTPGSTC 216

RESULT 13
US-10-156-761-8802
; Sequence 8802, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8802
; LENGTH: 211
; TYPE: PRT
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ORGANISM: Streptomyces avermitilis
US-10-156-761-8802

Query Match 41.2%; Score 42; DB 15; Length 211;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YFSSKDNVGTKT 13
:|||||:
Db 58 HFSSKDNLTGAT 69

RESULT 14

US-10-021-811-54
; Sequence 54, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odell, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BBI294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 54
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Glycine max
US-10-021-811-54

Query Match 41.2%; Score 42; DB 15; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGTKG 15
:|||||:
Db 197 CYASSADNIAIWMKG 211

RESULT 15

US-10-128-714-3467
; Sequence 3467, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Weng
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3467

LENGTH: 993
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3467

Query Match 40.7%; Score 41.5; DB 15; Length 993;
Best Local Similarity 40.9%; Pred. No. 4.3e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 9; Gaps 1;

QY 5 SKDNV-----GKVTGKT 17
:|||||:
Db 102 TKDNICFQIDAEKGTGKT 123

Search completed: October 15, 2003, 17:47:01
Job time : 27.2695 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 13.6886 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115A-15
Perfect score: 102
Sequence: 1 CYFSSKDNVNGKVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	266	1 ENSAC1	enterotoxin C-1 pr
2	102	100.0	266	2 A60114	enterotoxin C-2 pr
3	102	100.0	266	2 S11885	enterotoxin C3 - S
4	46	45.1	199	2 AG1583	weakly phosphoglyc
5	46	45.1	375	1 DEHUA4	alcohol dehydrogen
6	46	45.1	375	1 DEHUA6	alcohol dehydrogen
7	44	43.1	246	2 JQ1472	trypsin (EC 3.4.21
8	44	43.1	246	2 JQ1471	trypsin (EC 3.4.21
9	44	43.1	275	2 T32005	hypothetical prote
10	44	43.1	1403	1 A47328	natural killer cel
11	44	43.1	1507	2 B47328	natural killer cel
12	43	42.2	274	2 T13010	hypothetical prote
13	43	42.2	346	2 AE3434	lytB protein timpo
14	43	42.2	368	2 T26338	hypothetical prote
15	42	41.2	212	2 T05936	agglutinin isolect
16	42	41.2	235	2 E91097	hypothetical prote
17	42	41.2	235	2 A85943	hypothetical prote
18	42	41.2	260	2 B96944	2 deoxy-D-gluconat
19	42	41.2	358	2 T08477	inclusion membrane
20	42	41.2	375	1 A38405	alcohol dehydrogen
21	42	41.2	378	2 A61454	protein gp18 from
22	42	41.2	378	2 AD1090	protein gp18 from
23	42	41.2	430	2 A87634	peptidase, M20/M25
24	41	40.2	57	2 S70473	neurotoxin Ts-kapp
25	41	40.2	199	2 T08573	hypothetical prote
26	41	40.2	199	2 AD1230	phosphoglycerate m
27	41	40.2	269	2 B97113	protein serine/thr
28	41	40.2	368	1 DEHUA6	alcohol dehydrogen
29	41	40.2	375	1 A33909	alcohol dehydrogen

30	41	40.2	746	2 AD1622	probable integral
31	41	40.2	750	2 G81361	probable flagellin
32	41	40.2	1127	2 T03105	major single-stran
33	40.5	39.7	333	2 D83585	hypothetical prote
34	40.5	39.7	725	2 T17732	helicase-like prote
35	40.5	39.7	1102	2 A84480	probable retroelem
36	40	39.2	99	2 G84242	hypothetical prote
37	40	39.2	242	2 H69066	ribosomal protein
38	40	39.2	266	1 S18159	ribosomal protein
39	40	39.2	320	2 H95136	hypothetical prote
40	40	39.2	320	2 B99005	ribonucleoside-dip
41	40	39.2	348	2 D70195	hypothetical prote
42	40	39.2	374	1 DEH0A5	alcohol dehydrogen
43	40	39.2	375	1 I55359	alcohol dehydrogen
44	40	39.2	375	1 DEHUA6	alcohol dehydrogen
45	40	39.2	375	1 DEH0A1	alcohol dehydrogen

ALIGNMENTS

RESULT 1

ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #ext_change 18-Jun-1999
C/Accession: S06356; A01816
R/Schmidt, J.J.; Spero, L.
Mol. Gen. Genet. 209, 15-20, 1987
A/Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to
A/Reference number: S06356; PMID:88038352; PMID:2823067
A/Accession: S06356
A/Molecule type: DNA
A/Residues: 1-266 <BOH>
A/Cross-references: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R/Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A/Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A/Reference number: A01816; PMID:83213327; PMID:6189824
A/Accession: A01816
A/Molecule type: protein
A/Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C/Genetics:
A/Gene: entC1
C/Superfamily: enterotoxin B
C/Keywords: enterotoxin
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-266/Product: enterotoxin C-1 #status experimental <MAT>
F/120-137/Diulfide bonds: #status experimental

Query Match 100.0%; Score 102; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVNGKVTGKTC 18
Db 120 CYFSSKDNVNGKVTGKTC 137

RESULT 2

A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N/Alternate names: enterotoxin C-3 precursor
C/Species: Staphylococcus aureus
C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #ext_change 16-Jul-1999
C/Accession: A60114; B60114; A33866
R/Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A/Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A/Reference number: A60114; PMID:89277549; PMID:2543637
A/Accession: A60114
A/Status: not compared with conceptual translation
A/Molecule type: DNA

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A;Residues: 1-266 <BOH>
A;Accession: B60114
A;Molecule type: protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Beley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <CCU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA6624.1; PID:g153004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match          100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGKTC 18
Db      120  CYFSSKDNVKGKVTGKTC 137

RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compar
A;Reference number: S11885; MUID:9020508; PMID:2325627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HCV>
A;Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B

Query Match          100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYFSSKDNVKGKVTGKTC 18
Db      120  CYFSSKDNVKGKVTGKTC 137

RESULT 4
AG1583
weakly phosphoglycerate mutase 1 homolog lin1208 [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
A;Accession: AG1583
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entliam, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurpakt, G.; Madueno, E.; Maicournam, A.; Ma
ok, C.; Schluefer, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <GAA>
A;Cross-references: GB:AL592022; PIDN:CAC96439.1; PID:g16413682; GSPDB:GN00178

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A;Experimental source: strain Clp11262
C;Genetics: 0
A;Gene: lin1208

Query Match          45.1%; Score 46; DB 2; Length 199;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      2  YFSSKDNVKGKVTGKTC 18
Db      151  YMEKTSKIGKVTGKTC 167

RESULT 5
DEHUA
alcohol dehydrogenase (EC 1.1.1.1) 1 - human
N;Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
C;Accession: S02265; A25428; A24408; I39398; I39397
R;Matsuo, Y.; Yokoyama, S.
FEBS Lett. 243, 57-60, 1989
A;Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
A;Reference number: S02265; MUID:89153548; PMID:2920825
A;Accession: S02265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1375 <MATS>
R;Ikuta, T.; Szeto, S.; Yoshida, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
A;Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and ev
A;Reference number: A94120; MUID:86120995; PMID:2935875
A;Accession: A25428
A;Molecule type: mRNA
A;Residues: 1-375 <IKU>
A;Cross-references: GB:M12271; NID:g178091; PIDN:AAA68131.1; PID:g178092
R;von Bahr-Lindstrom, H.; Hoog, J.O.; Hedden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K.
Biochemistry 25, 2465-2470, 1986
A;Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
A;Reference number: A24408; MUID:86243367; PMID:3013304
A;Accession: A24408
A;Molecule type: mRNA
A;Residues: 1-375 <YON>
A;Cross-references: GB:M12963; NID:g178089; PIDN:AAA51590.1; PID:g178090
R;Yasunami, M.; Kikuchi, I.; Sarapat, D.; Yoshida, A.
Genomics 7, 152-158, 1990
A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
A;Reference number: I39398; MUID:90269803; PMID:2347582
A;Accession: I39398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <YAS>
A;Cross-references: GB:M37066; NID:g178095; PIDN:AAA51591.1; PID:g178096
R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
Gene 90, 271-279, 1990
A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
A;Reference number: I39397; MUID:90382676; PMID:2169444
A;Accession: I39397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <STB>
A;Cross-references: GB:M32656; NID:g178093; PIDN:AAA52276.1; PID:g178094
C;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
C;Genetics:
A;Gene: GDB:ADH1
A;Cross-references: GDB:119650; OMIM:103700
A;Map position: 4q21-4q23
A;Intons: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
C;Function: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: ethanol degradation
A;Note: human alcohol dehydrogenase 1 is expressed predominately in fetal and neonatal li

```

C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C/Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F1:2-375/Product: alcohol dehydrogenase 1 #status predicted <MAT>
 F1:32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F1:95-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F1:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F1:47,68,115/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F1:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 45.1%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

1 CYP5----SKDNVGYTKGKTC 18
 175 CCFSTGVGSANVAKVTPGSTC 196

RESULT 6
 DEHUB
 Alcohol dehydrogenase (BC 1.1.1.1) 2 [validated] - human
 N/Alternate names: alcohol dehydrogenase beta chain; class I alcohol dehydrogenase
 C/Species: Homo sapiens (man)
 C/Date: 25-Feb-1985 #sequence, revision 02-Aug-1994 #text, change 15-Sep-2000
 C/Accession: A23607; A38916; I39399; A26281; I39401; S05202; S10621; I39400; A00
 R/Heden, L.O.; Hooq, J.O.; Larsson, K.; Lake, M.; Lagerholm, E.; Holmgren, A.; Vallée, E
 FEBS Lett. 194, 327-332, 1986
 A/Title: CDNA clones coding for the beta-subunit of human liver alcohol dehydrogenase ha
 A/Reference number: A23607; MUID:86082371; PMID:3000832
 A/Accession: A23607
 A/Molecule type: mRNA
 A/Residues: 1-375 <HEB>
 A/Cross-references: EMBL:G28415; PIDN:G28416
 R/Kuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2703-2707, 1985
 A/Title: Molecular cloning of a full-length cDNA for human alcohol dehydrogenase.
 A/Reference number: A38916; MUID:85190565; PMID:2986130
 A/Accession: A38916
 A/Molecule type: mRNA
 A/Residues: 1-375 <IKU>
 A/Cross-references: GB:M24317; NID:G178097
 A/Note: this sequence has been revised in reference A38917
 R/Kuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5578, 1985
 A/Reference number: A38917
 A/Contents: annotation; erratum
 R/Yokoyama, S.; Yokoyama, R.; Rotwein, P.
 Jpn. J. Genet. 62, 241-256, 1987
 A/Title: Molecular characterization of cDNA clones encoding the human alcohol dehydrogen
 A/Reference number: I39399
 A/Accession: I39399
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-375 <YOK>
 A/Cross-references: GB:000137; NID:G219427; PIDN:BA00084.1; PID:G219428
 R/Bueser, G.; Smith, M.; Blanchone, V.; Hatfield, G.W.
 J. Biol. Chem. 261, 2027-2033, 1986
 A/Title: Molecular analysis of the human class I alcohol dehydrogenase gene family and r
 A/Reference number: A26281; MUID:86111889; PMID:2935533
 A/Accession: A26281
 A/Molecule type: DNA
 A/Residues: 1-229,'K',231-375 <DUE>
 A/Cross-references: GB:M24317; NID:G178097; PIDN:AAA51884.1; PID:G178098
 A/Note: the authors translated the codon AAA for residue 230 as Phe
 R/Tasunam, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
 Genomics 7, 152-158, 1990
 A/Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly
 A/Reference number: I39398; MUID:90269803; PMID:2347582
 A/Accession: I39402
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-6 <YAS>
 A/Cross-references: GB:M37067; NID:G178114; PIDN:AAA51593.1; PID:G178115

R/Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990
 A/Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
 A/Reference number: I39397; MUID:90382676; PMID:2169444
 A/Accession: I39401
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-6 <STR>
 A/Cross-references: GB:M32657; NID:G178112; PIDN:AAA52277.1; PID:G178113
 R/Matsumoto, Y.; Yokoyama, R.; Yokoyama, S.
 Eur. J. Biochem. 185, 317-320, 1989
 A/Title: The genes for human alcohol dehydrogenases beta(1) and beta(2) differ by only o
 A/Reference number: S05202; MUID:89338401; PMID:2547609
 A/Accession: S05202
 A/Molecule type: DNA
 A/Residues: 1-47,'H',49-375 <MAT>
 A/Cross-references: EMBL:X15447; NID:G28385
 A/Note: allelic beta-2 variant found predominately in oriental populations
 A/Note: the sequence in GenBank entry HSADH221, release 103 (PID:8228260), has an incorr
 R/Hirig, T.; von Wartburg, J.P.; Wermuth, B.
 FEBS Lett. 234, 53-55, 1988
 A/Title: CDNA sequence of the beta(2)-subunit of human liver alcohol dehydrogenase.
 A/Reference number: S10621; MUID:88271624; PMID:2968918
 A/Accession: S10621
 A/Molecule type: mRNA
 A/Residues: 1-47,'H',49-343 <EHR>
 A/Note: only a list of differences from various previously published sequences is shown
 R/Xu, Y.L.; Carr, L.G.; Boston, W.F.; Li, T.K.; Edenberg, H.J.
 Genomics 2, 209-214, 1988
 A/Title: Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci following t
 A/Reference number: G139400; MUID:88284699; PMID:3397059
 A/Accession: I39400
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-7,'W',9-56,'K',58-165,'K',167-224,'V',236-375 <RR3>
 A/Cross-references: GB:M21692; NID:G178099; PIDN:AAA51592.1; PID:G178100
 R/Hempel, R.; Buhler, R.; Kaiser, R.; von Wartburg, J.P.; Vallée, B.L.; Jornvall, H.
 Eur. J. Biochem. 145, 437-445, 1984
 A/Title: Human liver alcohol dehydrogenase. 1. The primary structure of the beta-beta-1
 A/Reference number: A00335; MUID:85076637; PMID:6391520
 A/Accession: A00335
 A/Molecule type: protein
 A/Residues: 2-129,131-375 <HEM>
 A/Note: allelic beta-1 variant found predominately in caucasian and negroid populations
 R/Buhler, R.; Hempel, R.; Kaiser, R.; von Wartburg, J.P.; Vallée, B.L.; Jornvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6320-6324, 1984
 A/Title: Human alcohol dehydrogenase: structural differences between the beta and gamma s
 ndants in livers of different mammals.
 A/Reference number: A05182; MUID:85038508; PMID:6387702
 A/Accession: A05182
 A/Molecule type: protein
 A/Residues: 12-34,'V',36-38,41-85,101-114,131-160,170-213,273-313,317-331,341-367 <BUH>
 R/Burnell, J.C.; Carr, L.G.; Dwyer, F.E.; Edenberg, H.J.; Li, T.K.; Boston, W.F.
 Biochem. Biophys. Res. Commun. 146, 1227-1233, 1987
 A/Title: The human beta-3 alcohol dehydrogenase subunit differs from beta-1 by a Cys for
 A/Reference number: A26826
 A/Accession: A26826
 A/Molecule type: protein
 A/Residues: 368-369,'C',371-375 <BUR>
 A/Note: allelic beta-3 variant found as a minor form occurring to a greater extent in neg
 R/Hurley, T.D.; Boston, W.F.; Hamilton, J.A.; Amzel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8149-8153, 1991
 A/Title: Structure of human beta-1beta-1-alcohol dehydrogenase: catalytic effects of non
 A/Reference number: A40987; MUID:91376103; PMID:1896463
 A/Contents: annotation; X-ray crystallography, 3.0 angstroms
 A/Note: structure of beta-1 variant dimer
 R/Hurley, T.D.; Boston, W.F.; Hamilton, J.A.; Amzel, L.M.
 submitted to the Brookhaven Protein Data Bank, January 1993
 A/Reference number: A52127; PDB:3HND
 A/Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 2-375
 C/Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C/Genes: ADH2
 A/Genes: GDB:ADH2

A;Cross-references: GDB:119651; OMIM:103720
A;Map position: 4q22-4q22
A;Intons: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded b
C;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
A;Pathway: alcohol degradation
A;Note: human alcohol dehydrogenase beta is expressed predominantly in fetal lung and ne
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
F;2-375/Product: alcohol dehydrogenase 2 #status experimental <MAT>
F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match 45.1%; Score 46; DB 1; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CYS-----SKDNVKGVTGKTC 18
Db 175 CGFSTGYGSANVAKVTPGSGTC 196

RESULT 7
J01472
trypsin (EC 3.4.21.4) V precursor, b-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: J01472
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: J01471; MUID:92165057; PMID:1537555
A;Accession: J01472
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59013; NID:957414; PIDN:CAA41752.1; PID:957415
A;Experimental source: pancreas
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, b-form #status predicted <MAT>
F;25-239/Domain: trypsin homology <TRY>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVKGVTGKTC 18
Db 16 FPTEDNDTRIVGSGTC 31

RESULT 8
J01471
trypsin (EC 3.4.21.4) V precursor, a-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: J01471; S23784
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: J01471; MUID:92165057; PMID:1537555
A;Accession: J01471
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59012; NID:957412; PIDN:CAA41751.1; PID:957413

A;Experimental source: pancreas
C;Superfamily: trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, a-form #status predicted <MAT>
F;25-239/Domain: trypsin homology <TRY>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVKGVTGKTC 18
Db 16 FPTEDNDTRIVGSGTC 31

RESULT 9
T32005
hypothetical protein F36H9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32005
R;Dante, M.; Kramer, J.; Twyman, B.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F36H9.
A;Reference number: Z21110
A;Accession: T32005
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-275 <DAN>
A;Cross-references: EMBL:AF016668; PIDN:AA866090.1; GSPDB:GN00020; CESP:F36H9.2
A;Experimental source: strain Bristol N2; clone F36H9
C;Genetics:
A;Gene: CESP:F36H9.2
A;Map position: 2
A;Intons: 26/2; 54/3; 80/1; 128/3; 152/1; 212/1

Query Match 43.1%; Score 44; DB 2; Length 275;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 10 CYNNSGKRGNTIPGMKTC 18
Db 193 CYNNSGKRGNTIPGMKTC 210

RESULT 10
A47328
natural killer cell tumor-recognition protein - human
N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: A47328
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortolano, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
A;Reference number: A47328; MUID:93133824; PMID:8421688
A;Accession: A47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1403 <AND>
A;Cross-references: GB:I04288; NID:g181251; PIDN:AAA5734.1; PID:g181252
A;Experimental source: NK killer cells from adult blood
A;Note: sequence extracted from NCBI backbone (NCBIN:122798, NCBI:P.122800)
C;Genetics:
A;Gene: GDB:NKTR
A;Cross-references: GDB:137171; OMIM:161565
A;Map position: 3p23-3p21
C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C;Keywords: alternative splicing; lymphocyte

Plant Physiol. 91, 124-129, 1989
A;Title: Cloning and characterization of root-specific barley lectin.
A;Reference number: Z15461
A;Accession: T05936
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <LER>
A;Cross-references: EMBL:M29280; NID:G167070; PIDN:AAA32969.1; PID:G167071
C;Superfamily: wheat agglutinin; hevein chitin-binding domain homology
C;Keywords: lectin
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-212/Product: agglutinin isolectin 1 #status predicted <MAT>
F;27-69/Domain: hevein chitin-binding domain homology <HCB>

Query March 41.2%; Score 42; DB 2; Length 212;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CYFSSKDNVGVKVTGKTC 18
|||:|||||
Db 66 CYTSKR--CGTQAGKTC 81

Search completed: October 15, 2003, 17:05:25
Job time : 13.6886 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 7.32934 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-15
Perfect score: 102
Sequence: 1 CYFSSKDNVGVKTKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	266	1	ETC1_STAAU
2	102	100.0	266	1	ETC2_STAAU
3	102	100.0	266	1	ETC3_STAAU
4	46	45.1	263	1	ITMA_MOUSE
5	46	45.1	374	1	ADHA_HUMAN
6	46	45.1	374	1	ADHB_HUMAN
7	44	43.1	246	1	TRVA_RAT
8	44	43.1	246	1	TRVB_RAT
9	44	43.1	1453	1	NKCR_MOUSE
10	44	43.1	1462	1	NKCR_HUMAN
11	43	42.2	346	1	ISPH_BRUME
12	42	41.2	212	1	AGI_HORVU
13	42	41.2	358	1	INCI_ECOLI
14	42	41.2	375	1	ADHI_RANPE
15	42	41.2	514	1	GUXC_FUSOX
16	41	40.2	35	1	SCCK_TITSE
17	41	40.2	336	1	OTCC_STRPY
18	41	40.2	368	1	ADHE_HUMAN
19	41	40.2	374	1	ADH_PAPPA
20	41	40.2	905	1	YD83_HUMAN
21	40	39.2	127	1	ACPS_THETN
22	40	39.2	242	1	PS4E_MERTH
23	40	39.2	263	1	ITMA_HUMAN
24	40	39.2	263	1	RLTA_CHICK
25	40	39.2	373	1	ADHS_HORSE
26	40	39.2	374	1	ADHI_RABIT
27	40	39.2	374	1	ADHA_MOUSE
28	40	39.2	374	1	ADHA_PERMA
29	40	39.2	374	1	ADHE_HORSE
30	40	39.2	374	1	ADHG_HUMAN
31	40	39.2	375	1	ADHA_MACMU
32	40	39.2	375	1	ADHA_RAT
33	40	39.2	412	1	FKB4_SPOFR

34	40	39.2	523	1	TYD5_PAPSO
35	40	39.2	528	1	ACH2_CHICK
36	40	39.2	612	1	UN37_GABEL
37	40	39.2	761	1	VPA_BRP2
38	40	39.2	867	1	PHLI_MOUSE
39	40	39.2	1170	1	TSP1_MOUSE
40	40	39.2	1235	1	DNBI_HCMVA
41	39.5	38.7	664	1	SVW_LISIN
42	39.5	38.7	664	1	SVW_LISMO
43	39	38.2	187	1	RECK_YERPE
44	39	38.2	256	1	YDCC_ECOLI
45	39	38.2	259	1	KCK2_RAT

ALIGNMENTS

RESULT 1	ID	ETC1_STAAU	STANDARD	PRT	266 AA.
AC	P01553	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Enterotoxin type C-1 precursor (SECI).				
GN	ENTC1.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88038352; PubMed=2823067;				
RA	Bohach G.A., Schlievert P.M.;				
RT	"Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic toxins.";				
RL	Mol. Gen. Genet. 209:15-20(1987).				
RN	[2]				
RP	SEQUENCE OF 28-266.				
RX	MEDLINE=83213327; PubMed=6189824;				
RA	Schmidt J.J., Spero L.;				
RT	"The complete amino acid sequence of staphylococcal enterotoxin C1.";				
RL	J. Biol. Chem. 258:6300-6306(1983).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION				
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.				
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN				
CC	FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL: X05815; CAA29260.1; -				
DR	PIR: S06356; ENSACI.				
DR	HSSP: P34071; 1SR2.				
DR	InterPro: IPR006177; Bactrl tox.				
DR	InterPro: IPR006123; Staph/Strep toxin.				
DR	InterPro: IPR006126; Staph/Strep tox.				
DR	InterPro: IPR006173; Staph tox OB.				
DR	PIfam: PF02876; Staph_Strep_tox_C1.				
DR	PIfam: PF01123; Staph_Strep_toxin; 1.				
DR	PRINTS: PR00279; BACTRILTOXIN.				
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.				
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.				
KM	Enterotoxin: Toxin; Signal; Superantigen.				
FT	SIGNAL	1	27		
FT	CHAIN	28	266		ENTEROTOXIN TYPE C-1.
FT	DISULFID	120	137		
FT	CONFLICT	177	177		D -> N (IN REF. 2).

SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYPSSKDNVKGKVTGKTC 18
 Db 120 CYPSSKDNVKGKVTGKTC 137
 RESULT 2
 ETC3 STAAU STANDARD; PRT; 266 AA.
 ID ETC3 STAAU STANDARD; PRT; 266 AA.
 AC P3407;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN ENT2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_taxonomy:1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "conservation of the biologically active portions of staphylococcal
 RT enterotoxins C1 and C2.";
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RT Staphylococcus aureus reveals a zinc-binding site.";
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 DR PIR; A60114; A60114.
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR PDB; 1COV; 19-SEP-01.
 DR PDB; 114P; 19-SEP-01.
 DR PDB; 114Q; 19-SEP-01.
 DR PDB; 114R; 19-SEP-01.
 DR PDB; 114X; 19-SEP-01.
 DR InterPro; IPR006177; Bcrl tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF02876; Staph_tox_Cf_1.

DR Pfam; PF01123; Staph Strep toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; zinc;
 KW 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT HELIX 49 55
 FT STRAND 60 65
 FT STRAND 69 69
 FT TURN 72 74
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 145 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYPSSKDNVKGKVTGKTC 18
 Db 120 CYPSSKDNVKGKVTGKTC 137
 RESULT 3
 ETC3 STAAU STANDARD; PRT; 266 AA.
 ID ETC3 STAAU STANDARD; PRT; 266 AA.
 AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN ENT3 OR SAIV2009 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878, 158879, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699, and N315;
 RX MEDLINE=M50 / PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Hiraoka H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT sequence comparison of all three type C staphylococcal
 RT enterotoxins";
 RL Mol. Genet. 220:329-333(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=97064178; PubMed=8906797;
 RA Fields B.A., Malchiodi E.L., Li H., Yeern X., Stauffer C.V.,
 RA Schlievert P.M., Karjalainen K., Martinza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen";
 RL Nature 384:188-192(1996).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC EMBL; AP003365; BAB43097.1; -;
 CC EMBL; X51661; CA35972.1; -;
 CC PIR; S11885; S11885.
 CC PDB; 1JCK; 12-NOV-97.
 CC PDB; 1JCG; 02-AUG-02.
 CC PDB; 1KLU; 14-AUG-02.
 CC InterPro: IPR006177; Bactl tox.
 CC InterPro: IPR006123; Staph/Strep toxin.
 CC InterPro: IPR006126; Staph/Strep tox.
 CC InterPro: IPR006173; Staph_tox_OB.
 CC Pfam; PF02876; Staph_Scrlp_tox_C; 1.
 CC Pfam; PF01123; Staph_Scrlp_toxin; 1.
 CC PRINTS; PR00279; BACTRLTOXIN.
 CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 CC Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
 CC Complete proteome.
 CC FT SIGNAL 1 27
 CC CHAIN 1 266 ENTEROTOXIN TYPE C-3.
 CC DISULFID 120 137
 CC SEQUENCE 266 AA; 30671 MW; 5ED8A32D1FFCA59 CRC64;
 CC
 CC Query Match 100.0%; Score 102; DB 1; Length 266;
 CC Best Local Similarity 100.0%; Pred. No. 3; 7e-09;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVGVKTKC 18
 DB 120 CYFSSKDNVGVKTKC 137
 RESULT 4
 ITMA MOUSE
 ID ITMA_MOUSE SE STANDARD; PRT; 263 AA.
 AC 06150:
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integral membrane protein 2A (E25 protein).
 GN ITM2A OR ITM2 OR E25.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Mandible;
 RX MEDLINE=96325063; PubMed=8702637;
 RA Deleersnijder W., Hong G., Cortvriend R., Poirier C., Tylianowski P.,
 RA Pittois K., Vanmarck E., Merregaert J.;
 RT "Isolation of markers for chondro-osteogenic differentiation using
 RT cDNA library subtraction. Molecular cloning and characterization of a
 RT gene belonging to a novel multigene family of integral membrane
 RT proteins";
 RL J. Biol. Chem. 271:19475-19482(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=99113395; PubMed=9892734;
 RA Pittois K., Wauters J., Bossuyt P., Deleersnijder W., Merregaert J.;
 RT "Genomic organization and chromosomal localization of the Itm2a
 RT gene";
 RL Mamm. Genome 10:54-56(1999).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANDIBULAR CONDYLES, IN BONE AND
 CC IN HAIR FOLLICLES. STRONG EXPRESSION IN OSTEOGENIC TISSUES, SUCH
 CC AS NEONATAL CALVARIA, PAMS, TAIL AND SKIN.
 CC -1- SIMILARITY: BELONGS TO THE ITM2 FAMILY.
 CC -----
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 CC -----
 CC EMBL; U38971; AAC37700.1; -;
 CC EMBL; AF074020; AAD14549.1; -;
 CC MGD; MGI:107706; Itm2a.
 CC Pfam; PF04089; BRICHOS; 1.
 CC Transmembrane; Signal-anchor.
 CC FT TRANSMEM 54 74
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT CARBOHYD 166 166
 CC SEQUENCE 263 AA; 29705 MW; CFF089834ABEC85A CRC64;
 CC
 CC Query Match 45.1%; Score 46; DB 1; Length 263;
 CC Best Local Similarity 43.8%; Pred. No. 4.1;
 CC Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

RESULT 5
 ADHA_HUMAN STANDARD; PRT; 374 AA.

AC P07327;
 DR 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase alpha chain (BC 1.1.1.1).
 GN ADH1A OR ADH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=66243367; PubMed=3013304;
 RA von Bahr-Lindstrom H., Hoeseg J.-O., Heden L.-O., Kaiser R.,
 RA Fleetwood L., Larsson K., Lake M., Holmquist B., Holmgren A.,
 RA Hempel J., Vallee B.L., Joernvall H.;
 RT "CDNA and protein structure for the alpha subunit of human liver
 RT alcohol dehydrogenase.";
 RL Biochemistry 25:2465-2470(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=69153548; PubMed=2920825;
 RA Matsuo Y., Yokoyama S.;
 RT "Molecular structure of the human alcohol dehydrogenase 1 gene.";
 RL FEBS Lett. 243:57-60(1989).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=90269803; PubMed=2347582;
 RA Ysuanami M., Kikuchi I., Sarapata D., Yoshida A.;
 RT "The human class I alcohol dehydrogenase gene cluster: three genes
 RT are tandemly organized in an 80-kb-long segment of the genome.";
 RL Genomics 7:152-158(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC P., ONE TO CLASS-III: CH1, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL: M12971; AAA68131.1; -;
 DR EMBL: M12963; AAA51590.1; -;
 DR EMBL: M37066; AAA51591.1; -;
 DR PIR: S02265; DEHUA.
 DR PDB: 1HSO; 27-APR-01.
 DR Genew: HGNC:249; ADH1A.
 DR GK: P07327; -;
 DR MIM: 103700; -;
 DR GO: GO:0005737; C:cytoplasm; NAS.
 DR GO: GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; NAS.
 DR GO: GO:0006066; P:alcohol metabolism; NAS.
 DR InterPro: IPR002326; ADH_zinc.

DR InterPro: IPR002085; Adh zn family.
 DR Pfam: PF00107; Adh_zinc_N; I.
 DR PROSITE: PS00059; Adh_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 KW Acetylation; 3D-structure.
 FT INIT MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 174 174 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 374 AA; 39727 MW; 5D2F5F6E31C4962C CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best local 61ilarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CYFS---SKDVGKTYGKTC 18
 Db 174 CGFSTGYGSAVNAVKTPTGTC 195
 RESULT 6
 ADHB_HUMAN STANDARD; PRT; 374 AA.
 ID ADHB_HUMAN
 AC P00325; Q13711; Q96K17;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase beta chain (BC 1.1.1.1).
 GN ADH1B OR ADH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yokoyama S., Yokoyama R., Rotwein P.;
 RT "Molecular characterization of cDNA clones encoding the human alcohol
 RT dehydrogenase beta 1 and the evolutionary relationship to the other
 RT class I subunits alpha and gamma.";
 RL Jpn. J. Genet. 62:241-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=66082371; PubMed=3000832;
 RA Heden L.O., Hoeseg J.-O., Larsson K., Lake M., Lagerholm B.,
 RA Holmgren A., Vallee B.L., Joernvall H., von Bahr-Lindstrom H.;
 RT "CDNA clones coding for the beta-subunit of human liver alcohol
 RT dehydrogenase have differentially sized 3'-non-coding regions.";
 RL FEBS Lett. 194:327-332(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=6611889; PubMed=2935533;
 RA Duester G., Smith M., Bilanchone V., Hatfield G.W.;
 RT "Molecular analysis of the human class I alcohol dehydrogenase gene
 RT family and nucleotide sequence of the gene encoding the beta
 RT subunit.";
 RL J. Biol. Chem. 261:2027-2033(1986).
 RN [5]
 RP SEQUENCE (BETA-1).
 RX MEDLINE=5076637; PubMed=6391920;
 RA Hempel J., Buhler R., Kaiser R., Holmquist B., de Zalenski C.,
 RA von Warburg J.-P., Vallee B.L., Joernvall H.;

RT "Human liver alcohol dehydrogenase. 1. The primary structure of the
 RT beta 1 isoenzyme.";
 RL Eur. J. Biochem. 145:437-445(1984).
 RN [6]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=89338401; PubMed=2547609;
 RA Matsuo Y., Yokoyama R., Yokoyama S.;
 RT "The genes for human alcohol dehydrogenases beta 1 and beta 2 differ
 RT by only one nucleotide.";
 RL Eur. J. Biochem. 183:317-320(1989).
 RN [7]
 RP SEQUENCE FROM N.A. (BETA-3).
 RX MEDLINE=90024225; PubMed=2679216;
 RA Carr L.G., Xu Y., Ho W.H., Edenberg H.J.;
 RT "Nucleotide sequence of the ADH2(3) gene encoding the human alcohol
 RT dehydrogenase beta 3 subunit.";
 RL Alcohol. Clin. Exp. Res. 13:594-596(1989).
 RN [8]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX TISSUE=Liver;
 RC Polin L., Hey-Chi H.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88284699; PubMed=3397059;
 RA Xu Y.L., Carr L.G., Bosron W.F., Li T.-K., Edenberg H.J.;
 RT "Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci
 RT following DNA sequence amplification.";
 RL Genomics 2:209-214(1988).
 RN [10]
 RP SEQUENCE OF 40-85 FROM N.A.
 RA Oeier M., Speed W.C., Seaman M.T., Kidd K.K.;
 RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP VARIANT BETA-2.
 RX MEDLINE=84221897; PubMed=6374651;
 RA Joernvall H., Hempel J., Vallee B.L., Bosron W.F., Li T.-K.;
 RT "Human liver alcohol dehydrogenase: amino acid substitution in the
 RT beta 2 beta 2 Oriental isozyme explains functional properties,
 RT establishes an active site structure, and parallels mutational
 RT exchanges in the yeast enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3024-3028(1984).
 RN [12]
 RP VARIANT BETA-3.
 RX MEDLINE=87298549; PubMed=3619918;
 RA Burnell J.C., Carr L.G., Dwyer F.E., Edenberg H.J., Li T.-K.,
 RA Bosron W.F.;
 RT "The human beta 3 alcohol dehydrogenase subunit differs from beta 1
 RT by a Cys for Arg-369 substitution which decreases NAD(H) binding.";
 RL Biochem. Biophys. Res. Commun. 146:1127-1133(1987).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=91376103; PubMed=1896463;
 RA Hurley T.D., Bosron W.F., Hamilton J.A., Amzel L.M.;
 RT "Structure of human beta 1 beta 1 alcohol dehydrogenase: catalytic
 RT effects of non-active-site substitutions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8149-8153(1991).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94260547; PubMed=8201622;
 RA Hurley T.D., Bosron W.F., Stone C.L., Amzel L.M.;
 RT "Structures of three human beta alcohol dehydrogenase variants.
 RT Correlations with their functional differences.";
 RL J. Mol. Biol. 239:415-429(1994).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=96291846; PubMed=8663387;
 RA Davis G.J., Bosron W.F., Stone C.L., Owsu-Dekyi K., Hurley T.D.;
 RT "X-ray structure of ionic interactions to coenzyme binding.";
 RL J. Biol. Chem. 271:17057-17061(1996).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +

CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
 CC MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
 CC ORIENTALS.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH ISOZYMS IN HUMAN:
 CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC -----
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 CC -----
 DR EMBL; D00137; BAA00084.1; -;
 DR EMBL; X03350; CAA27056.1; -;
 DR EMBL; M24316; AAB59496.1; -;
 DR EMBL; M24308; AAB59496.1; JOINED.
 DR EMBL; M24309; AAB59496.1; JOINED.
 DR EMBL; M24310; AAB59496.1; JOINED.
 DR EMBL; M24311; AAB59496.1; JOINED.
 DR EMBL; M24312; AAB59496.1; JOINED.
 DR EMBL; M24313; AAB59496.1; JOINED.
 DR EMBL; M24314; AAB59496.1; JOINED.
 DR EMBL; M24317; AAB51884.1; -;
 DR EMBL; X15447; CAA33487.1; -;
 DR EMBL; X15448; CAA33487.1; JOINED.
 DR EMBL; X15449; CAA33487.1; JOINED.
 DR EMBL; X15450; CAA33487.1; JOINED.
 DR EMBL; X15451; CAA33487.1; JOINED.
 DR EMBL; X15452; CAA33487.1; JOINED.
 DR EMBL; X15453; CAA33487.1; JOINED.
 DR EMBL; X15454; CAA33487.1; JOINED.
 DR EMBL; X15455; CAA33487.1; JOINED.
 DR EMBL; X38290; AAB48003.1; -;
 DR EMBL; X38283; AAB48003.1; JOINED.
 DR EMBL; X38284; AAB48003.1; JOINED.
 DR EMBL; X38285; AAB48003.1; JOINED.
 DR EMBL; X38286; AAB48003.1; JOINED.
 DR EMBL; X38287; AAB48003.1; JOINED.
 DR EMBL; X38288; AAB48003.1; JOINED.
 DR EMBL; X38289; AAB48003.1; JOINED.
 DR EMBL; AF153821; AAD37446.1; -;
 DR EMBL; M21692; AAA51592.1; -;
 DR EMBL; AF040967; AAB96912.1; -;
 DR PIR; A23607; DEHUB.
 DR PDB; 1HDY; 31-JAN-94.
 DR PDB; 1HDZ; 31-JAN-94.
 DR PDB; 3HUD; 31-JAN-94.
 DR PDB; 1DEH; 08-MAR-96.
 DR PDB; 1HTB; 07-DEC-95.
 DR PDB; 1HSZ; 27-APR-01.
 DR Genew; HGNC:250; ADH1B.
 DR GK; P00325; -;
 DR MIM; 103720; -;
 DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; TAS.
 DR GO; GO:0005489; F:electron transporter activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR GO; GO:0006069; F:ethanol oxidation; TAS.
 DR InterPro; IPR002328; Adh_zn family.
 DR InterPro; IPR02085; Adh_zn family.
 DR Pfam; PF00107; Adh_zn N; 1.
 DR PROSITE; PS00059; Adh_ZINC; 1.

KM	Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;			
KM	Acetylation; Polymorphism; 3d-structure.			
FT	INT_MFT	0	0	
FT	MOD_RES	1	1	ACETYLATION.
FT	METAL	46	46	ZINC 1 (CATALYTIC).
FT	METAL	67	67	ZINC 1 (CATALYTIC).
FT	METAL	97	97	ZINC 2.
FT	METAL	100	100	ZINC 2.
Query Match		45.1%;	Score 46;	DB 1;
Best Local Similarity		54.5%;	Pred. No. 5.8;	
Matches	12;	Conservative	0;	Mismatches
			6;	Indels
			4;	Gaps
			1;	
Qy	1	CYFS----	SKNCGKVTGKTC	18
Db	174	CGFTGSGAVNAVATPGSTC	195	
RESULT 7				
TRYA_RAT		STANDARD;	PRT;	246 AA.
AC	P32821;			
DT	01-OCT-1993	(Rel. 27, Created)		
DT	01-OCT-1993	(Rel. 27, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Trypsin V-A precursor (EC 3.4.21.4).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxId=10116;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=pancreas;			
RX	MEDLINE=92165057; PubMed=1537555;			
RA	Kang J., Wiegand U., Mueller-Hill B.;			
RT	"Identification of cDNAs encoding two novel rat pancreatic serine			
RL	proteases.";			
RL	Gene 110:181-187(1992).			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg -Xaa, Lys -Xaa.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X59012; CAA41751.1; -.			
DR	PIR; J01471; J01471.			
DR	HSSP; P00763; IDPO.			
DR	MEROPS; S01.092; -.			
DR	InterPro; IPR001314; Chymotrypsin.			
DR	InterPro; IPR001254; Ser_protease_Try.			
DR	Pfam; PF00089; trypsin.1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SMO0020; Tryp_SPC. 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM. 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS. 1.			
DR	PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.			
KW	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;			
KW	Multigene family.			
FT	SIGNAL	1	15	
FT	PROPEP	16	24	ACTIVATION PEPTIDE.
FT	CHAIN	25	246	TRYPSIN V-A.
FT	ACT_SITE	64	64	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	108	108	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	200	200	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	31	160	BY SIMILARITY.
FT	DISULFID	49	65	BY SIMILARITY.
FT	DISULFID	133	233	BY SIMILARITY.

FT	DISULFID	140	206	BY SIMILARITY.
FT <th>DISULFID</th> <td>171</td> <td>185</td> <td>BY SIMILARITY.</td>	DISULFID	171	185	BY SIMILARITY.
FT <th>DISULFID</th> <td>196</td> <td>220</td> <td>BY SIMILARITY.</td>	DISULFID	196	220	BY SIMILARITY.
FT <th>SITE</th> <td>194</td> <td>194</td> <td>REQUIRED FOR SPECIFICITY (BY SIMILARITY).</td>	SITE	194	194	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SO <th>SEQUENCE</th> <td>246 AA;</td> <td>26900 MW;</td> <td>1EBE59D88BA1715 CRC64;</td>	SEQUENCE	246 AA;	26900 MW;	1EBE59D88BA1715 CRC64;
Query Match		43.1%;	Score 44;	DB 1;
Best Local Similarity		43.8%;	Pred. No. 8.1;	
Matches	7;	Conservative	4;	Mismatches 5; Indels 0; Gaps 0;
QY		3	FSKDNVGVKVTGKTC	18
		:: ::		
Db		16	FPTEDDNDRIYGVYTC	31
RESULT 8	0	*		
TRYB_RAT				
ID_TRYB_RAT	STANDARD;	PRT;	246 AA.	
AC	P33822;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Trypsin V-B precursor (EC 3.4.21.4).			
OC	Rattus norvegicus (Rat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OK	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancreas;			
RX	MEDLINE=92165057; PubMed=1537555;			
RA	Kang J., Wiegand U., Mueller-Hill B.,			
RT	"Identification of cDNAs encoding two novel rat pancreatic serine			
RL	proteases.";			
CC	Gene 110:181-187(1992).			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- Xaa, Lys- -Xaa.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-----			
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CC	-----			
DR	EMBL; X59013; CAA11752.1; -.			
DR	PIR; J01472; J01472.			
DR	HSSP; P00763; IDPO.			
DR	MEROPS; S01.093; -.			
DR	InterPro; IPR001254; Ser_protease_Try.			
DR	Pfam; PF00089; trypsin; 1.			
DR	SMART; SM00020; *Tryp_SPC; 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.			
KW	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; signal;			
KW	Multigene family.			
FT <th>SIGNAL</th> <td>1</td> <td>15</td> <td></td>	SIGNAL	1	15	
FT <th>PROPEP</th> <td>16</td> <td>24</td> <td>ACTIVATION PEPTIDE.</td>	PROPEP	16	24	ACTIVATION PEPTIDE.
FT <th>CHAIN</th> <td>25</td> <td>246</td> <td>TRYPSIN V-B.</td>	CHAIN	25	246	TRYPSIN V-B.
FT <th>ACT_SITE</th> <td>64</td> <td>64</td> <td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td>	ACT_SITE	64	64	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT <th>ACT_SITE</th> <td>108</td> <td>108</td> <td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td>	ACT_SITE	108	108	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT <th>ACT_SITE</th> <td>200</td> <td>200</td> <td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td>	ACT_SITE	200	200	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT <th>DISULFID</th> <td>31</td> <td>160</td> <td>BY SIMILARITY.</td>	DISULFID	31	160	BY SIMILARITY.
FT <th>DISULFID</th> <td>49</td> <td>65</td> <td>BY SIMILARITY.</td>	DISULFID	49	65	BY SIMILARITY.
FT <th>DISULFID</th> <td>133</td> <td>233</td> <td>BY SIMILARITY.</td>	DISULFID	133	233	BY SIMILARITY.
FT <th>DISULFID</th> <td>140</td> <td>206</td> <td>BY SIMILARITY.</td>	DISULFID	140	206	BY SIMILARITY.
FT <th>DISULFID</th> <td>171</td> <td>185</td> <td>BY SIMILARITY.</td>	DISULFID	171	185	BY SIMILARITY.
FT <th>DISULFID</th> <td>196</td> <td>220</td> <td>BY SIMILARITY.</td>	DISULFID	196	220	BY SIMILARITY.
FT <th>SITE</th> <td>194</td> <td>194</td> <td>REQUIRED FOR SPECIFICITY (BY SIMILARITY).</td>	SITE	194	194	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SO <th>SEQUENCE</th> <td>246 AA;</td> <td>26819 MW;</td> <td>1EB899CAlBA80025 CnC64;</td>	SEQUENCE	246 AA;	26819 MW;	1EB899CAlBA80025 CnC64;

Query Match 43.1%; Score 44; DB 1; Length 246;
 Best Local Similarity 43.8%; Pred. No. 8.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 PFSKDNVGVKGTGKTC 18
 DB 16 FPTEDNDRIYGVGYTC 31

RESULT 9

NCRC MOUSE STANDARD; PRT; 1453 AA.
 AC P30415;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NK-tumor recognition protein (Natural-killer cells cyclophilin-related protein) (NK-TR protein).
 DE NKTR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93133824; PubMed=8421688;
 RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,
 RT "A cyclophilin-related protein involved in the function of natural killer cells."
 RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RC STRAIN=BAH/c; TISSUE=Blood;
 RA Anderson S.K.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
 CC INVOLVED IN THE FUNCTION OF NK CELLS.
 CC -1- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.
 CC -----
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 CC -----
 DR EMBL; L04289; AAA37500.2; ALT_INIT.
 DR HSSP; Q27450; IA33.
 DR MGD; MGI:97346; NKTR.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PROSITE; PS00170; CSA_PPIASE 1; 1.
 DR PROSITE; PS50072; CSA_PPIASE 2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Repeat; Transmembrane.
 FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.
 FT DOMAIN 222 241 ARG/LYS-RICH (BASIC).
 FT DOMAIN 422 459 ARG/LYS-RICH (BASIC).
 FT DOMAIN 964 1003 ARG/LYS-RICH (BASIC).
 FT DOMAIN 198 273 ARG/SER-RICH.
 FT DOMAIN 468 565 ARG/SER-RICH.
 FT DOMAIN 658 812 ARG/SER-RICH.
 FT DOMAIN 1303 1453 ARG-SER TANDEM REPEAT-RICH.
 SQ SEQUENCE 1453 AA; 163439 MW; DF1173F814B283E CRC64;

Query Match 43.1%; Score 44; DB 1; Length 1453;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKGTGKTC 18
 DB 1 CYFSSKDNVGVKGTGKTC 18

DB 41 CLCSEKGLGKTTGKLC 58

RESULT 10
 NCRC HUMAN STANDARD; PRT; 1462 AA.

AC P30414;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NK-tumor recognition protein (Natural-killer cells cyclophilin-related protein) (NK-TR protein).
 DE NKTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93133824; PubMed=8421688;
 RA Anderson S.K., Gallinger S., Roder J., Frey J., Young H.A.,
 RT "A cyclophilin-related protein involved in the function of natural killer cells."
 RT Proc. Natl. Acad. Sci. U.S.A. 90:542-546(1993).
 RN [2]
 RP REVISIONS.
 RA Anderson S.K.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
 CC INVOLVED IN THE FUNCTION OF NK CELLS.
 CC -1- SUBCELLULAR LOCATION: Membrane-anchored. Attached to the membrane via its N-terminus.
 CC -1- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.
 CC -----
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 CC -----
 DR EMBL; L04288; AAA3754.2; -
 DR EMBL; AF184110; AAD56402.1; -
 DR HSSP; Q27450; IA33.
 DR GeneW; HGNC:7833; NKTR.
 DR MIM; 161565; -
 DR GO; GO:0004600; F:cyclophilin; TAS.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE 1; 1.
 DR PROSITE; PS50072; CSA_PPIASE 2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Repeat; Membrane.
 FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.
 FT DOMAIN 219 240 ARG/LYS-RICH (BASIC).
 FT DOMAIN 421 457 ARG/LYS-RICH (BASIC).
 FT DOMAIN 970 1010 ARG/LYS-RICH (BASIC).
 FT DOMAIN 194 244 ARG/SER-RICH.
 FT DOMAIN 466 574 ARG/SER-RICH.
 FT DOMAIN 664 814 ARG/SER-RICH.
 FT DOMAIN 1311 1348 ARG-SER TANDEM REPEAT-RICH.
 SQ SEQUENCE 1462 AA; 165676 MW; D98A1147763EF527 CRC64;

Query Match 43.1%; Score 44; DB 1; Length 1462;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKGTGKTC 18
 DB 41 CLCSEKGLGKTTGKLC 58

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RESULT 11
ISPH BRUME STANDARD; PRT; 346 AA.
AC O8YFRL;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
ISPH protein.
GN ISPH OR LYTB OR BME1459.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Muijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Bizer P.H., Hagius S., O'Callaghan D., Leveson J.-C.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
CC -----
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CC -----
DR EMBL; AE009582; AAL52640.1; -.
DR PIR; AE3434; AE3434.
DR HAMAP; MF_00191; -.
DR InterPro; IPR003451; LytB.
DR Pfam; PF02401; LytB; 1.
DR TIGRFAMs; TIGR00216; isph_lytB; 1.
KW Isoprene biosynthesis; Complete proteome.
SQ SEQUENCE 346 AA; 37747 MW; EB9C1D60EF73421B CRC64;

Query Match 42.2%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYSSKDNVGVKT 13
| : | : | : | : |
Db 161 CHFDDEDNLGFTV 173

RESULT 12
AGI HORVU STANDARD; PRT; 212 AA.
AC P15312;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Root-specific lectin precursor.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;

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```

RN [1]
SEQUENCE FROM N.A.
RA Ierner D.R., Raikhel N.V.;
RT "Cloning and characterization of root-specific barley lectin.";
RL Plant Physiol. 91:124-129 (1989).
CC -1- FUNCTION: CARBOHYDRATE BINDING.
CC -1- SIMILARITY: Contains 4 chitin-binding domains.
CC -----
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CC -----
DR EMBL; M28280; AAA32969.1; -.
DR PIR; T05936; T05936.
DR HSP; P10969; 1MGT.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00187; Chitin bind 1; 4.
DR PRINTS; PR00451; CHITINBINDING.
DR SMART; SM00270; CHCBD; 4.
DR PROSITE; PS00026; CHITIN-BINDING; 4.
KW Lectin; Repeat; Chitin-binding; Glycoprotein; Signal;
KW Pyroliidone carboxylic acid.
FT SIGNAL 0 1* 26
FT CHAIN 27 212
FT DOMAIN 27 69
FT DOMAIN 70 112
FT DOMAIN 113 155
FT DOMAIN 156 197
FT MOD_RES 27 27
FT FT
FT DISULFID 29 44
FT DISULFID 38 50
FT DISULFID 43 57
FT DISULFID 61 66
FT DISULFID 72 87
FT DISULFID 81 93
FT DISULFID 86 100
FT DISULFID 104 109
FT DISULFID 115 130
FT DISULFID 124 136
FT DISULFID 129 143
FT DISULFID 147 152
FT DISULFID 158 173
FT DISULFID 167 179
FT DISULFID 172 186
FT DISULFID 190 195
FT CARBOHYD 206 206
SQ SEQUENCE 212 AA; 21209 MW; 8D948245DB625A5 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 212;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 CYSSKDNVGVKTGKTC 18
| : | : | : | : |
Db 66 CYTSKR--CGTQAGKTC 81

RESULT 13
INCL_ECOLI STANDARD; PRT; 358 AA.
AC Q52312; P71175; Q52283;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein inc.
GN INCC.
OS Escherichia coli.
OG Plasmid Incp-beta R751.

```


OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 RX NCBI_TaxId=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macartney D.P., Williams D.R., Stafford T., Foster A., Thomas C.M.;
 RT "Evolution of the partitioning and global regulation functions of
 the Incp central control region."
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-109 FROM N.A.
 RC STRAIN=K12 / C600;
 RX MEDLINE=95291464; PubMed=7773415;
 RA Thomas C.M., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;
 RT "Evolution of the korA-oriV segment of promiscuous Incp plasmids."
 RL Microbiology 141:1201-1210(1995).
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS ENCODED BY THE TRFB OPERON;
 IT IS INVOLVED IN PLASMID MAINTENANCE AND REPLICATION (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U67194; AAC64421.1; -
 DR InterPro: IPR000707; ATPase_Para.
 DR Pfam: PF00991; Para. 1.
 KW Plasmid; DNA replication.
 SQ SEQUENCE 358 AA; 38246 MW; 44859F07844167BE CRC64;

Query Match 41.2%; Score 42; DB 1; Length 358;
 Best Local Similarity 41.2%; Pred. No. 25;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CYFSKDNVKGVTGKTC 17
 Db 45 CHFGADGGGAGGGS 61

RESULT 14
 ADHI_RANPE STANDARD; PRT; 375 AA.
 ID ADHI_RANPE
 AC P22797;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase, major (EC 1.1.1.1).
 OS Rana perezi (Perez's frog) (Western Mediterranean green frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 RX NCBI_TaxId=8403;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=91175722; PubMed=2007119;
 RA Cederslund E., Peralba J.M., Pares X., Joernvall H.;
 RT "Amphibian alcohol dehydrogenase, the major frog liver enzyme.
 Relationships to other forms and assessment of an early gene
 duplication separating vertebrate class I and class III alcohol
 dehydrogenases."
 RL Biochemistry 30:2811-2816(1991).
 RN [2]
 RP SEQUENCE OF 1-5.
 RX MEDLINE=90353571; PubMed=2387402;
 RA Beegsted B., Batoniis M., Danielson O., Persson B., Cederslund E.,
 Kaiser R., Holmquist B., Vallee B., Pares X., Jeffery J.,
 Joernvall H.;
 RT "Fast atom bombardment mass spectrometry and chemical analysis in

RT determinations of acyl-blocked protein structures."
 RL FEBS Lett. 269:194-196(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 FAMILY. MORE CLOSELY RELATED TO CLASS I MAMMALIAN ENZYMES.
 DR PIR: A38405; A38405.
 DR HSSP: P00325; 1DEH.
 DR InterPro: IPR002328; ADH_zinc.
 DR InterPro: IPR002085; Adh_zn_family.
 DR Pfam: PF00107; ADH_zinc_N; 1.
 DR PROSITE: PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Acetylation.
 FT MOD_RES 1 1
 FT METAL 46 46 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 68 68 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 98 98 ZINC 2 (BY SIMILARITY).
 FT METAL 101 101 ZINC 2 (BY SIMILARITY).
 FT METAL 104 104 ZINC 2 (BY SIMILARITY).
 FT METAL 112 112 ZINC 2 (BY SIMILARITY).
 FT METAL 175 175 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 375 AA; 40184 MW; 283E0A60E339195 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 375;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 CYFSKDNVKGVTGKTC 18
 Db 175 CGFSTGYGSANVTGKPKGSTC 196

RESULT 15
 GUXC_FUSOX STANDARD; PRT; 514 AA.
 ID GUXC_FUSOX
 AC P46238;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Putative exoglucanase type C precursor (EC 3.2.1.91)
 DE (Exocellulohydrolase I) (1,4-beta-cellulohydrolase)
 DE (Beta-glucanocellulohydrolase).
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 RX NCBI_TaxId=5507;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95047531; PubMed=7959045;
 RA Shepard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
 Hagen F.S., Uphall A., McKnight G.L., O'Hara P.J.;
 RT "The use of conserved cellulase family-specific sequences to clone
 cellulase homologue cDNAs from Fusarium oxysporum."
 RL Gene 150:163-167(1994).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 in cellulose and cellobiose, releasing cellobiose from the non-
 reducing ends of the chains.
 CC -1- SIMILARITY: Contains 1 fungal-type cellulose-binding (CBD) domain.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GHYCOSYL
 HYDROLASES).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L29379; AAA65587.1; -
 DR HSSP: P00725; 8CEL.

DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR001722; Glyco_hydro_7.
 DR Pfam; PF00734; CBM_1; 1.
 DR Pfam; PF00840; Glyco_hydro_7; 1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR ProDom; PD186135; Glyco_hydro_7; 1.
 DR SMART; SM00236; fCBD; 1.
 DR PROSITE; PS00562; CBD_FUNGAL; 1.
 KM Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 17 POTENTIAL
 FT CHAIN 18 514 PUTATIVE EXOGLUCANASE TYPE C.
 FT DOMAIN 18 439 CATALYTIC.
 FT DOMAIN 440 482 LINKER.
 FT DOMAIN 483 514 CELLULOSE-BINDING (BY SIMILARITY).
 FT ACT_SITE 229 229 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 234 234 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 486 503 BY SIMILARITY.
 FT DISULFID 497 513 BY SIMILARITY.
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 514 AA; 54704 MM; 6A4617323A46E062 CRC64;

Query March 41.2%; Score 42; DB 1; Length 514;
 Best Local Similarity 44.4%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Oy 1 CYFSSKDNVGVKVTGKTC 18
 || : | : |||
 Db 66 CYTGKMKWDTISICTDGKTC 83

Search completed: October 15, 2003, 16:58:17
 Job time : 7.42934 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 : Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-15

Perfect score: 102

Sequence: 1 CYFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	234	2	Q9RSX4 staphylococ
2	102	100.0	239	2	Q05157 staphylococ
3	102	100.0	239	2	Q53678 staphylococ
4	102	100.0	239	2	Q06532 staphylococ
5	102	100.0	239	2	Q06531 staphylococ
6	102	100.0	239	2	Q06533 staphylococ
7	102	100.0	266	16	Q8NXJ6 staphylococ
8	102	100.0	271	2	Q9F0L6 staphylococ
9	96	94.1	239	2	Q06535 staphylococ
10	93	91.2	239	2	Q06534 staphylococ
11	55	53.9	511	16	Q8RI66 fusobacteri
12	47	46.1	2108	5	Q815C7 plasmodium
13	46.5	45.6	505	2	Q50203 xanthobacte
14	46	45.1	199	16	Q92CG4 listeria in
15	46	45.1	233	11	Q9CRM4 mus musculi
16	46	45.1	263	11	Q8KH04 mus musculi

17	46	45.1	269	6	Q8WMN3 gorilla gor
18	45	44.1	276	4	Q9NP00 homo sapien
19	44.5	43.6	107	4	Q9UL82 homo sapien
20	44.5	43.6	457	12	Q9YQZ1 ranid herpe
21	44	43.1	275	5	Q16622 caenorhabd
22	44	43.1	299	10	Q8LAK6 arabidopsis
23	44	43.1	966	11	Q8CBP6 mus musculi
24	44	43.1	2301	5	Q95281 oikopleura
25	43	42.2	126	5	Q95U05 branchiost
26	43	42.2	159	5	Q817X7 branchiost
27	43	42.2	274	10	Q9STR7 arabidopsis
28	43	42.2	315	10	Q93VX9 arabidopsis
29	43	42.2	368	5	Q9XXJ6 caenorhabd
30	43	42.2	372	16	Q8G257 bruceella su
31	43	42.2	765	5	Q26018 plasmodium
32	43	42.2	765	5	Q81KT6 plasmodium
33	43	42.2	1022	5	Q9W3E1 drosophila
34	42	41.2	148	16	Q8DRX5 streptococ
35	42	41.2	161	17	Q8TLN3 methanosarc
36	42	41.2	224	8	Q9Z2S7 ceratocolen
37	42	41.2	235	16	Q8XEI9 escherichia
38	42	41.2	260	16	Q97M39 clostridium
39	42	41.2	278	2	Q51311 nostoc punc
40	42	41.2	377	11	Q9QY99 mus musculi
41	42	41.2	378	16	Q92FD6 listeria in
42	42	41.2	378	16	Q8YAK1 listeria mo
43	42	41.2	430	16	Q9A3U5 caulobacter
44	42	41.2	1064	16	Q8XK16 clostridium
45	41.5	40.7	731	16	Q8RG00 fusobacteri

ALIGNMENTS

RESULT 1

Q9RSX4 PRELIMINARY; PRT; 234 AA.
ID Q9RSX4
AC Q9RSX4;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcstr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
DB 88 CYFSSKDNVGVTKGKTC 105

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RESULT 2
005157 ID 005157 PRELIMINARY; PRT; 239 AA.
AC 005157;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; JICK.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph toxin OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27536 MW; D66064460DE4191 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 3
053678 ID 053678 PRELIMINARY; PRT; 239 AA.
AC 053678;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph toxin OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;
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Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 4
006532 ID 006532 PRELIMINARY; PRT; 239 AA.
AC 006532;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph toxin OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC080645 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 5
006531 ID 006531 PRELIMINARY; PRT; 239 AA.
AC 006531;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; ISE2.
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DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
PT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 6
ID Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
DE Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCCopeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL: L13378; AAA26622.1; -.
DR HSSP: P34071; 1STE.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
PT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 93 CYFSSKDNVGVKVTGKTC 110

RESULT 7
ID Q8NXJ6 PRELIMINARY; PRT; 266 AA.
AC Q8NXJ6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
SECA SEC4 OR MM0759.
OS Staphylococcus aureus (strain MM2).
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OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94624.1; -.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 100.0%; Score 102; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 120 CYFSSKDNVGVKVTGKTC 137

RESULT 8
ID Q9F0L6 PRELIMINARY; PRT; 271 AA.
AC Q9F0L6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meany W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70(2001).
DR EMBL: AF217235; AAG29599.1; -.
DR HSSP: P34071; 1SE2.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 9.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
Db 125 CYFSSKDNVGVKVTGKTC 142
```

RESULT 9

Q06535 PRELIMINARY; PRT; 239 AA.
 AC Q06535; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRI 909;
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13377; AA26621.1; -.
 DR HSSP; P23313; 1JCK.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_tox; 1.
 DR Pfam; PF02876; Staph_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 27648 MW; CC3C3B04E4119E0 CRC64;

Query Match 94.4%; Score 96; DB 2; Length 239;
 Best Local Similarity 94.4%; Pred. No. 8.3e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
 Db 93 CYPSSKDNVKGVTGKTC 110

RESULT 10

Q06534 PRELIMINARY; PRT; 239 AA.
 AC Q06534; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13379; AA26623.1; -.
 DR HSSP; P34071; 1SE2.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_tox; 1.
 DR Pfam; PF02876; Staph_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON TER 1
 SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 91.2%; Score 93; DB 2; Length 239;
 Best Local Similarity 94.4%; Pred. No. 2.6e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 18
 Db 93 CYPSSKDNVKGVTGKTC 110

RESULT 11

Q8R166 PRELIMINARY; PRT; 511 AA.
 AC Q8R166; 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Cysteine permease.
 GN FN1747.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=11889109;
 RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Coleman E., Bernal A.,
 RA Larsen N., D'Souza M., Malinas T., Fusch G., Haselkorn R.,
 RA Fongstein M., Kyrides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018 (2002).
 DR EMBL; AE010479; AAL93862.1; -.
 DR InterPro; IPR002293; AA/tel_permeasel.
 DR InterPro; IPR001463; Na/Ala_sympor.
 DR Pfam; PF01235; Na_Ala_symp; 1.
 DR TIGRFAMs; TIGR00835; agcs; 1.
 DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
 KM Complete proteome.
 SQ SEQUENCE 511 AA; 56196 MW; 03D8A2859135ER3D CRC64;

Query Match 53.9%; Score 55; DB 16; Length 511;
 Best Local Similarity 52.9%; Pred. No. 1.3;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYPSSKDNVKGVTGKTC 17
 Db 128 CYPSSKDNVKGVTGKTC 144

RESULT 12

Q8I5C7 PRELIMINARY; PRT; 2108 AA.
 AC Q8I5C7; 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Hypothetical protein.
 GN PFL1410C.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=2255705; PubMed=12368864;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

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RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiolli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairland A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AB014848; AAN36368.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2108 AA; 248300 MW; 2B0464D22291B2D9 CRC64;

Query Match 46.1%; Score 47; DB 5; Length 2108;
Best Local Similarity 32.4%; Pred. No. 1.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 20; Gaps 1;

QY 1 YFSSKDN-----VGKVTGKTC 17
DB 763 CYFSSKNDYIKANINLTAKNSVYIIIGNVSGKT 799

RESULT 13
ID 050203 PRELIMINARY; PRT; 505 AA.
AC 050203;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chloroacetaldehyde dehydrogenase.
GN ALDA.
OS Xanthobacter autotrophicus.
OC Plasmid linear plasmid pXAU1.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_Taxid=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJ10;
RX MEDLINE=98172729; PubMed=9511738;
RA Bergeron H., Labbe D., Turmel C., Lau P.C.;
RT "Cloning, sequence and expression of a linear plasmid-based and a
RT chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
RT in Xanthobacter autotrophicus GJ10."
RL Gene 207:9-18(1998).
CC -|- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; AF029733; AAC13641.1; -.
DR HSSP; P05091; 1CM3.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF00171; aldehyd.1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KM Oxidoreductase; Plasmid.
SQ SEQUENCE 505 AA; 54945 MW; AD6A9EDB0297BD04 CRC64;

Query Match 45.6%; Score 46.5; DB 2; Length 505;
Best Local Similarity 58.8%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 2 YFSSKDNVGVKVTGKTC 18
DB 34 YF--DNTSPVTGKTC 47

RESULT 14
ID 092CG4 PRELIMINARY; PRT; 199 AA.
AC 092CG4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein lin1208.

```

```

GN LIN1208.
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_Taxid=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX PubMed=11679669;
RA Glaeser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Denoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Ertlan K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunat F., Kurupkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjati H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tietze P.,
RA Vazquez-Boland J.-A., Voss H., Wehlend J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
DR EMBL; AL596168; CAC96439.1; -.
DR ListList; LIN01208; -.
DR InterPro; IPR001345; PG/BPGW_mutase.
DR Pfam; PF00300; PGAM; 1.
DR PROSITE; PS00175; PG_MUTASE; 1.
KM Hypothetical protein Complete proteome.
SQ SEQUENCE 199 AA; 22902 MW; E14DD962F4C6BFB5 CRC64;

Query Match 45.1%; Score 46; DB 16; Length 199;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 YFSSKDNVGVKVTGKTC 18
DB 151 YWEKTSKIGKVTGLNRC 167

RESULT 15
ID 09CRW4 PRELIMINARY; PRT; 233 AA.
AC 09CRW4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Integral membrane protein 2 (Fragment).
GN ITM2A OR ITM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Niemi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Schor K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
RA Hayashizaki Y.;

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-16
Perfect score: 102
Sequence: 1 CYFSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	18	20	AAV06249
2	102	100.0	18	24	ABG71377
3	102	100.0	18	24	ABG71380
4	102	100.0	238	12	AA13208
5	102	100.0	238	14	AA45016
6	102	100.0	238	22	AA67343
7	102	100.0	238	23	AB76239
8	102	100.0	239	12	AA13207
9	102	100.0	239	14	AA45015

10	102	100.0	239	20	AAV06255	Staphylococcal gro
11	102	100.0	239	20	AAV06256	Staphylococcal gro
12	102	100.0	239	20	AAV06251	Staphylococcal gro
13	102	100.0	239	20	AAV06252	Staphylococcal gro
14	102	100.0	239	20	AAV06253	Staphylococcal gro
15	102	100.0	239	22	AA67342	Staphylococcus aur
16	102	100.0	239	23	AB76238	Staphylococcus aur
17	102	100.0	240	24	ABG71367	Staphylococcal ent
18	102	100.0	240	24	ABG71368	Staphylococcal ent
19	102	100.0	240	24	ABG71369	Staphylococcal ent
20	102	100.0	240	24	ABG71371	Staphylococcal ent
21	102	100.0	240	24	ABG71372	Staphylococcal ent
22	102	100.0	266	21	AAV70108	Staphylococcal SEC
23	102	100.0	266	21	AB79507	Staphylococcal gro
24	96	94.1	18	20	AAV06250	Staphylococcal ent
25	96	94.1	18	24	ABG71378	Staphylococcal gro
26	96	94.1	239	20	AAV06254	Staphylococcal gro
27	96	94.1	239	20	AAV06257	Staphylococcal gro
28	96	94.1	240	24	ABG71370	Staphylococcal ent
29	96	94.1	240	24	ABG71373	Staphylococcal ent
30	93	91.2	18	24	ABG71379	Staphylococcal ent
31	87	85.3	239	20	AAV06258	Staphylococcal gro
32	87	85.3	240	24	ABG71374	Staphylococcal ent
33	66	64.7	14	20	AAV06259	Staphylococcal ent
34	66	64.7	14	24	ABG71381	Staphylococcal ent
35	47	46.1	77	21	AA661245	Arabidopsis thalia
36	47	46.1	103	21	AA661244	Arabidopsis thalia
37	46	45.1	374	20	AAV43983	Human alcohol dehy
38	46	45.1	374	20	AAV43984	Human alcohol dehy
39	46	45.1	375	23	ABG79657	Invertebrate forag
40	46	45.1	395	21	AA658159	Lung cancer associ
41	45	44.1	277	23	AB897515	Novel human protei
42	45	44.1	513	22	AA673600	Zinc finger protei
43	44	43.1	299	21	AA606436	Arabidopsis thalia
44	44	43.1	315	21	AA606435	Arabidopsis thalia
45	44	43.1	340	21	AA606434	Arabidopsis thalia

ALIGNMENTS

RESULT 1
ID AAV06249 standard; Peptide; 18 AA.
XX AAV06249;
XX 23-AUG-1999 (first entry)
XX DT 23-AUG-1999 (first entry)
XX DE Staphylococcal group C enterotoxin disulfide loop.
XX KW Enterotoxin; SEC1; SEC2; SEC3 FRI 913; SEC3 4446; SEC-Bovine;
XX SEC-Ovine; toxin; disulfide loop; protein engineering.
XX OS Staphylococcus aureus.
XX PN MO9927889-A2.
XX PD 10-JUN-1999.
XX PF 01-DEC-1998; 98WO-US25107.
XX PR 02-DEC-1997; 97US-0067357.
XX (IDAH-) IDAH RES FOUND INC.
XX Bohach GI;
XX WPI: 1999-358008/30.
XX N-PSDB; AAX58884.
XX Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 3; 25pp; English.
XX
CC This peptide corresponds to the disulfide loop, i.e. amino acids
CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,
CC SEC3, FRI 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AA006251-53
CC and AA006255-58). The invention relates to pyrogenic toxins, such as
CC staphylococcal enterotoxins, modified in the disulfide loop region.
CC Typically, the modification involves deletions within the disulfide
CC loop region of SEC (see AA006261). The modified toxins retain useful
CC biological properties, such as the ability to induce cytokine
CC production, but have substantially reduced toxicity compared to the
CC corresponding unmodified native toxin. Emetic response inducing
CC activity and fever inducing activity are typically decreased by at
CC least about 100-fold, while LD50 (in Dutch Belted rabbits) is at
CC least 100-fold higher than the native toxin.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 102; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CYFSSKDNVKGKVTGGKTC 18
DB 1 CYFSSKDNVKGKVTGGKTC 18
XX
RESULT 2
ABG71377
ID ABG71377 standard; Peptide; 18 AA.
XX
AC ABG71377;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin disulphide loop region.
XX
KM Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KM emetic response-inducing activity; staphylococcal enterotoxin;
KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KM SEC1; SEC2; SEC3-FRI913; SEC-4446; SEC-Bovine.
XX
OS Staphylococcus aureus.
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11619.
XX
PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX
PT New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning -
XX
PS Disclosure; Fig 15; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC for vaccination against diseases such as toxic shock syndrome and

CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC disulphide loop region, occurring in several enterotoxins.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 102; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CYFSSKDNVKGKVTGGKTC 18
DB 1 CYFSSKDNVKGKVTGGKTC 18
XX
RESULT 3
ABG71380
ID ABG71380 standard; Peptide; 18 AA.
XX
AC ABG71380;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin C1 (SEC1) protein fragment.
XX
KM Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KM emetic response-inducing activity; staphylococcal enterotoxin; SEC1;
KM toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
XX
OS Staphylococcus aureus.
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11619.
XX
PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX
DR N-PADB; ABS56822.
XX
PD New modified staphylococcal enterotoxin derived from a native disulfide
PD loop-containing pyrogenic toxin, useful for non-specifically enhancing
PD an immune function and as a vaccine against toxic shock syndrome or
PD food poisoning -
XX
PS Example 1; Fig 1; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC protein fragment.
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 102; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CYFSSKDNVKGKVTGGKTC 18
DB 1 CYFSSKDNVKGKVTGGKTC 18

```
RESULT 4
AAR13208
ID AAR13208 standard; Protein; 238 AA.
XX
AC AAR13208;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C3.
XX
KW SEC3; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1991; 91WO-US00342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
PS Disclosure; Fig 1; 74pp; English.
XX
XX
CC SEC3 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems; augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
CC See AAR13203-R13211.
XX
XX
SQ Sequence 238 AA;
XX
XX
Query Match 100.0%; Score 102; DB 12; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVGVKVTGKTC 18
Db 92 CYFSSKDNVGVKVTGKTC 109
XX
XX
RESULT 5
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
AC AAR45016;
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEC3.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
```

```
PN WO9324136-A1.
XX
XX
PD 09-DEC-1993.
XX
XX
PF 01-JUN-1993; 93WO-US05213.
XX
XX
PR 01-JUN-1992; 92US-0891718.
XX
XX
PA (STON/) STONE J L.
PA (TERM/) TERMAN D S.
XX
XX
PI Stone JL, Terman DS;
XX
DR WPI; 1993-405418/50.
XX
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
XX
PS Disclosure; Fig 1; 90pp; English.
XX
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 238 AA;
XX
XX
Query Match 100.0%; Score 102; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVGVKVTGKTC 18
Db 92 CYFSSKDNVGVKVTGKTC 109
XX
XX
RESULT 6
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
XX
AC AAB67343;
XX
XX
DT 23-APR-2001 (first entry)
XX
XX
DE Staphylococcus aureus enterotoxin C3 protein.
XX
XX
KW Tumour; cancer; immune; enterotoxin.
XX
XX
OS Staphylococcus aureus.
XX
XX
PN US6180097-B1.
XX
XX
PD 30-JAN-2001.
XX
XX
PF 30-OCT-1998; 98US-0183437.
XX
XX
PR 31-JUN-1994; 94US-0189424.
PR 19-JUN-1995; 95US-0491746.
PR 03-OCT-1989; 89US-0416530.
PR 17-JAN-1990; 90US-0466577.
PR 17-JAN-1991; 91WO-US00342.
PR 01-JUN-1992; 92US-0891718.
PR 02-MAR-1993; 93US-0025144.
XX
XX
PA (TERM/) TERMAN D S.
XX
XX
PI Terman DS;
XX
```

DR WPI; 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro

PT or in vivo comprises exogenous nucleic acids encoding a superantigen

PT and a costimulatory molecule -

XX

PS Disclosure; Fig 2; 16pp; English.

XX

CC The present invention relates to a tumour cell capable of stimulating

CC antitumor immune reactivity in vitro or in vivo contains and

CC expresses an exogenous nucleic acid molecule encoding a superantigen

CC or its active fragment and an exogenous nucleic acid molecule

CC encoding a costimulatory molecule that activates T cells in

CC conjunction with an antigenic stimulus. The invention may be used

CC for cancer therapy by stimulating an anticancer immune response

CC in vivo or ex vivo.

XX

SQ Sequence 238 AA;

QY Query Match 100.0%; Score 102; DB 22; Length 238;

Db Best Local Similarity 100.0%; Pred. No. 4.7e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVGKTC 18

Db 92 CYFSSKDNVGVKVGKTC 109

RESULT 7

ABB76239

ID ABB76239 standard; Protein; 238 AA.

XX

AC ABB76239;

XX

DT 09-AUG-2002 (first entry)

XX

DE Staphylococcus aureus enterotoxin C3.

XX

XX Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;

KM antitumour; therapy.

XX

OS Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Misc-difference 208 /note= "given as 'O' in the specification"

XX

PN US2002051765-A1.

XX

PD 02-MAY-2002.

XX

PF 19-DEC-2000; 2000US-0741503.

XX

PR 31-JAN-1994; 94US-0189424.

PR 19-JUN-1995; 95US-0491746.

PR 03-OCT-1989; 89US-0416530.

PR 17-JAN-1990; 90US-0466577.

PI 17-JAN-1991; 91MO-US00342.

PR 01-JUN-1992; 92US-0891718.

PR 02-MAR-1993; 93US-0025144.

XX

PA (TERM/) TERMAN D S.

XX

PI Terman DS;

XX

DR WPI; 2002-415198/44.

XX

PT Reagent for treating cancer without the need for e.g. radiotherapy,

PT comprises a specific V beta subset of T cells sensitized to a growing

PT tumor and stimulated with superantigens -

XX

PS Disclosure; Fig 2; 17pp; English.

XX

CC The present sequence is the protein sequence of enterotoxin C3

CC (SEC3) of Staphylococcus aureus. Similarity is shown, in several

CC stretches of sequence, between staphylococcal enterotoxins,

CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative

CC toxins (see ABB76234-44). In the present invention, synthetic

CC polypeptides useful in tumour therapy and in blocking or destroying

CC autoreactive T and B lymphocyte populations are characterised by

CC substantial structural homology to staphylococcal enterotoxin A and

CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with

CC statistically significant sequence homology and similarity (Z value

CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding

CC 6) to include alignment of cysteine residues and similar hydrophathy

CC profiles. These superantigens are used to treat solid tumours,

CC including their metastases, without radiation, surgery or

CC standard chemotherapeutic agents. A claimed method of human cancer

CC treatment involves contacting haematopoietic cells from a patient

CC with one or more superantigens ex vivo to generate stimulated cells,

CC selecting a specific V beta subset of cells, and reintroducing

CC these cells into the patient to induce an in vivo therapeutic,

CC tumoricidal reaction.

XX

SQ Sequence 238 AA;

QY Query Match 100.0%; Score 102; DB 23; Length 238;

Db Best Local Similarity 100.0%; Pred. No. 4.7e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVGKTC 18

Db 92 CYFSSKDNVGVKVGKTC 109

RESULT 8

AAR13207

ID AAR13207 standard; Protein; 239 AA.

XX

AC AAR13207;

XX

DT 15-OCT-1991 (first entry)

XX

DE Staphylococcal enterotoxin C1.

XX

XX SEC1; cancer treatment; pyrogen; tumouricide.

KM

XX Staphylococcus aureus.

OS

XX WO9110680-A.

PN

PD 25-JUL-1991.

XX

PF 17-JAN-1991; 91MO-US00342.

XX

PR 17-JAN-1990; 90US-0466577.

XX

PA (TERM/) TERMAN D S.

XX

PI Terman DS;

XX

DR WPI; 1991-237984/32.

XX

PT Treating cancer with enterotoxin from Staphylococcus aureus -

PT administered by IV injection, having same tumoricidal activity

PT as Staphylococcal protein A without potential toxic reactions

XX

PS Disclosure; Fig 1; 74pp; English.

XX

CC SEC1 was isolated and purified from *S. aureus*. It can be used for

CC treating cancer, activating cytokine mediators and procoagulant

CC systems, augmenting natural killer cell cytotoxicity, etc. The

CC enterotoxin can be administered intravenously, optionally with

CC ibuprofen to attenuate toxic reaction to SEC1. Synthetic

CC polypeptides having structural homology to Staphylococcal exotoxins

CC are claimed, provided the homology includes statistically

CC significant sequence homology, alignment of Cysteine residues and
CC similar hydropathy profiles.
CC See AAR13203-R13211.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 9
AAR45015
ID AAR45015 standard; protein; 239 AA.

XX AAR45015;

XX 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)

XX Staphylococcal enterotoxin SECI.

XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
XX autoimmune disease; toxicity; Protein A; perfusion system.

XX Staphylococcus aureus.

XX WO9324136-A1.

XX 09-DEC-1993.

XX 01-JUN-1993; 93WO-US05213.

XX 01-JUN-1992; 92US-0891718.

XX (STON/) STONE J L.
PA (TERM/) TERNAN D S.

XX Stone J L, Terman D S;

XX WPI; 1993-405418/50.

XX Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases

XX Disclosure; Fig 1; 90pp; English.

XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 10

AAV06255
ID AAV06255 standard; Protein; 239 AA.

XX AAV06255;

XX 23-AUG-1999 (first entry)

XX Staphylococcal group C enterotoxin SEC-MNCoPeland.

XX Enterotoxin; SEC-MNCoPeland; toxin; disulfide loop;
XX protein engineering.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
FH Disulfide-bond 93.110

XX WO927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins
PT
PS Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC-MNCoPeland. The invention relates to pyrogenic
CC toxins, such as staphylococcal enterotoxins, modified in the
CC disulfide loop region. Typically, the modification involves
CC deletions within the disulfide loop region of SEC (see AAV06261).
CC The modified toxins retain useful biological properties, such as
CC the ability to induce cytokine production, but have substantially
CC reduced toxicity compared to the corresponding unmodified native
CC toxin. Emetic response inducing activity and fever inducing
CC activity are typically decreased by at least about 100-fold, while
CC LD50 (in Dutch Belted rabbits) is at least 100-fold higher than
CC the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYFSSKDNVKGKVTGKTC 18
|||
DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 11
AAV06256
ID AAV06256 standard; Protein; 239 AA.

XX AAV06256;

XX 23-AUG-1999 (first entry)

XX Staphylococcal group C enterotoxin SEC-4446.

XX Enterotoxin; SEC-4446; toxin; disulfide loop;
XX protein engineering.

XX Staphylococcus aureus.

XX	Key	Location/Qualifiers
FH	Disulfide-bond	93..110
FT		
XX	MO9927889-A2.	
PM		
XX	10-JUN-1999.	
PD		
XX	01-DEC-1998;	98WO-US25107.
XX	02-DEC-1997;	97US-0067357.
PR		
XX	(IDAH-) IDAHO RES FOUND INC.	
PA		
XX		
PI	Bohach GI;	
XX		
DR	WPI; 1999-358008/30.	
XX		
FT	Non-toxic modified staphylococcal enterotoxins	
XX		
PS	Disclosure; Page 17; 25pp; English.	
XX		
CC	This protein represents the Staphylococcus aureus type C	
CC	enterotoxin SEC-4446. The invention relates to pyrogenic toxins,	
CC	such as staphylococcal enterotoxins, modified in the disulfide loop	
CC	region. Typically, the modification involves deletions within the	
CC	disulfide loop region of SEC (see AAY06261). The modified toxins	
CC	retain useful biological properties, such as the ability to induce	
CC	cyclokin production, but have substantially reduced toxicity	
CC	compared to the corresponding unmodified native toxin. Emetic	
CC	response inducing activity and fever inducing activity are	
CC	typically decreased by at least about 100-fold, while LD50 (in Dutch	
CC	Belted rabbits) is at least 100-fold higher than the native toxin.	
XX		
SQ	Sequence 239 AA;	
	Query Match 100.0%; Score 102; DB 20; Length 239;	
	Best Local Similarity 100.0%; Pred. No. 4.8e-08;	
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 CYFSSKDNVGVKVTGKTC 18	
DB	93 CYFSSKDNVGVKVTGKTC 110	
	RESULT 12	
ID	AAY06251 standard; Protein; 239 AA.	
XX	AAY06251;	
AC		
XX	23-AUG-1999 (first entry)	
DT		
XX	Staphylococcal group C enterotoxin SEC1.	
DE		
XX	Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.	
KW		
XX	Staphylococcus aureus.	
OS		
XX	Key Location/Qualifiers	
FH	Disulfide-bond 93..110	
FT		
XX	MO9927889-A2.	
PM		
XX	10-JUN-1999.	
PD		
XX	01-DEC-1998;	98WO-US25107.
PF	02-DEC-1997;	97US-0067357.
PR		
XX	(IDAH-) IDAHO RES FOUND INC.	
PA		
XX		
PI	Bohach GI;	

```

XX      WPI; 1999-358006/30.
DR      Non-toxic modified staphylococcal enterotoxins
XX
PS      Disclosure; Page 17; 25pp; English.
XX
XX      This protein represents the Staphylococcus aureus type C
CC      enterotoxin SEC1. The invention relates to pyrogenic toxins, such
CC      as staphylococcal enterotoxins, modified in the disulfide loop
CC      region. Typically, the modification involves deletions within the
CC      disulfide loop region of SEC (see AAU06261). The modified toxins
CC      retain useful biological properties, such as the ability to induce
CC      cytokine production, but have substantially reduced toxicity
CC      compared to the corresponding unmodified native toxin. Emetic
CC      response inducing activity and fever inducing activity are
CC      typically decreased by at least about 100-fold, while LD50 (in Dutch
CC      Belted rabbits) is at least 100-fold higher than the native toxin.
CX
SQ      Sequence     239 AA;
XX
Query Match          100.0%; Score 102; DB 20; Length 239;
Best Local Similarity 100.0%; Pred. No. 4,8e+08;
Matches    18; Conservative   0; Mismatches   0; Indels    0; Gaps    0.
OY              1 CYFSSKDNVNGKVATGSKTC 18
                ||| | | | | | | | | | | |
DB             93 CYFSSKDNVNGKVATGSKTC 110
               ||| | | | | | | | | | | |

RESULT 13
AAU06252
ID       AAY06252 standard; Protein; 239 AA.
XX
AC       AAY06252;
XX
DT       23-AUG-1999 (first entry)
XX
DE       Staphylococcal group C enterotoxin SEC2.
XX
KW       Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
XX
OS       Staphylococcus aureus.
XX
FH       Key           Location/Qualifiers
FT       Disulfide-bond 93..110
XX
PN       MO9927889-A2.
XX
PD       10-JUN-1999.
XX
PF       01-DEC-1998; 98WO-US25107.
XX
PR       02-DEC-1997; 97US-0067357.
XX
PA       (IDA#-) IDAHO RES FOUNDD INC.
XX
PI       Bohach GI;
XX
DR       WPI; 1999-358006/30.
XX
Non-toxic modified staphylococcal enterotoxins
XX
Disclosure; Page 17; 25pp; English.
XX
This protein represents the Staphylococcus aureus type C
enterotoxin SEC2. The invention relates to pyrogenic toxins, such
as staphylococcal enterotoxins, modified in the disulfide loop
region. Typically, the modification involves deletions within the
disulfide loop region of SEC (see AAU06261). The modified toxins
retain useful biological properties, such as the ability to induce
cytokine production, but have substantially reduced toxicity
compared to the corresponding unmodified native toxin. Emetic
response inducing activity and fever inducing activity are
typically decreased by at least about 100-fold, while LD50 (in Dutch
Belted rabbits) is at least 100-fold higher than the native toxin.
```

CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while ID50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18

DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 14
AAV06253 standard; Protein; 239 AA.

XX AAV06253;

XX 23-AUG-1999 (first entry)

XX Staphylococcal group C enterotoxin SEC3-FR1913.

XX Enterotoxin; SEC3-FR1913; toxin; disulfide loop;

XX protein engineering.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Disulfide-bond 93..110

XX W09927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
XX enterotoxin SEC3-FR1913. The invention relates to pyrogenic toxins,
XX such as staphylococcal enterotoxins, modified in the disulfide loop
XX region. Typically, the modification involves deletions within the
XX disulfide loop region of SEC (see AAV06261). The modified toxins
XX retain useful biological properties, such as the ability to induce
XX cytokine production, but have substantially reduced toxicity
XX compared to the corresponding unmodified native toxin. Emetic
XX response inducing activity and fever inducing activity are
XX typically decreased by at least about 100-fold, while ID50 (in Dutch
XX Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 20; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18

DB 93 CYFSSKDNVKGKVTGKTC 110

RESULT 15
AAB67342 standard; peptide; 239 AA.

XX AAB67342;

XX 23-APR-2001 (first entry)

XX Staphylococcus aureus enterotoxin C1 protein.

XX Tumour; cancer; immune; enterotoxin.

XX Staphylococcus aureus.

XX US6180097-B1.

XX 30-JAN-2001.

XX 30-OCT-1998; 98US-0183437.

XX 31-JAN-1994; 94US-0189424.

XX 19-JUN-1995; 95US-0491746.

XX 03-OCT-1989; 89US-0416530.

XX 17-JAN-1990; 90US-0466577.

XX 17-JAN-1991; 91US-0500342.

XX 01-JUN-1992; 92US-0891718.

XX 02-MAR-1993; 93US-0025144.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro

XX or in vivo comprises exogenous nucleic acids encoding a superantigen

XX and a costimulatory molecule -

XX Disclosure; Fig 2; 16pp; English.

XX The present invention relates to a tumour cell capable of stimulating

XX antitumor immune reactivity in vitro or in vivo contains and

XX expresses an exogenous nucleic acid molecule encoding a superantigen

XX or its active fragment and an exogenous nucleic acid molecule

XX encoding a costimulatory molecule that activates T cells in

XX conjunction with an antigenic stimulus. The invention may be used

XX for cancer therapy by stimulating an anticancer immune response

XX in vivo or ex vivo.

XX Sequence 239 AA;

Query Match 100.0%; Score 102; DB 22; Length 239;

Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGKVTGKTC 18

DB 93 CYFSSKDNVKGKVTGKTC 110

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Job time : 49.3575 secs

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OM protein - protein search, using sw model

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Perfect score: 102
Sequence: 1 CYPSSKDNVKGVTGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	102	100.0	89	4	US-09-144-776B-22
3	102	100.0	89	4	US-09-144-776B-23
4	102	100.0	238	4	US-08-896-933-28
5	102	100.0	238	4	US-09-314-235-28
6	102	100.0	239	3	US-08-896-933-27
7	102	100.0	239	4	US-09-314-235-27
8	102	100.0	266	4	US-09-144-776B-14
9	48	47.1	170	4	US-09-252-991A-29047
10	46	45.1	263	2	US-08-892-690-3
11	46	45.1	374	2	US-07-857-224B-82
12	46	45.1	374	2	US-07-857-224B-83
13	46	45.1	375	4	US-09-347-878-56
14	44	43.1	134	2	US-08-482-728A-14
15	44	43.1	176	1	US-08-145-995A-4
16	44	43.1	176	2	US-08-481-747-4
17	44	43.1	176	3	US-09-134-852-4
18	42	41.2	514	1	US-08-361-920-21
19	42	41.2	514	1	US-08-479-939-21
20	42	41.2	514	1	US-08-483-432-21
21	40.5	39.7	155	4	US-09-252-991A-19995
22	40	39.2	210	4	US-09-247-155-121
23	40	39.2	264	3	US-08-924-570A-2
24	40	39.2	320	3	US-09-092-437-2
25	40	39.2	374	2	US-07-857-224B-80
26	40	39.2	374	2	US-07-857-224B-81
27	40	39.2	374	2	US-07-857-224B-84

28	40	39.2	374	2	US-07-857-224B-85	Sequence 85, Appl
29	40	39.2	375	2	US-07-857-224B-86	Sequence 86, Appl
30	40	39.2	412	2	US-08-741-134-2	Sequence 2, Appl
31	40	39.2	690	4	US-09-252-991A-29429	Sequence 29429, A
32	40	39.2	1053	4	US-09-328-352-6788	Sequence 6788, Ap
33	39.5	38.7	765	4	US-09-252-991A-24791	Sequence 24791, A
34	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
35	39	38.2	94	2	US-07-728-215-35	Sequence 35, Appl
36	39	38.2	94	4	US-08-938-085A-35	Sequence 35, Appl
37	39	38.2	94	4	US-08-938-085A-37	Sequence 37, Appl
38	39	38.2	94	4	US-10-072-844-35	Sequence 35, Appl
39	39	38.2	94	4	US-10-072-844-37	Sequence 37, Appl
40	39	38.2	95	4	US-09-107-532A-6140	Sequence 6140, Ap
41	39	38.2	228	1	US-08-278-091-7	Sequence 7, Appl
42	39	38.2	228	1	US-08-483-859-7	Sequence 7, Appl
43	39	38.2	228	1	US-08-472-173-7	Sequence 7, Appl
44	39	38.2	228	2	US-08-487-167-7	Sequence 7, Appl
45	39	38.2	228	2	US-08-482-816-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-144-776B-21
Sequence 21, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MPMC -504 Scott Street
MCMB-JA (Charles H. Harris-Patent
Acty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21
Query Match 100.0%; Score 102; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
54 CYFSSKDNVGVKVTGKTC 71

RESULT 2

US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen
Vaccines

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B

FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714

SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-144-776B-22

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
54 CYFSSKDNVGVKVTGKTC 71

RESULT 3

US-09-144-776B-23

; Sequence 23, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson

Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B

FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714

SEQUENCE CHARACTERISTICS:
LENGTH: 89
TYPE: Amino Acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-144-776B-23

Query Match 100.0%; Score 102; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGKTC 18
|||||
54 CYFSSKDNVGVKVTGKTC 71

RESULT 4

US-08-896-933028

; Sequence 28, Application US/08896933
; Patent No. 6221351

GENERAL INFORMATION:
APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILIPIN REAGENT, AND RELATED COMPOUNDS

FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933

CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978

EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28

LENGTH: 238
TYPE: PRT

ORGANISM: Staphylococcus aureas
US-08-896-933-28

Query Match 100.0%; Score 102; DB 3; Length 238;

Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVGVGTGKTC 18
Db 92 CFFSSKDNVGVGTGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 633845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-28

Query Match 100.0%; Score 102; DB 4; Length 238;

Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVGVGTGKTC 18
Db 92 CFFSSKDNVGVGTGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 622351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-27

Query Match 100.0%; Score 102; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVGVGTGKTC 18
Db 93 CFFSSKDNVGVGTGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 633845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-27

Query Match 100.0%; Score 102; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVGVGTGKTC 18
Db 93 CFFSSKDNVGVGTGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match      100.0%; Score 102; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CYSSKDNVKGKTK 18
Db      120  CYSSKDNVKGKTK 137

RESULT 9
US-09-252-991A-29047
; Sequence 29047, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29047
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29047

Query Match      47.1%; Score 48; DB 4; Length 170;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CYSSKDNVKGKTK 14
Db      116  CSFAARDNAGRATG 129

RESULT 10
US-08-892-690-3
; Sequence 3, Application US/08892690
; Patent No. 5932420
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Puri
; TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

```

; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,690
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0339 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624778
US-08-892-690-3

Query Match      45.1%; Score 46; DB 2; Length 263;
Best Local Similarity 43.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1  CYSSKDNVKGKTKGK 16
Db      90  CFPDSEDPVNSIPGGE 105

RESULT 11
US-07-857-224B-82
; Sequence 82, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlustrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (international) 41 1 632 2830
; TELEFAX: (international) 41 1 262 2437
; TELEX: none
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INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: human
FEATURE: Alcohol dehydrogenase, Table 3 Column 3
PUBLICATION INFORMATION:
AUTHORS: Joernvall, H.
AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-82

Query Match 45.1%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVKVTGKTC 18
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Db 174 CGFSTGYGSVAVNAKVTPGSTC 195

RESULT 12
US-07-857-224B-83
; Sequence 83, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; TOPOLOGY: linear
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: human
FEATURE: Alcohol dehydrogenase, Table 3 Column 4
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Joernvall, H.

AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-83

Query Match 45.1%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVKVTGKTC 18
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Db 174 CGFSTGYGSVAVNAKVTPGSTC 195

RESULT 13
US-09-347-878-56
; Sequence 56, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-878-56

Query Match 45.1%; Score 46; DB 4; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVGVKVTGKTC 18
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Db 175 CGFSTGYGSVAVNAKVTPGSTC 196

RESULT 14
US-08-482-728A-14
; Sequence 14, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSEE: & Herbert
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-14

Query Match 43.1%; Score 44; DB 2; Length 134;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKTC 18
Db 21 CLCSGKGLGKTKKLC 38

RESULT 15
US-08-145-995A-4
Sequence 4, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-4

Query Match 43.1%; Score 44; DB 1; Length 176;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVKGKTC 18
Db 41 CLCSGKGLGKTKKLC 58
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Job time : 14.7964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 27.2695 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115A-16
Perfect score: 102
Sequence: 1 CYFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 60653 seqs, 161128416 residues
Total number of hits satisfying chosen parameters: 60653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	89	15	US-10-002-784A-36
2	102	100.0	89	15	US-10-002-784A-37
3	102	100.0	89	15	US-10-002-784A-38
4	102	100.0	266	8	US-08-882-431-14
5	102	100.0	266	10	US-09-870-759-12
6	102	100.0	266	12	US-09-751-708A-12
7	102	100.0	266	15	US-10-002-784A-14
8	46	45.1	263	9	US-09-265-710-3
9	46	45.1	263	12	US-10-366-020-3
10	46	45.1	375	10	US-09-981-353-113
11	46	45.1	375	12	US-09-738-630-92
12	46	45.1	395	9	US-09-925-302-497
13	42	41.2	211	15	US-10-156-761-8802
14	42	41.2	332	15	US-10-021-811-54
15	41.5	40.7	993	15	US-10-128-714-3467

16	41.5	40.7	1105	15	US-10-128-714-8467	Sequence 8467, Ap
17	41	40.2	163	12	US-10-238-075-786	Sequence 786, App
18	41	40.2	307	11	US-09-764-891-4188	Sequence 4188, App
19	40.5	39.7	1139	15	US-10-156-761-10856	Sequence 10856, A
20	40	39.2	152	12	US-10-040-895-2	Sequence 2, Appli
21	40	39.2	210	12	US-09-903-190-121	Sequence 121, App
22	40	39.2	263	9	US-09-823-356-13	Sequence 13, Appl
23	40	39.2	263	11	US-09-946-374-43	Sequence 43, Appl
24	40	39.2	263	12	US-10-015-387A-43	Sequence 43, Appl
25	40	39.2	263	12	US-10-006-130A-43	Sequence 43, Appl
26	40	39.2	263	12	US-10-199-672-184	Sequence 184, App
27	40	39.2	263	12	US-10-006-172A-43	Sequence 43, Appl
28	40	39.2	263	12	US-10-187-749-184	Sequence 184, App
29	40	39.2	263	12	US-10-194-457-184	Sequence 184, App
30	40	39.2	263	12	US-10-184-642-184	Sequence 184, App
31	40	39.2	263	12	US-10-196-747-184	Sequence 184, App
32	40	39.2	263	12	US-10-015-392A-43	Sequence 43, Appl
33	40	39.2	263	12	US-10-017-253A-43	Sequence 43, Appl
34	40	39.2	263	12	US-10-173-689-184	Sequence 184, App
35	40	39.2	263	12	US-10-173-690-184	Sequence 184, App
36	40	39.2	263	12	US-10-173-691-184	Sequence 184, App
37	40	39.2	263	12	US-10-173-692-184	Sequence 184, App
38	40	39.2	263	12	US-10-173-694-184	Sequence 184, App
39	40	39.2	263	12	US-10-173-698-184	Sequence 184, App
40	40	39.2	263	12	US-10-173-699-184	Sequence 184, App
41	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
42	40	39.2	263	12	US-10-174-569-184	Sequence 184, App
43	40	39.2	263	12	US-10-174-583-184	Sequence 184, App
44	40	39.2	263	12	US-10-174-587-184	Sequence 184, App
45	40	39.2	263	12	US-10-174-589-184	Sequence 184, App

ALIGNMENTS

RESULT 1
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin CI
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match 100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
Db 54 CYFSSKDNVGVTKGKTC 71

RESULT 2
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33

```
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-37

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
      |||||
Db      54 CYFSSKDNVKGVTGGKTC 71

RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-38

Query Match      100.0%; Score 102; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
      |||||
Db      54 CYFSSKDNVKGVTGGKTC 71

RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRMW -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
```

```
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match      100.0%; Score 102; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
      |||||
Db      120 CYFSSKDNVKGVTGGKTC 137

RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: FERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-12

Query Match      100.0%; Score 102; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CYFSSKDNVKGVTGGKTC 18
      |||||
Db      120 CYFSSKDNVKGVTGGKTC 137

RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
```



```
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match 100.0%; Score 102; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 7
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 100.0%; Score 102; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 8
US-09-265-710-3
; Sequence 3, Application US/09265710
; Patent No. US20020042126A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW INTEGRAL MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

Query Match 100.0%; Score 102; DB 12; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 9
US-10-366-020-3
; Sequence 3, Application US/10366020
; Publication No. US20030152989A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/366,020
; FILING DATE: 11-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,161
; FILING DATE: 1998-12-07
; APPLICATION NUMBER: US/08/791,338
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/892,690
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0339 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624778
US-09-265-710-3

Query Match 45.1%; Score 46; DB 9; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGCK 16
Db 90 CFFDSEDPVNSIPGGE 105

RESULT 9
US-10-366-020-3
; Sequence 3, Application US/10366020
; Publication No. US20030152989A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/366,020
; FILING DATE: 11-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,161
; FILING DATE: 1998-12-07
; APPLICATION NUMBER: US/08/791,338
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

```

; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0208 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624778
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-366-020-3

Query Match 45.1%; Score 46; DB 12; Length 263;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYPSSKDNVKGVTGGK 16
Db 90 CFFDSEDPVNSIPGGE 105

RESULT 10
US-09-981-353-113
; Sequence 113, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laeak, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 2512879CD1
US-09-981-353-113

Query Match 45.1%; Score 46; DB 10; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVKGVTGGKTC 18
Db 175 CGFSTGYGSVAVNAKVTPGTC 196

RESULT 11
US-09-738-630-92
; Sequence 92, Application US/09738630
; Publication No. US20030166213A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; APPLICANT: Shaw, Paul J.
; TITLE OF INVENTION: Methods For Identifying Compounds That
; TITLE OF INVENTION: Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
; TITLE OF INVENTION: Protein Kinase Signaling
; FILE REFERENCE: P-NI 3906
; CURRENT APPLICATION NUMBER: US/09/738,630
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92

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```

; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-630-92

Query Match 45.1%; Score 46; DB 12; Length 375;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVKGVTGGKTC 18
Db 175 CGFSTGYGSVAVNAKVTPGTC 196

RESULT 12
US-09-925-302-497
; Sequence 497, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 497
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-497

Query Match 45.1%; Score 46; DB 9; Length 395;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS-----SKDNVKGVTGGKTC 18
Db 195 CGFSTGYGSVAVNAKVTPGTC 216

RESULT 13
US-10-156-761-8802
; Sequence 8802, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8802
; LENGTH: 211
; TYPE: PRT

```

```

; ORGANISM: Streptomyces avermitilis
US-10-156-761-8802

Query Match      41.2%; Score 42; DB 15; Length 211;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YFSSKDNVKGVT 13
   :|||||:
Db 58 HFSSKNLTKAT 69

RESULT 14
US-10-021-811-54
; Sequence 54, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odell, Joan
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BB1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 54
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Glycine max
US-10-021-811-54

Query Match      41.2%; Score 42; DB 15; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CYFSSKDNVKGVTGG 15
   |||||:
Db 197 CYASSADNIARMLKG 211

RESULT 15
US-10-128-714-3467
; Sequence 3467, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3467

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; LENGTH: 993
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3467

Query Match      40.7%; Score 41.5; DB 15; Length 993;
Best Local Similarity 40.9%; Pred. No. 4.3e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 9; Gaps 1;

QY 5 SKDNV-----GKVTGGKT 17
   :|||:
Db 102 TKDNICFQOIDABEGTITGGKT 123

Search completed: October 15, 2003, 17:47:02
Job time : 28.2695 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 13.6886 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115A-16

Perfect score: 102
Sequence: 1 CYFSSKDNVGVKGGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	266	1 ENSAC1	enterotoxin C-1 pr
2	102	100.0	266	2 A60114	enterotoxin C-2 pr
3	102	100.0	266	2 S11885	enterotoxin C3 - S
4	46	45.1	199	2 AG1583	weakly phosphoglyc
5	46	45.1	375	1 DEHUA	alcohol dehydrogen
6	46	45.1	375	1 DEHUA	alcohol dehydrogen
7	44	43.1	246	2 JQ1472	trypsin (EC 3.4.21
8	44	43.1	246	2 JQ1471	trypsin (EC 3.4.21
9	44	43.1	275	2 T32005	hypothetical prote
10	44	43.1	1403	1 A47328	natural killer cel
11	44	43.1	1507	2 B47328	natural killer cel
12	43	42.2	274	2 T13010	hypothetical prote
13	43	42.2	346	2 AE3434	lytB protein (impo
14	43	42.2	368	2 T26338	hypothetical prote
15	42	41.2	212	2 T05936	agglutinin isolect
16	42	41.2	235	2 E91097	hypothetical prote
17	42	41.2	235	2 A85943	hypothetical prote
18	42	41.2	260	2 B96944	2 deoxy-D-gluconat
19	42	41.2	358	2 T08477	inclusion membrane
20	42	41.2	375	1 A38405	alcohol dehydrogen
21	42	41.2	378	2 AC1454	protein gp18 from
22	42	41.2	378	2 AD1090	protein gp18 from
23	42	41.2	430	2 A87634	peptidase, M20/M25
24	41	40.2	57	2 S70473	neurotoxin Ts-kapp
25	41	40.2	97	2 T08573	hypothetical prote
26	41	40.2	199	2 AD1230	phosphoglycerate m
27	41	40.2	269	2 B97113	protein serine/thr
28	41	40.2	368	1 DEHUA6	alcohol dehydrogen
29	41	40.2	375	1 A33909	alcohol dehydrogen

ALIGNMENTS

RESULT 1

ENSAC1

enterotoxin C-1 precursor - Staphylococcus aureus

C;Species: Staphylococcus aureus

C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999

C;Accession: S06356; A01816

R;Bohach, G.A.; Schlievert, P.M.

Mol. Gen. Genet. 209, 15-20, 1987

A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness t

A;Reference number: S06356; MUID:88038352; PMID:2823067

A;Accession: S06356

A;Molecule type: DNA

A;Residues: 1-266 <BOH>

A;Cross-references: EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567

R;Schmidt, J.J.; Spero, L.

J. Biol. Chem. 258, 6300-6306, 1983

A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.

A;Reference number: A01816; MUID:83213327; PMID:6189824

A;Accession: A01816

A;Molecule type: protein

A;Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>

C;Genetics:

A;Gene: entC1

C;Superfamily: enterotoxin B

C;Keywords: enterotoxin

F;1-27/Domain: signal sequence #status predicted <SIG>

F;28-266/Product: enterotoxin C-1 #status experimental <MAT>

F;120-137/Disulfide bonds: #status experimental

Query Match 100.0%; Score 102; DB 1; Length 266;

Best Local Similarity 100.0%; Pred No. 2,3e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0;

QY 1 CYFSSKDNVGVKGGKTC 18

Db 120 CYFSSKDNVGVKGGKTC 137

RESULT 2

A60114

enterotoxin C-2 precursor - Staphylococcus aureus

N;Alternate names: enterotoxin C-3 precursor

C;Species: Staphylococcus aureus

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999

C;Accession: A60114; B60114; A33866

R;Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2252, 1989

A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins

A;Reference number: A60114; MUID:89277549; PMID:2543837

A;Accession: A60114

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-266 <BOH>
A;Accession: B60114
A;Molecule type: protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests the
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA36624.1; PID:g153004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>
Query Match 100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 120 CYFSSKDNVKGVTGGKTC 137
RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S11885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison
A;Reference number: S11885; MUID:90220508; PMID:2325627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
A;Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B
Query Match 100.0%; Score 102; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 120 CYFSSKDNVKGVTGGKTC 137
RESULT 4
AG1583
weakly phosphoglycerate mutase 1 homolog lin1208 [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1583
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96439.1; PID:g16413682; GSPDB:GN00178

A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1208
Query Match 45.1%; Score 46; DB 2; Length 199;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 2 YFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 151 YWEKTSKIGKVTGLKNC 167
RESULT 5
DEHUA
alcohol dehydrogenase (EC 1.1.1.1) 1 - human
N;Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
C;Accession: S02265; A25428; A24408; I39398; I39397
R;Matsuoka, Y.; Yokoyama, S.
FEBS Lett. 243, 57-60, 1989
A;Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
A;Reference number: S02265; MUID:89153548; PMID:2920825
A;Accession: S02265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-375 <MATS>
R;Ikuta, T.; Szeto, S.; Yoshida, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
A;Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and ev
A;Reference number: A94120; MUID:86120995; PMID:2935875
A;Accession: A25428
A;Molecule type: mRNA
A;Residues: 1-375 <IKU>
A;Cross-references: GB:M12271; NID:g178091; PIDN:AAA68131.1; PID:g178092
R;von Bahr-Lindstrom, H.; Hoog, J.O.; Heden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K.
Biochemistry 25, 2465-2470, 1986
A;Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
A;Reference number: A24408; MUID:86243367; PMID:3013304
A;Accession: A24408
A;Molecule type: mRNA
A;Residues: 1-375 <VON>
A;Cross-references: GB:M12963; NID:g178089; PIDN:AAA51590.1; PID:g178090
R;Yasunani, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
Genomics 7, 152-158, 1990
A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
A;Reference number: I39398; MUID:90269803; PMID:2347582
A;Accession: I39398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <YAS>
A;Cross-references: GB:M37066; NID:g178095; PIDN:AAA51591.1; PID:g178096
R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
Gene 90, 271-279, 1990
A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
A;Reference number: I39397; MUID:90382676; PMID:2169444
A;Accession: I39397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <STE>
A;Cross-references: GB:M32656; NID:g178093; PIDN:AAA52276.1; PID:g178094
C;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
C;Genetics:
A;Gene: GDB:ADH1
A;Cross-references: GDB:119650; OMIM:103700
A;Map position: 4q21.4q23
A;Intons: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
C;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: ethanol degradation
A;Note: human alcohol dehydrogenase 1 is expressed predominately in fetal and neonatal l

A;Cross-references: GDB:119651; OMIM:103720
A;Map position: 4q22-q22
A;Introns: 6/3; 40/3; 8/11, 116/2; 199/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
C;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: alcohol degradation
A;Note: human alcohol dehydrogenase beta is expressed predominantly in fetal lung and ne
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidore
F;2-375/Product: alcohol dehydrogenase 2 #status experimental <MAT>
F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match 45.1%; Score 46; DB 1; Length 375;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYFS----SKDNVGVKVTGGKTC 18
Db 175 CGFSTGYGSAAVNVAKVTPGSGTC 196

RESULT 7
JQ1472
trypsin (EC 3.4.21.4) V precursor, b-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: JQ1472
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: JQ1471; MUID:92165057; PMID:1537555
A;Accession: JQ1472
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59013; NID:g57414; PIDN:CAA41752.1; PID:g57415
A;Experimental source: pancreas
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, b-form #status predicted <MAT>
F;25-239/Domain: trypsin homology <TRY>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGGKTC 18
Db 16 FPTEDNDRIVGGYTC 31

RESULT 8
JQ1471
trypsin (EC 3.4.21.4) V precursor, a-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: JQ1471; S23784
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: JQ1471; MUID:92165057; PMID:1537555
A;Accession: JQ1471
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59012; NID:g57412; PIDN:CAA41751.1; PID:g57413

A;Experimental source: pancreas
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, a-form #status predicted <MAT>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 43.1%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGGKTC 18
Db 16 FPTEDNDRIVGGYTC 31

RESULT 9
T32005
hypothetical protein F36H9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32005
R;Dante, M.; Kramer, J.; Twyman, B.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F36H9.
A;Reference number: Z21110
A;Accession: T32005
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-275 <DAN>
A;Cross-references: EMBL:AF016668; PIDN:AAB66090.1; GSPDB:GN00020; CESP:F36H9.2
A;Experimental source: strain Bristol N2; clone F36H9
C;Genetics:
A;Gene: CESP:F36H9.2
A;Map position: 2
A;Introns: 26/2; 54/3; 80/1; 128/3; 152/1; 212/1

Query Match 43.1%; Score 44; DB 2; Length 275;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
Db 193 CYNNSNGKPGNIPGMKYC 210

RESULT 10
A47328
natural killer cell tumor-recognition protein - human
N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: A47328
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
A;Reference number: A47328; MUID:93133824; PMID:8421688
A;Accession: A47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1403 <AND>
A;Cross-references: GB:I04288; NID:g181251; PIDN:AAA35734.1; PID:g181252
A;Experimental source: NK killer cells from adult blood
A;Note: sequence extracted from NCBI backbone (NCBIN:122798, NCBI:P:122800)
C;Genetics:
A;Gene: GDB:NKTR
A;Cross-references: GDB:137171; OMIM:161565
A;Map position: 3p23-3p21
C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C;Keywords: alternative splicing; lymphocyte

F;60-230/Domain: cyclophilin homology <CYP>

Query Match 43.1%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
| : : : : :
DB 95 CLCGSGKGLGKTKGKLC 112

RESULT 11

B47328
natural killer cell tumor-recognition protein - mouse
N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 05-Nov-1999
C;Accession: B47328; I77662
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
A;Reference number: A47328; MUID:93133824; PMID:8421688
A;Accession: B47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1507 <AND>
A;Cross-references: GB:L04289; NID:G192866
A;Note: authors translated the codon AGT for residue 972 as Arg
R;Rinfret, A.; Anderson, S.K.
Mol. Immunol. 30, 1307-1313, 1993
A;Title: IL-2 regulates the expression of the NK-TR gene via an alternate RNA splicing m
A;Reference number: I57820; MUID:94019422; PMID:8413330
A;Accession: I77662
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 235-237;263-294 <RIN>
A;Cross-references: GB:S65998; NID:G425701; PIDN:AAB28500.1; PID:G425702
C;Genetics:
A;Gene: NK-TR
C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C;Keywords: alternative splicing; lymphocyte
F;60-230/Domain: cyclophilin homology <CYP>

Query Match 43.1%; Score 44; DB 2; Length 1507;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVTGGKTC 18
| : : : : :
DB 95 CLCGSGKGLGKTKGKLC 112

RESULT 12

T13010
hypothetical protein T24C20.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999
C;Accession: T13010
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17586
A;Accession: T13010
A;Molecule type: DNA
A;Residues: 1-274 <CHO>
A;Cross-references: EMBL:AL096856; GSPDB:GN000061; ATSP:T24C20.90
A;Experimental source: cultivar Columbia; BAC clone T24C20
C;Genetics:
A;Gene: ATSP:T24C20.90
A;Map position: 3
A;Introns: 62/1; 84/1; 133/1; 171/1; 201/1; 271/3
Query Match 42.2%; Score 43; DB 2; Length 274;
Best Local Similarity 75.0%; Pred. No. 41;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SKDNVGVKVTGGK 16
| : : : : :
DB 137 SKDNAGKVTEDK 148

RESULT 13

AE3434
lytB protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AE3434
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, V.
; Mazur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AJ3252; PMID:11756688
A;Accession: AE3434
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52640.1; PID:G17983462; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1459
A;Map position: 1
C;Superfamily: penicillin tolerance protein
Query Match 42.2%; Score 43; DB 2; Length 346;
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVT 13
| : : : : :
DB 161 CHFDEEDNLGPT 173

RESULT 14

T26338
hypothetical protein Y102A5B.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26338
R;Gardner, A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20203
A;Accession: T26338
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-368 <WIL>
A;Cross-references: EMBL:AL023821; PIDN:CAA19437.1; CESP:Y102A5B.3
A;Experimental source: clone Y102A5B
C;Genetics:
A;Introns: 61/3; 76/3; 136/3; 185/1; 245/1
Query Match 42.2%; Score 43; DB 2; Length 368;
Best Local Similarity 43.8%; Pred. No. 54;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSSKDNVGVKVTGGKTC 18
| : : : : :
DB 144 FASKNIGNIWTGLJC 159

RESULT 15

T05936
agglutinin isolectin 1 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
C;Accession: T05936
R;Lerner, D.R.; Raikhel, N.V.

Plant Physiol. 91, 124-129, 1989
A;Title: Cloning and characterization of root-specific barley lectin.
A;Reference number: Z15461
A;Accession: T05936
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <LER>
A;Cross-references: EMBL:M29280; NID:g167070; PIDN:AAA32969.1; PID:g167071
C;Superfamily: wheat agglutinin; hevein chitin-binding domain homology
C;Keywords: lectin
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-212/Product: agglutinin isolectin 1 #status predicted <MAT>
F;27-69/Domain: hevein chitin-binding domain homology <HCB>

Query Match 41.2%; Score 42; DB 2; Length 212;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 CYFSSKDNVGVKVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 66 CYTSKR--CGTQAGGKTC 81

Search completed: October 15, 2003, 17:06:25
Job time : 13.6886 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 7.32934 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-16

Perfect score: 102

Sequence: 1 CYFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	102	100.0	266	1 ETC1_STAAU	P01553 staphylococ
2	102	100.0	266	1 ETC2_STAAU	P34071 staphylococ
3	102	100.0	266	1 ETC3_STAAU	P23313 staphylococ
4	46	45.1	263	1 ITMA_MOUSE	Q61500 mus musculu
5	46	45.1	374	1 ADHA_HUMAN	P07327 homo sapien
6	46	45.1	374	1 ADHE_HUMAN	P00325 homo sapien
7	44	43.1	246	1 TRYA_RAT	P32821 rattus norv
8	44	43.1	246	1 TRYB_RAT	P32822 rattus norv
9	44	43.1	1453	1 NKCR_MOUSE	P30415 mus musculu
10	44	43.1	1462	1 NKCR_HUMAN	P30414 homo sapien
11	43	42.2	346	1 ISPH_BRUME	Q8YFR1 brucella me
12	42	41.2	212	1 AGI_HORVU	P15312 hordeum vul
13	42	41.2	358	1 INCI_ECOLI	Q52312 escherichia
14	42	41.2	375	1 ADHI_RANPE	P22797 rana perezi
15	42	41.2	514	1 GUXC_FUSOX	P46238 fusarium ox
16	41	40.2	35	1 SKCK_TITSE	P56219 titvys serr
17	41	40.2	336	1 OTCC_STRPY	P16964 streptococ
18	41	40.2	368	1 ADH6_HUMAN	P28332 homo sapien
19	41	40.2	374	1 ADH_FAPHA	P14139 papio hamad
20	41	40.2	905	1 YD83_HUMAN	Q9P294 homo sapien
21	40	39.2	127	1 ACPS_THETN	Q8R857 thermoanaer
22	40	39.2	242	1 RS4E_METTH	Q26123 methanobact
23	40	39.2	263	1 ITMA_HUMAN	Q43736 homo sapien
24	40	39.2	265	1 RL7A_CHICK	P32429 gallus gall
25	40	39.2	373	1 ADHS_HORSE	P00328 equus cabal
26	40	39.2	374	1 ADHI_RABIT	Q03505 oryctolagus
27	40	39.2	374	1 ADHA_MOUSE	P00329 mus musculu
28	40	39.2	374	1 ADHA_PERMA	P41680 peromyscus
29	40	39.2	374	1 ADHE_HORSE	P00327 equus cabal
30	40	39.2	374	1 ADHC_HUMAN	P00326 homo sapien
31	40	39.2	374	1 ADH_MACMU	P28469 macaca mula
32	40	39.2	375	1 ADHA_RAT	P06757 rattus norv
33	40	39.2	412	1 PKB4_SPOFR	Q26486 spodoptera

ALIGNMENTS

RESULT 1

ID	ETC1_STAAU	STANDARD;	PRT;	266 AA.
AC	P01553;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Enterotoxin type C-1 precursor (SEC1).			
GN	ENTC1.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88038352; PubMed=2823067;			
RA	Bohach G.A., Schlievert P.M.;			
RT	"Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic toxins.";			
RL	Mol. Gen. Genet. 209:15-20(1987).			
RN	[2]			
RP	SEQUENCE OF 28-266.			
RX	MEDLINE=83213327; PubMed=6189824;			
RA	Schmidt J.J., Spero L.;			
RT	"The complete amino acid sequence of staphylococcal enterotoxin Cl.";			
RL	J. Biol. Chem. 258:6300-6306(1983).			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION			
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.			
CC	-!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; X05815; CAA29260.1; .			
DR	PIR; S06356; ENSACL.			
DR	HSSP; P34071; LS22.			
DR	InterPro; IPR006177; Bctrl tox.			
DR	InterPro; IPR006123; Staph/Strep toxin.			
DR	InterPro; IPR006126; Staph/Strep tox.			
DR	InterPro; IPR006173; Staph tox OB.			
DR	Pfam; PF02876; Staph_Strp_tox_C; 1.			
DR	Pfam; PF01123; Staph_Strp_toxin; 1.			
DR	PRINTS; PR00279; BACTRLTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Enterotoxin; Toxin; Signal; Superantigen.			
FT	SIGNAL 1 27			
FT	CHAIN 28 266			
FT	DISULFID 120 137			
FT	CONFLICT 177 177			
FT				ENTEROTOXIN TYPE C-1.
FT				D -> N (IN REF. 2).

P54771 papaver som
P09480 gallus gall
O02482 caenorhabdi
O06419 bacterioph
O54990 mus musculu
P35441 mus musculu
P17147 human cytom
Q92490 listeria in
Q8vaf2 listeria mo
P37867 versinia pe
Q48809 escherichia
P00759 rattus norv

34 40 39.2 523 1 TVD5_PAPSO
35 40 39.2 528 1 ACH2_CHICK
36 40 39.2 612 1 UN37_CAEEL
37 40 39.2 761 1 VPA_BPP2
38 40 39.2 867 1 PML1_MOUSE
39 40 39.2 1170 1 TSP1_MOUSE
40 40 39.2 1235 1 DNBI_HCMVA
41 39.5 38.7 664 1 SYM_LISIN
42 39.5 38.7 664 1 SYM_LISMO
43 39 38.2 187 1 RECK_YERPE
44 39 38.2 256 1 YQEC_ECOLI
45 39 38.2 259 1 KLK2_RAT

SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;

Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGGKTC 18
 |||||
 DB 120 CYFSSKDNVGVGGKTC 137

RESULT 2

ETC2_STAAU STANDARD; PRT; 266 AA.

AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN ENTC2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bonach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 enterotoxins C1 and C2.";
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 Staphylococcus aureus reveals a zinc-binding site.";
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 FAMILY.
 CC PIR; A60114.
 CC PDB; 1STE: 23-DEC-96.
 CC PDB; 1SE2: 08-MAR-96.
 CC PDB; 1CQV: 19-SEP-01.
 CC PDB; 1I4P: 19-SEP-01.
 CC PDB; 1I4Q: 19-SEP-01.
 CC PDB; 1I4R: 19-SEP-01.
 CC PDB; 1I4X: 19-SEP-01.
 CC InterPro; IPR006177; Bctrl tox.
 CC InterPro; IPR006123; Staph/Strep_toxin.
 CC InterPro; IPR006126; Staph/Strep_tox.
 CC InterPro; IPR006173; Staph_tox_OB.
 CC Pfam; PF02876; Staph_Strep_tox_C; 1.

DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLETOXIN
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 3D-structure.

FT SIGNAL 1 27 ENTEROTOXIN TYPE C-2.
 FT CHAIN 28 266
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT TURN 49 55
 FT STRAND 60 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT STRAND 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT STRAND 242 246
 FT TURN 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGGKTC 18
 |||||
 DB 120 CYFSSKDNVGVGGKTC 137

RESULT 3

ETC3_STAAM STANDARD; PRT; 266 AA.

AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN ENIC3 OR SAV2009 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 1280;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=MUSO / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=1418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Shiba T.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hirumatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240 (2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT sequence comparison of all three type C staphylococcal
 RT enterotoxins";
 RL Mol. Gen. Genet. 220:329-333 (1990).
 RN [3]
 RX X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RP MEDLINE=97064178; PubMed=8906797;
 RA Fields B.A., Malchiodi E.L., Li H., Yeern X., Stauffacher C.V.,
 RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen";
 RL Nature 384:188-192 (1996).
 RN [4]
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 DR EMBL; AP003364; BAB58171.1; -;
 DR EMBL; AP003135; BAB43097.1; -;
 DR EMBL; X51661; CAA35972.1; -;
 DR PIR; S11885; S11885.
 DR PDB; 1JCK; 12-NOV-97.
 DR PDB; 1KLG; 02-AUG-02.
 DR PDB; 1KLU; 14-AUG-02.
 DR InterPro; IPR006177; Bactrl_tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB-
 DR Pfam; PF02876; Staph_Strep_tox_C7_1.
 DR Pfam; PF01123; Staph_Strep_tox_C7_1.
 DR PRINTS; PR0279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
 KW Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137
 SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;

Query Match 100.0%; Score 102; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVKVGKTC 18
 DB 120 CYFSSKDNVGVKVGKTC 137
 RESULT 4
 ITMA_MOUSE
 ID ITMA_MOUSE STANDARD; PRT; 263 AA.
 AC Q61500;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integral membrane protein 2A (E25 protein).
 GN ITM2A OR ITM2 OR E25.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Mandible;
 RX MEDLINE=96325063; PubMed=8702637;
 RA Deleersnijder W., Hong G., Cortvriindt R., Poirier C., Tylzanowski P.,
 RA Pittois K., Vanmarck E., Merregaert J.;
 RT "Isolation of markers for chondro-osteogenic differentiation using
 RT cDNA library subtraction. Molecular cloning and characterization of a
 RT gene belonging to a novel multigene family of integral membrane
 RT proteins";
 RL J. Biol. Chem. 271:19475-19482 (1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=99111395; PubMed=9892734;
 RA Pittois K., Wauters J., Bossuyt P., Deleersnijder W., Merregaert J.;
 RT "Genomic organization and chromosomal localization of the Itm2a
 RT gene";
 RL Mamm. Genome 10:54-56 (1999).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANDIBULAR CONDYLES, IN BONE AND
 CC IN HAIR FOLLICLES, STRONG EXPRESSION IN OSTEOGENIC TISSUES, SUCH
 CC AS NEONATAL CALVARIA, PAMS, TAIL AND SKIN.
 CC -!- SIMILARITY: BELONGS TO THE ITM2 FAMILY.
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 CC -----
 DR EMBL; L38971; AAC37700.1; -;
 DR EMBL; AF074020; AAD14549.1; -;
 DR MGD; MGI:107706; Itm2a.
 DR Pfam; PF04089; BRICHOS; 1.
 KW Transmembrane; Signal-anchor.
 FT TRANSMEM 54 74
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 263 AA; 29705 MW; CF809834ABECDB85A CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 263;
 Best Local Similarity 43.8%; Pred. No. 4.1;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVGVKVGKTC 16
 DB 90 CFFDSEDVPVNSIPGGE 105
 RESULT 5
 ADHA_HUMAN
 ID ADHA_HUMAN STANDARD; PRT; 374 AA.

AC P07327;
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase alpha chain (EC 1.1.1.1).
 GN ADH1A OR ADH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=86241367; PubMed=3013304;
 RA von Bahr-Lindstrom H., Hoesoe J.-O., Heden L.-O., Kaiser R.,
 RA Fleetwood L., Larsson K., Lake M., Holmquist B., Holmgren A.,
 RA Hempel J., Vallee B.L., Joernvall H.;
 RT "cDNA and protein structure for the alpha subunit of human liver
 RT alcohol dehydrogenase.";
 RL Biochemistry 25:2465-2470(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89153548; PubMed=2920825;
 RA Matsuo Y., Yokoyama S.;
 RT "Molecular structure of the human alcohol dehydrogenase 1 gene.";
 RL FEBS Lett. 243:57-60(1989).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=90269803; PubMed=2347582;
 RA Yasunami M., Kikuchi I., Sarapata D., Yoshida A.;
 RT "The human class I alcohol dehydrogenase gene cluster: three genes
 RT are tandemly organized in an 80-kb-long segment of the genome.";
 RL Genomics 7:152-158(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 CC alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
 CC PI, ONE TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 CC CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 CC
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 CC -----
 CC EMBL; M12271; AAA68131.1; -;
 CC EMBL; M12963; AAA51590.1; -;
 CC EMBL; M37066; AAA51591.1; -;
 CC PIR; S02265; DEHUA.
 CC PDB; 1HSO; 27-APR-01.
 CC Genew; HGNC:249; ADH1A.
 CC GK; P07327; -;
 CC MIM; 103700; -;
 CC GO; GO:0005737; C:cytoplasm; NAS.
 CC GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; NAS.
 CC GO; GO:0006066; P:alcohol metabolism; NAS.
 CC InterPro; IPR002328; ADH_zinc.

DR InterPro9 IPR002085; Adh zn family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; zinc; Metal-binding; NAD; Multigene family;
 KW Acetylation; 3D-structure.
 FT INIT MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 174 174 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 374 AA; 39727 MW; 5D2F5F6E31C4962C CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CYFS----SKDNVGVKVGKTC 18
 Db 174 CGFSTGYGSANVAKVTPGTC 195
 RESULT 6
 ID ADHB HUMAN STANDARD; PRT; 374 AA.
 AC P00325; Q13711; Q96K17;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase beta chain (EC 1.1.1.1).
 GN ADHB OR ADH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] 0
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120995; PubMed=2935875;
 RA Ikuta T., Szeto S., Yoshida A.;
 RT "Three human alcohol dehydrogenase subunits: cDNA structure and
 RT molecular and evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:634-638(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Yokoyama S., Yokoyama R., Rotwein P.;
 RT "Molecular characterization of cDNA clones encoding the human alcohol
 RT dehydrogenase beta 1 and the evolutionary relationship to the other
 RT class I subunits alpha and gamma.";
 RL Jpn. J. Genet. 62:241-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=86082371; PubMed=3000832;
 RA Heden L.O., Hoesoe J.-O., Larsson K., Lake M., Lagerholm B.,
 RA Holmgren A., Vallee B.L., Joernvall H., von Bahr-Lindstrom H.;
 RT "cDNA clones coding for the beta-subunit of human liver alcohol
 RT dehydrogenase have differently sized 3'-non-coding regions.";
 RL FEBS Lett. 194:327-332(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (BETA-1).
 RX MEDLINE=86111889; PubMed=2935533;
 RA Duyster G., Smith M., Bilanchone V., Hatfield G.W.;
 RT "Molecular analysis of the human class I alcohol dehydrogenase gene
 RT family and nucleotide sequence of the gene encoding the beta
 RT subunit.";
 RL J. Biol. Chem. 261:2027-2033(1986).
 RN [5]
 RP SEQUENCE (BETA-1).
 RX MEDLINE=85076637; PubMed=6391920;
 RA Hempel J., Buhler R., Kaiser R., Vallee B.L., Joernvall H.;
 RA von Wartburg J.-P., Vallee B.L., Joernvall H.;

RT "Human liver alcohol dehydrogenase. 1. The primary structure of the
RL beta 1 isoenzyme.";
RT Eur. J. Biochem. 145:437-445(1984).
RN [6]
RP SEQUENCE FROM N.A. (BETA-2).
RX MEDLINE=89338401; PubMed=2547609;
RA Matsuo Y., Yokoyama R., Yokoyama S.;
RT "The genes for human alcohol dehydrogenases beta 1 and beta 2 differ
RL by only one nucleotide.";
RT Eur. J. Biochem. 183:317-320(1989).
RN [7]
RP SEQUENCE FROM N.A. (BETA-3).
RC TISSUE=Liver;
RX MEDLINE=90024225; PubMed=2679216;
RA Carr L.G., Xu Y., Ho W.H., Edenberg H.J.;
RT "Nucleotide sequence of the ADH2(3) gene encoding the human alcohol
RL dehydrogenase beta 3 subunit.";
RL Alcohol. Clin. Exp. Res. 13:594-596(1989).
RN [8]
RP SEQUENCE FROM N.A. (BETA-2).
RC TISSUE=Liver;
RA Pollin L., Hey-Chi H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=88284699; PubMed=3397059;
RA Xu Y.L., Carr L.G., Bosron W.F., Li T.K., Edenberg H.J.;
RT "Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci
RL following DNA sequence amplification.";
RL Genomics 2:209-214(1988).
RN [10]
RP SEQUENCE OF 40-85 FROM N.A.
RA Osier M., Speed W.C., Seaman M.I., Kidd K.K.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [11]
RP VARIANT BETA-2.
RX MEDLINE=84221897; PubMed=6374651;
RA Joernvall H., Hempel J., Vallee B.L., Bosron W.F., Li T.-K.;
RT "Human liver alcohol dehydrogenase: amino acid substitution in the
RL beta 2 beta 2 Oriental isozyme explains functional properties,
RT establishes an active site structure, and parallels mutational
RT exchanges in the yeast enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3024-3028(1984).
RN [12]
RP VARIANT BETA-3.
RX MEDLINE=87298549; PubMed=3619918;
RA Burnell J.C., Carr L.G., Dwulet F.E., Edenberg H.J., Li T.-K.,
RA Bosron W.F.;
RT "The human beta 3 alcohol dehydrogenase subunit differs from beta 1
RL by a Cys for Arg-369 substitution which decreases NAD(H) binding.";
RL Biochem. Biophys. Res. Commun. 146:1127-1133(1987).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=91376103; PubMed=1896463;
RA Hurley T.D., Bosron W.F., Hamilton J.A., Amzel L.M.;
RT "Structure of human beta 1 beta 1 alcohol dehydrogenase: catalytic
RL effects of non-active-site substitutions.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8149-8153(1991).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
RX MEDLINE=94260547; PubMed=8201622;
RA Hurley T.D., Bosron W.F., Stone C.L., Amzel L.M.;
RT "Structures of three human beta alcohol dehydrogenase variants.
RL Correlations with their functional differences.";
RL J. Mol. Biol. 239:415-429(1994).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=96291846; PubMed=8663387;
RA Davis G.J., Bosron W.F., Stone C.L., Owsun-Dekyi K., Hurley T.D.;
RT "X-ray structure of human betabeta3 alcohol dehydrogenase. The
RL contribution of ionic interactions to coenzyme binding.";
RL J. Biol. Chem. 271:17057-17061(1996).
CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +

CC NADH.
CC -!- COFACTOR: Binds 2 zinc ions per subunit.
CC -!- SUBUNIT: Dimer of identical or nonidentical chains of three types;
CC alpha, beta and gamma.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
CC MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
CC ORIENTALS.
CC -!- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
CC PI ONE TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
CC PI ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
CC CLASS-V: ADH6.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
CC -----
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CC -----
CC EMBL: D00137; BAA00084.1; -;
DR EMBL: X03350; CAA27056.1; -;
DR EMBL: M24316; AAB59496.1; -;
DR EMBL: M24308; AAB59496.1; JOINED.
DR EMBL: M24309; AAB59496.1; JOINED.
DR EMBL: M24310; AAB59496.1; JOINED.
DR EMBL: M24311; AAB59496.1; JOINED.
DR EMBL: M24312; AAB59496.1; JOINED.
DR EMBL: M24313; AAB59496.1; JOINED.
DR EMBL: M24314; AAB59496.1; JOINED.
DR EMBL: M24317; AAB51884.1; -;
DR EMBL: X15447; CAA33487.1; -;
DR EMBL: X15448; CAA33487.1; JOINED.
DR EMBL: X15449; CAA33487.1; JOINED.
DR EMBL: X15450; CAA33487.1; JOINED.
DR EMBL: X15451; CAA33487.1; JOINED.
DR EMBL: X15452; CAA33487.1; JOINED.
DR EMBL: X15453; CAA33487.1; JOINED.
DR EMBL: X15454; CAA33487.1; JOINED.
DR EMBL: X15455; CAA33487.1; JOINED.
DR EMBL: X38290; AAB48003.1; -;
DR EMBL: X38283; AAB48003.1; JOINED.
DR EMBL: X38284; AAB48003.1; JOINED.
DR EMBL: X38285; AAB48003.1; JOINED.
DR EMBL: X38286; AAB48003.1; JOINED.
DR EMBL: X38287; AAB48003.1; JOINED.
DR EMBL: X38288; AAB48003.1; JOINED.
DR EMBL: X38289; AAB48003.1; JOINED.
DR EMBL: AF153821; AAD37446.1; -;
DR EMBL: M21692; AAB51592.1; -;
DR EMBL: AF040967; AAB96912.1; -;
DR PIR: A23607; DEHUAB.
DR PDB: 1HDX; 31-JAN-94.
DR PDB: 1HDY; 31-JAN-94.
DR PDB: 1HDZ; 31-JAN-94.
DR PDB: 3HOD; 31-JAN-94.
DR PDB: 1DEH; 08-MAR-96.
DR PDB: 1HTB; 07-DEC-95.
DR PDB: 1HSZ; 27-APR-01.
DR Genew; HGNC:250; ADH1B.
DR GK; P00325; -;
DR MIM; 103720; -;
DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; TAS.
DR GO; GO:0005489; F:electron transporter activity; TAS.
DR GO; GO:0008270; F:zinc ion binding activity; TAS.
DR GO; GO:0006069; P:ethanol oxidation; TAS.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.

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KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
KW Acetylation; Polymorphism; 3D-structure.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT METAL 46 46 ZINC 1 (CATALYTIC).
FT METAL 67 67 ZINC 1 (CATALYTIC).
FT METAL 97 97 ZINC 2.
FT METAL 100 100 ZINC 2.

Query Match 45.1%; Score 46; DB 1; Length 374;
Best Local Similarity 54.5%; Pred. No. 5.8;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CYES----SKDNVKGKVGKTC 18
Db 174 CGFTGYGSVAVKVTGKTC 195

RESULT 7
TRYB_RAT
ID TRYB_RAT STANDARD; PRT; 246 AA.
AC P32821;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin V-A precursor (EC 3.4.21.4).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=92165057; PubMed=1537555;
RA Kang J., Wiegand U., Mueller-Hill B.;
RT "Identification of cDNAs encoding two novel rat pancreatic serine
RT proteases.";
RL Gene 110:181-187(1992).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-----
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-----
DR EMBL; X59012; CAA41751.1; -.
DR PIR; JQ1471; JQ1471.
DR HSP; P00763; IDPO.
DR MEROPS; S01.092; -.
DR InterPro; IPR001314; Chymotrypsin.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 15 ACTIVATION PEPTIDE.
FT PROPEP 16 24 TRYPSIN V-A.
FT CHAIN 25 246 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 64 64 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 31 160 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 133 233 BY SIMILARITY.
FT DISULFID 140 206 BY SIMILARITY.
FT DISULFID 171 185 BY SIMILARITY.
FT DISULFID 196 220 BY SIMILARITY.
FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 246 AA; 26819 MW; 1EB899CA1B8A0025 CRC64; BY SIMILARITY.

KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
KW Acetylation; Polymorphism; 3D-structure.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT METAL 46 46 ZINC 1 (CATALYTIC).
FT METAL 67 67 ZINC 1 (CATALYTIC).
FT METAL 97 97 ZINC 2.
FT METAL 100 100 ZINC 2.

Query Match 43.1%; Score 44; DB 1; Length 246;
Best Local Similarity 43.8%; Pred. No. 8.1;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSKDNVKGKVGKTC 18
Db 16 FPTEDNDDRIVGKTC 31

RESULT 8
TRYB_RAT
ID TRYB_RAT STANDARD; PRT; 246 AA.
AC P32822;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin V-B precursor (EC 3.4.21.4).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=92165057; PubMed=1537555;
RA Kang J., Wiegand U., Mueller-Hill B.;
RT "Identification of cDNAs encoding two novel rat pancreatic serine
RT proteases.";
RL Gene 110:181-187(1992).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-----
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-----
DR EMBL; X59013; CAA41752.1; -.
DR PIR; JQ1472; JQ1472.
DR HSP; P00763; IDPO.
DR MEROPS; S01.093; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR SMART; SM00089; trypsin; 1.
DR PROSITE; PS00240; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 15 ACTIVATION PEPTIDE.
FT PROPEP 16 24 TRYPSIN V-B.
FT CHAIN 25 246 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 64 64 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 31 160 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 133 233 BY SIMILARITY.
FT DISULFID 140 206 BY SIMILARITY.
FT DISULFID 171 185 BY SIMILARITY.
FT DISULFID 196 220 BY SIMILARITY.
FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 246 AA; 26819 MW; 1EB899CA1B8A0025 CRC64; BY SIMILARITY.

```



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RESULT 11
ISPH_BRUME STANDARD; PRT; 346 AA.
ID ISPH_BRUME
AC Q8YFR1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ISPH protein.
GN ISPH OR LYTB OR BME11459.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapural V., Redkar R.J., Patra G., Muij C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Resnik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Salikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
CC
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CC
CC EMBL; AE009582; AAL52640.1; -.
CC PIR; AE3434; AE3434.
CC HAMAP; MF_00191; -.
CC InterPro; IPR003451; LytB.
CC Pfam; PF02401; LytB; 1.
CC TIGRFAMs; TIGR00216; isph_lytB; 1.
CC Isoprene biosynthesis; Complete proteome.
CC KW ISOPRENE BIOSYNTHESIS; Complete proteome.
CC SEQUENCE 346 AA; 37747 MW; EB9C1D60EF73421B CRC64;
SQ
Query Match 42.2%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKT 13
Db 161 CHFDDEDNUGFVT 173
|:|:|:|:|:|
161 CHFDDEDNUGFVT 173

RESULT 12
AGI_HORVU STANDARD; PRT; 212 AA.
ID AGI_HORVU
AC P15312;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Root-specific lectin precursor.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapural V., Redkar R.J., Patra G., Muij C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Resnik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Salikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
CC
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CC
CC EMBL; AE009582; AAL52640.1; -.
CC PIR; AE3434; AE3434.
CC HAMAP; MF_00191; -.
CC InterPro; IPR003451; LytB.
CC Pfam; PF02401; LytB; 1.
CC TIGRFAMs; TIGR00216; isph_lytB; 1.
CC Isoprene biosynthesis; Complete proteome.
CC KW ISOPRENE BIOSYNTHESIS; Complete proteome.
CC SEQUENCE 346 AA; 37747 MW; EB9C1D60EF73421B CRC64;
SQ
Query Match 42.2%; Score 43; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CYFSSKDNVGVKT 13
Db 161 CHFDDEDNUGFVT 173
|:|:|:|:|:|
161 CHFDDEDNUGFVT 173
```

```

[1]
SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapural V., Redkar R.J., Patra G., Muij C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Resnik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Salikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: BELONGS TO THE ISPH FAMILY.
CC
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CC
CC EMBL; M29280; AAA32969.1; -.
CC PIR; T05936; T05936.
CC HSSP; P10969; LWGT.
CC InterPro; IPR001002; Chitin_binding_1.
CC Pfam; PF00187; Chitin_bind_1; 4.
CC PRINTS; PR00451; CHITINBINDING.
CC SMART; SM00270; ChtBD1; 4.
CC PROSITE; PS00026; CHITIN BINDING; 4.
CC Lectin; Repeat; Chitin-binding; Glycoprotein; Signal;
CC Pyroglutamate carboxylic acid.
CC SIGNAL 1 26 POTENTIAL.
CC CHAIN 27 212 ROOT-SPECIFIC LECTIN.
CC DOMAIN 27 69 CHITIN-BINDING 1.
CC DOMAIN 70 112 CHITIN-BINDING 2.
CC DOMAIN 113 155 CHITIN-BINDING 3.
CC DOMAIN 156 197 CHITIN-BINDING 4.
CC MOD_RES 27 27 PYRROLIDONE CARBOXYLIC ACID
CC (BY SIMILARITY).
CC DISULFID 29 44 BY SIMILARITY.
CC DISULFID 38 50 BY SIMILARITY.
CC DISULFID 43 57 BY SIMILARITY.
CC DISULFID 61 66 BY SIMILARITY.
CC DISULFID 72 87 BY SIMILARITY.
CC DISULFID 81 93 BY SIMILARITY.
CC DISULFID 96 100 BY SIMILARITY.
CC DISULFID 104 109 BY SIMILARITY.
CC DISULFID 115 130 BY SIMILARITY.
CC DISULFID 124 136 BY SIMILARITY.
CC DISULFID 129 143 BY SIMILARITY.
CC DISULFID 147 152 BY SIMILARITY.
CC DISULFID 158 173 BY SIMILARITY.
CC DISULFID 167 179 BY SIMILARITY.
CC DISULFID 172 186 BY SIMILARITY.
CC DISULFID 190 195 BY SIMILARITY.
CC CARBOHYD 206 206 N-LINKED (GLCNAC...).
CC SEQUENCE 212 AA; 21209 MW; 8D948245D6B625A5 CRC64;
Query Match 41.2%; Score 42; DB 1; Length 212;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;
QY 1 CYFSSKDNVGVKTGGKTC 18
Db 66 CYTSKR--CGTQAGGKTC 81
|:|:|:|:|:|
66 CYTSKR--CGTQAGGKTC 81

RESULT 13
INCL_ECOLI STANDARD; PRT; 358 AA.
ID INCL_ECOLI
AC Q52312; P71175; Q52283;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein incC.
GN INCC.
OS Escherichia coli.
OX Plasmid IncP-beta R751.
```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macartney D.P., Williams D.R., Stafford T., Foster A., Thomas C.M.;
 RA "Evolution of the partitioning and global regulation functions of
 RT the IncP central control region."
 RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-109 FROM N.A.
 RC STRAIN=K12 / C600;
 RX MEDLINE=95291464; PubMed=7773415;
 RA Thomas C.M., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;
 RA "Evolution of the kora-oxiv segment of promiscuous IncP plasmids."
 RL Microbiology 141:1201-1210(1995).
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS ENCODED BY THE TRFB OPERON;
 CC IT IS INVOLVED IN PLASMID MAINTENANCE AND REPLICATION (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY.
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 CC -----
 DR EMBL; U67194; AAC64421.1; -;
 DR InterPro; IPR000707; ATPase_ParA.
 DR Pfam; PF00991; ParA; 1.
 KW Plasmid; DNA replication.
 SQ SEQUENCE 358 AA; 38246 MW; 44859F07844167EE CRC64;
 Query Match 41.2%; Score 42; DB 1; Length 358;
 Best Local Similarity 41.2%; Pred. No. 25;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CYFSSKDNVKGKVTGGKT 17
 Db 45 CHFAGADQGGVAGGQS 61
 RESULT 14
 ADHI RANGE
 ID _ADHI_RANGE STANDARD; PRT; 375 AA.
 AC P22797;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase, major (EC 1.1.1.1).
 OS Rana perezi (Perez's frog) (Western Mediterranean green frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8403;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Liver;
 RX MEDLINE=91175722; PubMed=20071119;
 RA Cederlund E., Peralba J.M., Pares X., Joernvall H.;
 RA "Amphibian alcohol dehydrogenase, the major frog liver enzyme.
 RT Relationships to other forms and assessment of an early gene
 RT duplication separating vertebrate class I and class III alcohol
 RT dehydrogenases.";
 RL Biochemistry 30:2811-2816(1991).
 RN [2]
 RP SEQUENCE OF 1-5.
 RX MEDLINE=90353571; PubMed=2387402;
 RA Egestad B., Estonius M., Danielson O., Persson B., Cederlund E.,
 RA Kaiser R., Holmquist B., Vallee B., Pares X., Jefferey J.,
 RA Joernvall H.;
 RT "Fast atom bombardment mass spectrometry and chemical analysis in

RT determinations of acyl-blocked protein structures.";
 RL FEBS Lett. 269:194-196(1990).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 CC NADH.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY. MORE CLOSELY RELATED TO CLASS I MAMMALIAN ENZYMES.
 DR PIR; A38405; A38405.
 DR HSSP; P00325; IDEH.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Acetylation.
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 68 68 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 98 98 ZINC 2 (BY SIMILARITY).
 FT METAL 101 101 ZINC 2 (BY SIMILARITY).
 FT METAL 104 104 ZINC 2 (BY SIMILARITY).
 FT METAL 112 112 ZINC 2 (BY SIMILARITY).
 FT METAL 175 175 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 375 AA; 40184 MW; 283E0A60E339195 CRC64;
 Query Match 41.2%; Score 42; DB 1; Length 375;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
 QY 1 CYFSSKDNVKGKVTGGKT 18
 Db 175 CGFSTGYGSVNTGKVKPGSTC 196
 RESULT 15
 GUXC_FUSOX
 ID _GUXC_FUSOX STANDARD; PRT; 514 AA.
 AC P46238;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Putative exoglucanase type C precursor (EC 3.2.1.91)
 DE (Exocellobiohydrolase I) (1,4-beta-cellobiohydrolase)
 DE (Beta-glucanocellobiohydrolase).
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=5507;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95047531; PubMed=7959045;
 RA Sheppard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
 RA Hagen F.S., Upshall A., McKnight G.L., O'Hara P.J.;
 RA "The use of conserved cellulase family-specific sequences to clone
 RT cellulase homologue cDNAs from Fusarium oxysporum.";
 RL Gene 150:163-167(1994).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 CC in cellulose and cellotetraose, releasing cellobiose from the non-
 CC reducing ends of the chains.
 CC -1- SIMILARITY: Contains 1 fungal-type cellulose-binding (CBD) domain.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L29379; AAA65587.1; -;
 DR HSSP; P00725; 8CEL.

DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR001722; Glyco_hydro_7.
 DR Pfam; PF00734; CBM_1; 1.
 DR Pfam; PF00840; Glyco_hydro_7; 1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR ProDom; PD186135; Glyco_hydro_7; 1.
 DR SMART; SM0236; fCBD; 1.
 DR PROSITE; PS00562; CBD_FUNGAL; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 514
 FT DOMAIN 18 439
 FT DOMAIN 440 482
 FT DOMAIN 483 514
 FT ACT_SITE 229 229
 FT ACT_SITE 234 234
 FT DISULFID 486 503
 FT DISULFID 497 513
 FT CARBOHYD 287 287
 FT CARBOHYD 490 490
 SQ SEQUENCE 514 AA; 54704 MW; 6A4617323A46E062 CRC64;

Query Match 41.2%; Score 42; DB 1; Length 514;
 Best Local Similarity 44.4%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVTKGKTC 18
 DB 66 CYTGNKWDTSICTDGKTC 83

Search completed: October 15, 2003, 16:58:17
 Job time : 7.42934 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-16

Perfect score: 102
Sequence: 1 CYFSSKDNVGVGTGGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	102	100.0	234	2 Q9RSX4	Q9RSX4 staphylococ
2	102	100.0	239	2 Q05157	Q05157 staphylococ
3	102	100.0	239	2 Q53678	Q53678 staphylococ
4	102	100.0	239	2 Q06532	Q06532 staphylococ
5	102	100.0	239	2 Q06531	Q06531 staphylococ
6	102	100.0	239	2 Q06533	Q06533 staphylococ
7	102	100.0	266	16 Q8NXXJ6	Q8NXXJ6 staphylococ
8	102	100.0	271	2 Q9F0L6	Q9F0L6 staphylococ
9	96	94.1	239	2 Q06535	Q06535 staphylococ
10	93	91.2	239	2 Q06534	Q06534 staphylococ
11	55	53.9	511	16 Q8RI66	Q8RI66 fuscobacteri
12	47	46.1	2108	5 Q8I5C7	Q8I5C7 plasmodium
13	46.5	45.6	505	2 Q50203	Q50203 xanthobacte
14	46	45.1	199	16 Q92CG4	Q92CG4 listeria in
15	46	45.1	233	11 Q9CRW4	Q9CRW4 mus musculu
16	46	45.1	263	11 Q8K0H4	Q8K0H4 mus musculu

17	46	45.1	269	6 Q8WNN3	Q8WNN3 gorilla gor
18	45	44.1	276	4 Q9NPP0	Q9NPP0 homo sapien
19	44.5	43.6	107	4 Q9UL82	Q9UL82 homo sapien
20	44.5	43.6	457	12 Q9VQZ1	Q9VQZ1 ranid herpe
21	44	43.1	275	5 Q16622	Q16622 caenorhabdi
22	44	43.1	299	10 Q8IAK6	Q8IAK6 arabidopsis
23	44	43.1	966	11 Q8CBP6	Q8CBP6 mus musculu
24	44	43.1	2301	5 Q95Z81	Q95Z81 oikopleura
25	43	42.2	126	5 Q95UQ5	Q95UQ5 brachiosto
26	43	42.2	159	5 Q8I7X7	Q8I7X7 branchiosto
27	43	42.2	274	10 Q9STR7	Q9STR7 arabidopsis
28	43	42.2	315	10 Q93VK9	Q93VK9 arabidopsis
29	43	42.2	368	5 Q9XXJ6	Q9XXJ6 caenorhabdi
30	43	42.2	372	16 Q8G257	Q8G257 bruceella su
31	43	42.2	765	5 Q26018	Q26018 plasmodium
32	43	42.2	765	5 Q8IKT6	Q8IKT6 plasmodium
33	43	42.2	1022	5 Q9W3E1	Q9W3E1 drosophila
34	42	41.2	148	16 Q8DRX5	Q8DRX5 streptococc
35	42	41.2	161	17 Q8TLN3	Q8TLN3 methanosarc
36	42	41.2	224	8 Q9ZZS7	Q9ZZS7 ceratoholen
37	42	41.2	235	16 Q8XEI9	Q8XEI9 escherichia
38	42	41.2	260	16 Q97M39	Q97M39 clostridium
39	42	41.2	278	2 Q51311	Q51311 nostoc punc
40	42	41.2	377	11 Q9QYI9	Q9QYI9 mus musculu
41	42	41.2	378	16 Q92FD6	Q92FD6 listeria in
42	42	41.2	378	16 Q8YAK1	Q8YAK1 listeria mo
43	42	41.2	430	16 Q9A3U5	Q9A3U5 caulobacter
44	42	41.2	1064	16 Q8XK16	Q8XK16 clostridium
45	41.5	40.7	731	16 Q8RG00	Q8RG00 fusobacteri

ALIGNMENTS

RESULT 1

Q9RSX4 PRELIMINARY; PRT; 234 AA.
AC Q9RSX4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph toxin OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep toxin C; 1.
DR PRINTS; PR00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYFSSKDNVGVGTGGKTC 18
|||
Db 88 CYFSSKDNVGVGTGGKTC 105

```
RESULT 2
O05157      Query Match      100.0%; Score 102; DB 2; Length 239;
AC O05157      Best Local Similarity 100.0%; Pred. No. 8.3e-09;
AC O05157      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; IUCK.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strept tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match      100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVKGVTGGKTC 18
DB 93 CYFSSKDNVKGVTGGKTC 110

RESULT 3
O53678      Query Match      100.0%; Score 102; DB 2; Length 239;
AC Q53678      Best Local Similarity 100.0%; Pred. No. 8.3e-09;
AC Q53678      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strept tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match      100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVKGVTGGKTC 18
DB 93 CYFSSKDNVKGVTGGKTC 110

RESULT 4
O06532      Query Match      100.0%; Score 102; DB 2; Length 239;
AC Q06532      Best Local Similarity 100.0%; Pred. No. 8.3e-09;
AC Q06532      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strept tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match      100.0%; Score 102; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYFSSKDNVKGVTGGKTC 18
DB 93 CYFSSKDNVKGVTGGKTC 110

RESULT 5
O06531      Query Match      100.0%; Score 102; DB 2; Length 239;
AC Q06531      Best Local Similarity 100.0%; Pred. No. 8.3e-09;
AC Q06531      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; ISE2.
```

DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1 1
 SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731E024 CRC64;
 Query Match 100.0%; Score 102; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CYFSSKDNVGVGGKTC 18
 Db 93 CYFSSKDNVGVGGKTC 110
 RESULT 6
 Q06533 PRELIMINARY; PRT; 239 AA.
 AC Q06533;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MNCCopeland;
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications.";
 RL Infect Immun. 61:4254-4262(1993).
 DR EMBL; L13378; AAA26622.1; -.
 DR HSSP; P34071; ISTE.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1 1
 SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;
 Query Match 100.0%; Score 102; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CYFSSKDNVGVGGKTC 18
 Db 93 CYFSSKDNVGVGGKTC 110
 RESULT 7
 Q8NXXJ6 PRELIMINARY; PRT; 266 AA.
 ID Q8NXXJ6
 AC Q8NXXJ6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ENTEROTOXIN TYPE C PRECURSOR.
 GN SEC4 OR MW0759.
 OS Staphylococcus aureus (strain MW2).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AF004824; BAB94624.1; -.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;
 Query Match 100.0%; Score 102; DB 16; Length 266;
 Best Local Similarity 100.0%; Pred. No. 9.4e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CYFSSKDNVGVGGKTC 18
 Db 120 CYFSSKDNVGVGGKTC 137
 RESULT 8
 Q9F0L6 PRELIMINARY; PRT; 271 AA.
 ID Q9F0L6
 AC Q9F0L6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Staphylococcal enterotoxin C-bovine.
 GN SEC-BOV.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20566668; PubMed=11114901;
 RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
 RA Meaney W.J., Smyth C.J.;
 RT "Characterization of a putative pathogenicity island from bovine
 RT Staphylococcus aureus encoding multiple superantigens.";
 RL J. Bacteriol. 183:63-70(2001).
 DR EMBL; AF217235; AAG29599.1; -.
 DR HSSP; P34071; ISE2.
 DR InterPro; IPR006177; Bcrl1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;
 Query Match 100.0%; Score 102; DB 2; Length 271;
 Best Local Similarity 100.0%; Pred. No. 9.5e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CYFSSKDNVGVGGKTC 18
 Db 129 CYFSSKDNVGVGGKTC 142

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RESULT 9
Q06535
ID Q06535 PRELIMINARY; PRT; 239 AA.
AC Q06535;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 909;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13377; AAA26623.1; -.
DR HSP; P23313; IJCK.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E411950 CRC64;

Query Match 94.1%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 93 CYFSSKDNVGVGTGGKTC 110

RESULT 10
Q06534
ID Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13379; AAA26623.1; -.
DR HSP; P34071; ISE2.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E411950 CRC64;

Query Match 94.1%; Score 96; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 93 CYFSSKDNVGVGTGGKTC 110
```

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FT NON_TER
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 91.2%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 93 CCFSSKDNVGVGTGGKTC 110

RESULT 11
Q8RI66
ID Q8RI66 PRELIMINARY; PRT; 511 AA.
AC Q8RI66;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cysteine permease.
GN FN1747.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fontstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; A5010479; AAL93862.1; -.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR001463; Na/Ala_sympor.
DR Pfam; PF01235; Na_Ala_symp; 1.
DR TIGRFAMs; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.
SQ SEQUENCE 511 AA; 56196 MW; 03D8A2859135EF3D CRC64;

Query Match 53.9%; Score 55; DB 16; Length 511;
Best Local Similarity 52.9%; Pred. No. 1.3;
Matches 0; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVGTGGKTC 17
| | | | | | | | | | | | | | | | | |
Db 128 CYRSKDETGRYFGGST 144

RESULT 12
Q8I5C7
ID Q8I5C7 PRELIMINARY; PRT; 2108 AA.
AC Q8I5C7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFL1410C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
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RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shalloom S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Ralph S.A.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL: AB014848; AAN36368.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2108 AA; 248300 MW; 280464D22291B2D9 CRC64;

Query Match 46.1%; Score 47; DB 5; Length 2108;
Best Local Similarity 32.4%; Pred. No. 1.3e+02;
Matches 12; Conservative 2; Mismatches 20; Gaps 1;

QY 1 CYPSSKDN-----VGKVTGGKT 17
Db |||||:|
763 CYPSSKNDDYILKNILNLTKNNSVVIIILGNVSGKT 799

RESULT 13
OS0203 PRELIMINARY; PRT; 505 AA.
AC OS0203;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chloroacetaldehyde dehydrogenase.
GN ALDA.
OS Xanthobacter autotrophicus.
OG Plasmid linear plasmid pXAL.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiales; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJ10;
RX MEDLINE=9817279; PubMed=9511738;
RA Bergeron H., Labbe D., Turmel C., Lau P.C.;
RT "Cloning, sequence and expression of a linear plasmid-based and a
RT chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
RT in Xanthobacter autotrophicus GJ10.";
RL Gene 207:9-18(1998).
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL: AF029733; AAC13841.1; -.
DR HSSP: P05091; 1CW3.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR Pfam: PF00171; aldedh; 1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Oxidoreductase; Plasmid.
SQ SEQUENCE 505 AA; 54945 MW; AD6A9EBD0297BB04 CRC64;

Query Match 45.6%; Score 46.5; DB 2; Length 505;
Best Local Similarity 58.8%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 2 YFSSKDNVGVKVTGGKTC 18
Db |||||:|
34 YF---DNTSPVTGGKIC 47

RESULT 14
Q92CG4 PRELIMINARY; PRT; 199 AA.
AC Q92CG4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein lin1208.
```

```
GN LIN1208.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duesurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L.-M., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madieno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Norddick G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL596168; CAC96439.1; -.
DR ListList; LIN01208; -.
DR InterPro: IPR001345; PG/BPGM_mutase.
DR Pfam: PF00300; PGAM; 1.
DR PROSITE: PS00175; PG_MUTASE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 199 AA; 22902 MW; E14DD962F4C6BFE5 CRC64;

Query Match 45.1%; Score 46; DB 16; Length 199;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 YFSSKDNVGVKVTGGKTC 18
Db |||||:|
151 YWEKTSKIGKVIGLKNK 167

RESULT 15
Q9CRW4 PRELIMINARY; PRT; 233 AA.
AC Q9CRW4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Integral membrane protein 2 (Fragment).
GN ITM2A OR ITM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Mateuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
```

RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR ENBL; AK014024; BAE29119.1; -.
 DR MGD; MGI:107706; Icm2a.
 FT NON_TER 1 1
 SQ SEQUENCE 233 AA; 26321 MW; B073D1FD94DEF2E9 CRC64;

Query Match 45.1%; Score 46; DB 11; Length 233;
 Best Local Similarity 43.8%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CYFSSKDNVGVKVTGGK 16
 | : | : | : | : | : | :
 Db 60 CFFDSEDPVNSIRGGE 75

Search completed: October 15, 2003, 17:04:14
 Job time : 36.8623 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:19:13 ; Search time 49.2575 Seconds
(without alignments)
58.003 Million cell updates/sec

Title: US-09-555-115A-17
Perfect score: 104
Sequence: 1 CCFSSKDNVGVGGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	18	24	ABG71379
2	98	94.2	239	20	AAV06258
3	98	94.2	240	24	ABG71374
4	93	89.4	18	20	AAV06249
5	93	89.4	18	24	ABG71377
6	93	89.4	18	24	ABG71380
7	93	89.4	238	12	AAR13208
8	93	89.4	238	14	AAR45016
9	93	89.4	238	22	AAB67343

10	93	89.4	238	23	ABB76239	Staphylococcus aur
11	93	89.4	239	12	AAAR13207	Staphylococcal ent
12	93	89.4	239	14	AAAR45015	Staphylococcal ent
13	93	89.4	239	20	AAV06255	Staphylococcal gro
14	93	89.4	239	20	AAV06256	Staphylococcal gro
15	93	89.4	239	20	AAV06251	Staphylococcal gro
16	93	89.4	239	20	AAV06252	Staphylococcal gro
17	93	89.4	239	20	AAV06253	Staphylococcal gro
18	93	89.4	239	22	AAB67342	Staphylococcus aur
19	93	89.4	239	23	ABB76238	Staphylococcus aur
20	93	89.4	240	24	ABG71367	Staphylococcal ent
21	93	89.4	240	24	ABG71368	Staphylococcal ent
22	93	89.4	240	24	ABG71369	Staphylococcal ent
23	93	89.4	240	24	ABG71371	Staphylococcal ent
24	93	89.4	240	24	ABG71372	Staphylococcal ent
25	93	89.4	266	21	AAV70108	Staphylococcal ent
26	93	89.4	266	23	ABB79507	Staphylococcal SEC
27	87	83.7	18	20	AAV06250	Staphylococcal gro
28	87	83.7	18	24	ABG71378	Staphylococcal ent
29	87	83.7	239	20	AAV06254	Staphylococcal gro
30	87	83.7	239	20	AAV06257	Staphylococcal gro
31	87	83.7	240	24	ABG71370	Staphylococcal ent
32	87	83.7	240	24	ABG71373	Staphylococcal ent
33	57	54.8	14	20	AAV06259	Staphylococcal ent
34	57	54.8	14	24	ABG71381	Staphylococcal ent
35	46	44.2	99	22	AAU49262	Propionibacterium
36	46	44.2	374	20	AAV43983	Human alcohol dehy
37	46	44.2	374	20	AAV43984	Human alcohol dehy
38	46	44.2	375	23	ABG73657	Invertebrate forag
39	46	44.2	395	21	AAV58159	Lung cancer associ
40	45	43.3	163	22	ABG23337	Novel human diagno
41	45	43.3	222	22	ABG09780	Novel human diagno
42	44.5	42.8	212	15	AAAR45357	Barley clone BLC3
43	44.5	42.8	212	21	AAAR19645	Barley lectin BLC3
44	44	42.3	77	21	AAG61245	Arabidopsis thalia
45	44	42.3	103	21	AAG61244	Arabidopsis thalia

ALIGNMENTS

RESULT 1
ABG71379
ID ABG71379 standard; Peptide; 18 AA.

XX AC ABG71379;

XX DT 29-JAN-2003 (first entry)

XX Staphylococcal enterotoxin SEC-ovine disulphide loop region.

XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
XX emetic response-inducing activity; staphylococcal enterotoxin;
XX toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
XX SEC-ovine.

OS Staphylococcus aureus.

XX WO200283169-A1.

XX PD 24-OCT-2002.

XX PF 11-APR-2002; 2002WO-US11619.

XX PR 13-APR-2001; 2001US-283720P.

XX PA (IDAH-) IDAHO RES FOUND INC.

XX PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;

XX DR WPI; 2003-058608/05.

XX PT New modified staphylococcal enterotoxin derived from a native disulfide

QY 1 CCFSSKDNVGVKVTGGKTC 18
 Db 93 CCFSSKDNVGVKVTGGKTC 110

RESULT 4

AAV06249
 ID AAY06249 standard; Peptide; 18 AA.

AC AAY06249;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin disulfide loop.

KW Enterotoxin; SEC1; SEC2; SEC3 PRI 913; SEC3 4446; SEC-Bovine;

KW SEC-Ovine; toxin; disulfide loop; protein engineering.

OS Staphylococcus aureus.

PN WO9927889-A2.

PD 10-JUN-1999.

PF 01-DEC-1998; 98WO-US25107.

PR 02-DEC-1997; 97US-0067357.

PA (IDAH-) IDAHO RES FOUND INC.

PI Bohach GI;

DR WPI; 1999-358008/30.

DR N-PSDB; AAX58884.

XX Non-toxic modified staphylococcal enterotoxins

PS Disclosure; Page 3; 25pp; English.

XX This peptide corresponds to the disulfide loop, i.e. amino acids
 CC 93-110, of Staphylococcus aureus group C enterotoxins SEC1, SEC2,
 CC SEC3 PRI 913, SEC 4446, SEC-Bovine and SEC-Ovine (see also AAY06251-53
 CC and AAY06255-58). The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide
 CC loop region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine
 CC production, but have substantially reduced toxicity compared to the
 CC corresponding unmodified native toxin. Emetic response inducing
 CC activity and fever inducing activity are typically decreased by at
 CC least about 100-fold, while LD50 (in Dutch Belted rabbits) is at
 CC least 100-fold higher than the native toxin.

XX Sequence 18 AA;

Query Match 89.4%; Score 93; DB 20; Length 18;
 Best Local Similarity 94.4%; Pred. No. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVKVTGGKTC 18
 Db 1 CCFSSKDNVGVKVTGGKTC 18

RESULT 5

ABG71377
 ID ABG71377 standard; Peptide; 18 AA.

AC ABG71377;

DT 29-JAN-2003 (first entry)

XX Staphylococcal enterotoxin disulfide loop region.

XX

KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC1; SEC2; SEC3-FRI913; SEC-4446; SEC-bovine.

OS Staphylococcus aureus.

PN WO200283169-A1.

XX 24-OCT-2002.

PF 11-APR-2002; 2002WO-US11619.

PR 13-APR-2001; 2001US-283720P.

XX (IDAH-) IDAHO RES FOUND INC.

PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;

XX WPI; 2003-058608/05.

XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
 PT an immune function and as a vaccine against toxic shock syndrome or
 PT food poisoning

PS Disclosure; Fig 15; 67pp; English.

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic
 CC response-inducing activity decreased by about 100-fold in comparison to a
 CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents a staphylococcal enterotoxin
 CC disulphide loop region, occurring in several enterotoxins.

XX Sequence 18 AA;

Query Match 89.4%; Score 93; DB 24; Length 18;
 Best Local Similarity 94.4%; Pred. No. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVKVTGGKTC 18
 Db 1 CCFSSKDNVGVKVTGGKTC 18

RESULT 6

ABG71380
 ID ABG71380 standard; Peptide; 18 AA.

XX ABG71380;

DT 29-JAN-2003 (first entry)

XX Staphylococcal enterotoxin C1 (SEC1) protein fragment.

XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin; SEC1;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.

OS Staphylococcus aureus.

PN WO200283169-A1.

XX 24-OCT-2002.

PF 11-APR-2002; 2002WO-US11619.

XX

```

PR 13-APR-2001; 2001US-283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
DR N-PSDB; ABS56822.
XX
PT New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing
PT an immune function and as a vaccine against toxic shock syndrome or
PT food poisoning .
XX
PS Example 1; Fig 1; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulfide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulfide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic
CC response-inducing activity decreased by about 100-fold in comparison to a
CC native toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents a staphylococcal enterotoxin
CC protein fragment.
XX
SQ Sequence 18 AA;

Query Match 89.4%; Score 93; DB 24; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKGKTC 18
Db 1 CCFSSKDNVGVKGKTC 18

RESULT 7
AAR13208
ID AAR13208 standard; Protein; 238 AA.
XX
AC AAR13208;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin C3.
XX
KW SEC3; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1991; 91WO-US00342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SEC3 was isolated and purified from S.aureus. It can be used for

CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
CC polypeptides having structural homology to staphylococcal
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydrophathy profiles.
XX
SQ Sequence 238 AA;

Query Match 89.4%; Score 93; DB 12; Length 238;
Best Local Similarity 94.4%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKGKTC 18
Db 92 CCFSSKDNVGVKGKTC 109

RESULT 8
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
AC AAR45016;
XX
DT 25-MAR-2003 (updated)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEC3.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US05213.
XX
PR 01-JUN-1992; 92US-0891718.
XX
PA (STON/) STONE J L.
PA (TERM/) GERMAN P S.
XX
PI Stone JL, Terman DS;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 238 AA;

Query Match 89.4%; Score 93; DB 14; Length 238;
Best Local Similarity 94.4%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 CCFSSKDNVGVGGKTC 18
 Db 92 CYFSSKDNVGVGGKTC 109

RESULT 9
 AAB67343
 ID AAB67343 standard; peptide; 238 AA.
 AC AAB67343;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin C3 protein.
 XX
 KW Tumour; cancer; immune; enterotoxin.
 XX
 OS Staphylococcus aureus.
 XX
 PN US6180097-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 30-OCT-1998; 98US-0183437.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2001-158657/16.
 XX

PT Tumor cell capable of stimulating antitumor immune reactivity in vitro
 or in vivo comprises exogenous nucleic acids encoding a superantigen
 and a costimulatory molecule -
 PT
 PS Disclosure; Fig 2; 16pp; English.
 XX
 CC The present invention relates to a tumour cell capable of stimulating
 antitumor immune reactivity in vitro or in vivo contains and
 expresses an exogenous nucleic acid molecule encoding a superantigen
 or its active fragment and an exogenous nucleic acid molecule
 encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 XX
 SQ Sequence 238 AA;
 Query Match 89.4%; Score 93; DB 22; Length 238;
 Best Local Similarity 94.4%; Pred. No. 1.2e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVGGKTC 18
 Db 92 CYFSSKDNVGVGGKTC 109

RESULT 10
 ABB76239
 ID ABB76239 standard; Protein; 238 AA.
 AC ABB76239;
 XX
 DT 09-AUG-2002 (first entry)
 XX

DE Staphylococcus aureus enterotoxin C3.
 XX
 KW Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
 antitumour; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 208
 XX /note= "given as 'O' in the specification"
 PN US2002051765-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 19-DEC-2000; 2000US-0741503.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2002-415198/44.
 XX
 PT Reagent for treating cancer without the need for e.g. radiotherapy,
 comprises a specific V beta subset of T cells sensitized to a growing
 tumor and stimulated with superantigens -
 PT
 PS Disclosure; Fig 2; 17pp; English.
 XX

CC The present sequence is the protein sequence of enterotoxin C3
 (SEC3) of Staphylococcus aureus. Similarity is shown, in several
 stretches of sequence, between staphylococcal enterotoxins,
 streptococcal pyrogenic exotoxins and staphylococcal exfoliative
 toxins (see AB576234-44). In the present invention, synthetic
 polypeptides useful in tumour therapy and in blocking or destroying
 autoreactive T and B lymphocyte populations are characterised by
 CC substantial structural homology to staphylococcal enterotoxin A and
 enterotoxin B, and to streptococcal pyrogenic exotoxins, with
 statistically significant sequence homology and similarity (Z value
 of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
 CC 6) to include alignment of cysteine residues and similar hydropathy
 profiles. These superantigens are used to treat solid tumours,
 including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 treatment involves contacting haematopoietic cells from a patient
 with one or more superantigens ex vivo to generate stimulated cells,
 CC selecting a specific V beta subset of cells, and reintroducing
 these cells into the patient to induce an in vivo therapeutic,
 CC tumoricidal reaction.
 XX
 SQ Sequence 238 AA;

Query Match 89.4%; Score 93; DB 23; Length 238;
 Best Local Similarity 94.4%; Pred. No. 1.2e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVGGKTC 18
 Db 92 CYFSSKDNVGVGGKTC 109

RESULT 11
 AAR13207
 ID AAR13207 standard; Protein; 239 AA.
 XX

CC enterotoxin SEC-MNCopeland. The invention relates to pyrogenic
CC toxins, such as staphylococcal enterotoxins, modified in the
CC disulfide loop region. Typically, the modification involves
CC deletions within the disulfide loop region of SEC (see AAY06261).
CC The modified toxins retain useful biological properties, such as
CC the ability to induce cytokine production, but have substantially
CC reduced toxicity compared to the corresponding unmodified native
CC toxin. Emetic response inducing activity and fever inducing
CC activity are typically decreased by at least about 100-fold, while
CC LD50 (in Dutch Belted rabbits) is at least 100-fold higher than
CC the native toxin.

XX Sequence 239 AA;

Query Match 89.4%; Score 93; DB 20; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 93 CFFSSKDNVGVGTGGKTC 110

RESULT 14
AAY06256
ID AAY06256 standard; Protein; 239 AA.

XX AC AAY06256;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC-4446.

KW Enterotoxin; SEC-4446; toxin; disulfide loop;
protein engineering.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
FH Disulfide-bond 93..110

XX WO9927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC-4446. The invention relates to pyrogenic toxins,
CC such as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 89.4%; Score 93; DB 20; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 93 CFFSSKDNVGVGTGGKTC 110

RESULT 15
AAY06251
ID AAY06251 standard; Protein; 239 AA.

XX AC AAY06251;

DT 23-AUG-1999 (first entry)

DE Staphylococcal group C enterotoxin SEC1.

KW Enterotoxin; SEC1; toxin; disulfide loop; protein engineering.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
FH Disulfide-bond 93..110

XX WO9927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins

XX Disclosure; Page 17; 25pp; English.

XX This protein represents the Staphylococcus aureus type C
CC enterotoxin SEC1. The invention relates to pyrogenic toxins, such
CC as staphylococcal enterotoxins, modified in the disulfide loop
CC region. Typically, the modification involves deletions within the
CC disulfide loop region of SEC (see AAY06261). The modified toxins
CC retain useful biological properties, such as the ability to induce
CC cytokine production, but have substantially reduced toxicity
CC compared to the corresponding unmodified native toxin. Emetic
CC response inducing activity and fever inducing activity are
CC typically decreased by at least about 100-fold, while LD50 (in Dutch
CC Belted rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 239 AA;

Query Match 89.4%; Score 93; DB 20; Length 239;
Best Local Similarity 94.4%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 93 CFFSSKDNVGVGTGGKTC 110

Search completed: October 15, 2003, 16:56:57
Job time : 50.3575 secs

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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 104
Sequence: 1 CCFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	89.4	89	4	US-09-144-776B-21
2	93	89.4	89	4	US-09-144-776B-22
3	93	89.4	89	4	US-09-144-776B-23
4	93	89.4	238	3	US-08-896-933-28
5	93	89.4	238	4	US-09-314-235-28
6	93	89.4	239	3	US-08-896-933-27
7	93	89.4	239	4	US-09-314-235-27
8	93	89.4	266	4	US-09-144-776B-14
9	49	47.1	170	4	US-09-252-991A-29047
10	46	44.2	374	2	US-07-857-224B-82
11	46	44.2	374	2	US-07-857-224B-83
12	46	44.2	375	4	US-09-347-878-56
13	44	42.3	134	2	US-08-482-728A-14
14	44	42.3	176	1	US-08-145-995A-4
15	44	42.3	176	2	US-08-451-747-4
16	44	42.3	176	3	US-09-134-852-4
17	41	39.4	263	2	US-08-892-690-3
18	41	39.4	275	1	US-08-252-995D-13
19	41	39.4	275	4	US-08-834-108-13
20	41	39.4	1917	4	US-09-627-650B-5
21	41	39.4	1917	4	US-09-436-063C-5
22	40	38.5	320	3	US-09-092-437-2
23	40	38.5	374	2	US-07-857-224B-80
24	40	38.5	374	2	US-07-857-224B-81
25	40	38.5	374	2	US-07-857-224B-84
26	40	38.5	374	2	US-07-857-224B-85
27	40	38.5	375	2	US-07-857-224B-86

28	40	38.5	690	4	US-09-252-991A-29429	Sequence 29429, A
29	40	38.5	1053	4	US-09-328-352-6788	Sequence 6788, Ap
30	39	37.5	94	2	US-07-728-215-35	Sequence 35, Appl
31	39	37.5	94	2	US-07-728-215-37	Sequence 37, Appl
32	39	37.5	94	4	US-08-938-085A-35	Sequence 35, Appl
33	39	37.5	94	4	US-08-938-085A-37	Sequence 35, Appl
34	39	37.5	94	4	US-10-072-844-35	Sequence 35, Appl
35	39	37.5	94	4	US-10-072-844-37	Sequence 37, Appl
36	39	37.5	228	1	US-08-278-091-7	Sequence 7, Appli
37	39	37.5	228	1	US-08-483-859-7	Sequence 7, Appli
38	39	37.5	228	1	US-08-472-173-7	Sequence 7, Appli
39	39	37.5	228	2	US-08-487-167-7	Sequence 7, Appli
40	39	37.5	228	2	US-08-482-816-7	Sequence 7, Appli
41	39	37.5	228	2	US-08-296-149-7	Sequence 7, Appli
42	39	37.5	228	2	US-08-801-499-7	Sequence 7, Appli
43	39	37.5	228	2	US-08-615-271-7	Sequence 7, Appli
44	39	37.5	228	3	US-09-074-660-7	Sequence 7, Appli
45	39	37.5	228	3	US-09-074-659-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-144-776B-21
; Sequence 21, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-144-776B-21

Query Match 89.4%; Score 93; DB 4; Length 89;

Best Local Similarity 94.4%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 54 CYFSSKDNVKGVTGGKTC 71

RESULT 2

US-09-144-776B-22
; Sequence 22, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Query Match 89.4%; Score 93; DB 4; Length 89;
Best Local Similarity 94.4%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 54 CYFSSKDNVKGVTGGKTC 71

RESULT 3

US-09-144-776B-23
; Sequence 23, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson

; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 89.4%; Score 93; DB 4; Length 89;
Best Local Similarity 94.4%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | |
Db 54 CYFSSKDNVKGVTGGKTC 71

RESULT 4

US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

Query Match

89.4%; Score 93; DB 3; Length 238;

Best Local Similarity 94.4%; Pred. No. 6.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 92 CYFSSKDNVKGVTGGKTC 109

RESULT 5

US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845

; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235

; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933

; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718

; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342

; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577

; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530

; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28

; LENGTH: 238

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-314-235-28

Query Match 89.4%; Score 93; DB 4; Length 238;

Best Local Similarity 94.4%; Pred. No. 6.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 92 CYFSSKDNVKGVTGGKTC 109

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351

; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933

; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-08-896-933-27

Query Match 89.4%; Score 93; DB 3; Length 239;

Best Local Similarity 94.4%; Pred. No. 6.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 93 CYFSSKDNVKGVTGGKTC 110

RESULT 7

US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845

; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235

; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933

; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718

; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342

; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577

; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530

; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-314-235-27

Query Match 89.4%; Score 93; DB 4; Length 239;

Best Local Similarity 94.4%; Pred. No. 6.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 93 CYFSSKDNVKGVTGGKTC 110

RESULT 8

US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332

; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson

; Sina Bavari

; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris

; STREET: US Army MPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B

; FILING DATE: 01-Sep-1998

TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: human
FEATURE: Alcohol dehydrogenase, Table 3 Column 4
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Joernvall, H.
AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-83

Query Match 44.2%; Score 46; DB 2; Length 374;
Best Local Similarity 54.5%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CCFSTGYGSANVAVKVTGGKTC 18
DB 174 CGFSTGYGSANVAVKVTGGKTC 195

RESULT 12
US-09-347-878-56
Sequence 56, Application US/09347878C
Patent No. 6376210
GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-878-56

Query Match 44.2%; Score 46; DB 4; Length 375;
Best Local Similarity 54.5%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

QY 1 CCFSTGYGSANVAVKVTGGKTC 18
DB 175 CGFSTGYGSANVAVKVTGGKTC 196

RESULT 13
US-08-482-728A-14
Sequence 14, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Pavan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohnbach, Test, Albritton
ADDRESSES: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-14

Query Match 42.3%; Score 44; DB 2; Length 134;
Best Local Similarity 44.4%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVKVTGGKTC 18
DB 21 CLCSGKGLGKTTGKLC 38

RESULT 14
US-08-145-995A-4
Sequence 4, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-4

Query Match 42.3%; Score 44; DB 1; Length 176;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKVTGGKTC 18
| | | | | | | | | | | | | | | | | | | |
Db 41 CLCSGEKGLGKTTGKKLC 58

RESULT 15
US-08-451-747-4
Sequence 4, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-451-747-4

Query Match 42.3%; Score 44; DB 2; Length 176;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKVTGGKTC 18
| | | | | | | | | | | | | | | | | | | |
Db 41 CLCSGEKGLGKTTGKKLC 58

Search completed: October 15, 2003, 17:08:33
Job time : 13.7964 secs

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OM protein - protein search, using sw model

Run on: October 15, 2003, 17:04:29 ; Search time 27.2695 Seconds
(without alignments)
106.357 Million cell updates/sec

Title: US-09-555-115a-17
Perfect score: 104
Sequence: 1 CCFSSKDNVGVKGGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues
Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	89.4	89	15	US-10-002-784A-36
2	93	89.4	89	15	US-10-002-784A-37
3	93	89.4	89	15	US-10-002-784A-38
4	93	89.4	266	8	US-08-882-431-14
5	93	89.4	266	10	US-09-870-759-12
6	93	89.4	266	12	US-09-751-708A-12
7	93	89.4	266	15	US-10-002-784A-14
8	49	47.1	1204	12	US-10-140-472-505
9	49	47.1	1204	12	US-10-141-761-505
10	49	47.1	1204	12	US-10-142-885-505
11	49	47.1	1204	12	US-10-158-790-505
12	49	47.1	1204	16	US-10-123-155-505
13	49	47.1	1204	16	US-10-146-731-505
14	47	45.2	1532	15	US-10-184-644-121
15	47	45.2	1532	15	US-10-184-634-121

16	46	44.2	375	10	US-09-981-353-113	Sequence 113, App
17	46	44.2	375	12	US-09-738-630-92	Sequence 92, Appl
18	46	44.2	395	9	US-09-925-302-497	Sequence 497, App
19	45	43.3	1648	15	US-10-184-644-295	Sequence 295, App
20	45	43.3	1648	15	US-10-184-634-295	Sequence 295, App
21	45	43.3	2447	12	US-10-140-472-291	Sequence 291, App
22	45	43.3	2447	12	US-10-141-761-291	Sequence 291, App
23	45	43.3	2447	12	US-10-142-885-291	Sequence 291, App
24	45	43.3	2447	12	US-10-158-790-291	Sequence 291, App
25	45	43.3	2447	15	US-10-123-155-291	Sequence 291, App
26	45	43.3	2447	16	US-10-146-731-291	Sequence 39, Appl
27	45	43.3	2998	12	US-10-140-472-39	Sequence 39, Appl
28	45	43.3	2998	12	US-10-141-761-39	Sequence 39, Appl
29	45	43.3	2998	12	US-10-142-885-39	Sequence 39, Appl
30	45	43.3	2998	12	US-10-158-790-39	Sequence 39, Appl
31	45	43.3	2998	15	US-10-123-155-39	Sequence 39, Appl
32	45	43.3	2998	16	US-10-146-731-39	Sequence 39, Appl
33	45	43.3	3567	12	US-10-140-472-77	Sequence 77, Appl
34	45	43.3	3567	12	US-10-141-761-77	Sequence 77, Appl
35	45	43.3	3567	12	US-10-142-885-77	Sequence 77, Appl
36	45	43.3	3567	12	US-10-158-790-77	Sequence 77, Appl
37	45	43.3	3567	15	US-10-123-155-77	Sequence 77, Appl
38	45	43.3	3567	16	US-10-146-731-77	Sequence 347, App
39	44.5	42.8	311	15	US-10-212-679-347	Sequence 317, App
40	44	42.3	1875	12	US-10-140-472-317	Sequence 317, App
41	44	42.3	1875	12	US-10-141-761-317	Sequence 317, App
42	44	42.3	1875	12	US-10-142-885-317	Sequence 317, App
43	44	42.3	1875	12	US-10-158-790-317	Sequence 317, App
44	44	42.3	1875	15	US-10-123-155-317	Sequence 317, App
45	44	42.3	1875	16	US-10-146-731-317	Sequence 317, App

ALIGNMENTS

RESULT 1
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match 89.4%; Score 93; DB 15; Length 89;
Best Local Similarity 94.4%; Pred. No. 5.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKGGKTC 18
Db 54 CCFSSKDNVGVKGGKTC 71

RESULT 2
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; /33

; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-37

Query Match 89.4%; Score 93; DB 15; Length 89;
Best Local Similarity 94.4%; Pred. No. 5.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
Db 54 CYFSSKDNVGVGTGGKTC 71

RESULT 3
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33

; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-38

Query Match 89.4%; Score 93; DB 15; Length 89;
Best Local Similarity 94.4%; Pred. No. 5.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
Db 54 CYFSSKDNVGVGTGGKTC 71

RESULT 4
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK

; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match 89.4%; Score 93; DB 8; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
Db 120 CYFSSKDNVGVGTGGKTC 137

RESULT 5
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-12

Query Match 89.4%; Score 93; DB 10; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
Db 120 CYFSSKDNVGVGTGGKTC 137

RESULT 6
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1

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; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-751-708A-12

Query Match      89.4%; Score 93; DB 12; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCFSSKDNVGVKVTGGKTC 18
Db      120 CYFSSKDNVGVKVTGGKTC 137

RESULT 7
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
; US-10-002-784A-14

Query Match      89.4%; Score 93; DB 15; Length 266;
Best Local Similarity 94.4%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCFSSKDNVGVKVTGGKTC 18
Db      120 CYFSSKDNVGVKVTGGKTC 137

RESULT 8
US-10-140-472-505
; Sequence 505, Application US/10140472
; Publication No. US2003013888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/141,761
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-141-761-505

Query Match      47.1%; Score 49; DB 12; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCFSSKDNVGVKVTGGKTC 18
Db      896 CCACCTGGTGTGGTTC 913

RESULT 9
US-10-141-761-505
; Sequence 505, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/141,761
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-141-761-505

Query Match      47.1%; Score 49; DB 12; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCFSSKDNVGVKVTGGKTC 18
Db      896 CCACCTGGTGTGGTTC 913

RESULT 10

```

```

; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: US/10/140,472
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-472-505

Query Match      47.1%; Score 49; DB 12; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCFSSKDNVGVKVTGGKTC 18
Db      896 CCACCTGGTGTGGTTC 913

RESULT 9
US-10-141-761-505
; Sequence 505, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/141,761
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-141-761-505

Query Match      47.1%; Score 49; DB 12; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCFSSKDNVGVKVTGGKTC 18
Db      896 CCACCTGGTGTGGTTC 913

RESULT 10

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US-10-142-885-505
; Sequence 505, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-885-505

Query Match 47.1%; Score 49; DB 12; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVKVTGGKTC 18
Db 896 CCACCTGGTGTGGTTC 913

RESULT 11
US-10-158-790-505
; Sequence 505, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505

US-10-142-885-505
; Sequence 505, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-885-505

Query Match 47.1%; Score 49; DB 12; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVKVTGGKTC 18
Db 896 CCACCTGGTGTGGTTC 913

RESULT 12
US-10-123-155-505
; Sequence 505, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-505

Query Match 47.1%; Score 49; DB 15; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVKVTGGKTC 18
Db 896 CCACCTGGTGTGGTTC 913

RESULT 13
US-10-146-731-505
; Sequence 505, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

```

```
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C323
; CURRENT APPLICATION NUMBER: US/10/146,731
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-731-505

Query Match 47.1%; Score 49; DB 16; Length 1204;
Best Local Similarity 44.4%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKVTGGKTC 18
|| : |||||
Db 896 CCACCTGGTGTGGTTC 913

RESULT 14
US-10-184-644-121
; Sequence 121, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 121
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-121

Query Match 45.2%; Score 47; DB 15; Length 1532;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKVTGGKTC 18
|| : |||||
Db 1368 CCTGAGCGGTCTGGGTC 1385

RESULT 15
US-10-184-634-121
; Sequence 121, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 121
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-121

Query Match 45.2%; Score 47; DB 15; Length 1532;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVKVTGGKTC 18
|| : |||||
Db 1368 CCTGAGCGGTCTGGGTC 1385

Search completed: October 15, 2003, 17:47:02
Job time : 27.2695 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:47:38 ; Search time 13.6886 Seconds
(without alignments)
126.458 Million cell updates/sec

Title: US-09-555-115A-17
Perfect score: 104
Sequence: 1 CCFSSKDNVKGVTGGKTC 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	89.4	266	1 ENSAC1	enterotoxin C-1 pr
2	93	89.4	266	2 A60114	enterotoxin C-2 pr
3	93	89.4	266	2 S11885	enterotoxin C3 - S
4	46	44.2	375	1 DEHUA6	alcohol dehydrogen
5	46	44.2	375	1 DEHUA6	alcohol dehydrogen
6	44.5	42.8	212	2 T05936	agglutinin isolect
7	44.5	42.8	2533	2 T28675	alpha-51D immobili
8	44.5	42.8	2533	2 T28674	alpha-51D-immobili
9	44.5	42.8	2543	2 T31687	surface antigen - P
10	44	42.3	246	2 JQ1472	trypsin (EC 3.4.21
11	44	42.3	246	2 JQ1471	trypsin (EC 3.4.21
12	44	42.3	1403	1 A47328	natural killer cel
13	44	42.3	1507	2 B47328	natural killer cel
14	43.5	41.8	186	2 A28401	agglutinin isolect
15	43	41.3	170	2 A44307	calcineurin regula
16	43	41.3	274	2 T13010	hypothetical prote
17	43	41.3	368	2 T26338	hypothetical prote
18	42	40.4	283	2 T01454	hypothetical prote
19	42	40.4	375	1 A38405	alcohol dehydrogen
20	42	40.4	399	2 T28913	cut repeat and hom
21	42	40.4	430	2 A87634	peptidase, M20/M25
22	42	40.4	1487	2 G96837	protein F20817.10
23	41.5	39.9	319	2 AH2849	transcription regu
24	41.5	39.9	319	2 F97626	probable transcrip
25	41	39.4	97	2 T08573	hypothetical prote
26	41	39.4	139	1 PSTV	phospholipase A2 (
27	41	39.4	270	2 AH1188	transporters (form
28	41	39.4	270	2 AH1546	transporters (form
29	41	39.4	319	2 A70102	conserved hypothet

30 41 39.4 368 1 DEHUA6 alcohol dehydrogen
31 41 39.4 375 1 A33909 alcohol dehydrogen
32 41 39.4 558 2 H81416 dihydroxy-acid deh
33 41 39.4 705 2 A48144 protein kinase CDC
34 41 39.4 1127 2 T03105 major single-stran
35 41 39.4 4377 2 A55575 ankylin 3, long sp
36 40.5 38.9 152 2 D64870 ychJ protein - Esc
37 40.5 38.9 152 2 G90845 hypothetical prote
38 40.5 38.9 152 2 F85703 hypothetical prote
39 40.5 38.9 725 2 T17732 helicase-like prot
40 40 38.5 99 2 G84242 hypothethical prote
41 40 38.5 129 2 A30554 Ig lambda chain pr
42 40 38.5 183 2 T42240 cut repeat homeobo
43 40 38.5 242 2 H69066 ribosomal protein
44 40 38.5 266 1 S18159 ribosomal protein
45 40 38.5 320 2 H95136 hypothethical prote

ALIGNMENTS

RESULT 1
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness t
A;Reference number: S06356; MUID:98038352; PMID:2823067
A;Accession: S06356
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: EMBL:X05815; NID:g45666; PIDN:CAA29260.1; PID:g46567
R;Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75,'IL',78-176,'N',178-266 <SCH>
C;Genetics:
A;Gene: entC1
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental

Query Match 89.4%; Score 93; DB 1; Length 266;
Best Local Similarity 94.4%; Pred.No. 1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 120 CYPSSKDNVKGVTGGKTC 137

RESULT 2
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N;Alternate names: enterotoxin C-3 precursor
C;Species: Staphylococcus aureus
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
C;Accession: A60114; B60114; A33866
R;Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A;Reference number: A60114; MUID:89277549; PMID:2543637
A;Accession: A60114
A;Status: not compared with conceptual translation
A;Molecule type: DNA

A;Residues: 1-266 <BOH>
A;Accession: B60114
A;Molecule type: protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A;Reference number: A33866; MUID:89321714; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:gl53003; PIDN:AAA26624.1; PID:gl53004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 89.4%; Score 93; DB 2; Length 266;
Best Local Similarity 94.4%; Pred. No. 1e-06; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 0;

Qy 1 CCFSSKDNVGVGTGGKTC 18
Db 120 CYFSSKDNVGVGTGGKTC 137

RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S11885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
A;Reference number: S11885; MUID:90220508; PMID:2325627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOW>
A;Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B

Query Match 89.4%; Score 93; DB 2; Length 266;
Best Local Similarity 94.4%; Pred. No. 1e-06; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 0;

Qy 1 CCFSSKDNVGVGTGGKTC 18
Db 120 CYFSSKDNVGVGTGGKTC 137

RESULT 4
DEHUAA
alcohol dehydrogenase (EC 1.1.1.1) 1 - human
N;Alternate names: alcohol dehydrogenase alpha chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Feb-2000
C;Accession: S02265; A25428; A24408; I39398; I39397
R;Matsumoto, Y.; Yokoyama, S.
FEBS Lett. 243, 57-60, 1989
A;Title: Molecular structure of the human alcohol dehydrogenase 1 gene.
A;Reference number: S02265; MUID:89153548; PMID:2920825
A;Accession: S02265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-375 <MATS>
R;Ikuta, T.; Szeto, S.; Yoshida, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 634-638, 1986
A;Title: Three human alcohol dehydrogenase subunits: cDNA structure and molecular and ev
A;Reference number: A94120; MUID:86120995; PMID:2935875

A;Accession: A25428
A;Molecule type: mRNA
A;Residues: 1-375 <IKU>
A;Cross-references: GB:M12271; NID:gl78091; PIDN:AAA68131.1; PID:gl78092
R;von Bahr-Lindstrom, H.; Hoog, J.O.; Heden, L.O.; Kaiser, R.; Fleetwood, L.; Larsson, K
Biochemistry 25, 2465-2470, 1986
A;Title: cDNA and protein structure for the alpha subunit of human liver alcohol dehydrog
A;Reference number: A24408; MUID:86243367; PMID:3013304
A;Accession: A24408
A;Molecule type: mRNA
A;Residues: 1-375 <VON>
A;Cross-references: GB:M12963; NID:gl78089; PIDN:AAA51590.1; PID:gl78090
R;Yasunami, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
Genomics 7, 152-158, 1990
A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly c
A;Reference number: I39398; MUID:90269803; PMID:2347582
A;Accession: I39398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <YAS>
A;Cross-references: GB:M37066; NID:gl78095; PIDN:AAA51591.1; PID:gl78096
R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
Gene 90, 271-279, 1990
A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
A;Reference number: I39397; MUID:90382676; PMID:2169444
A;Accession: I39397
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <STE>
A;Cross-references: GB:M32656; NID:gl78093; PIDN:AAA52276.1; PID:gl78094
C;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity;
C;Genetics:
A;Gene: GDB:ADH1
A;Cross-references: GDB:119650; OMIM:103700
A;Map position: 4q21-4q23
A;Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
C;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
C;Function:
A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
A;Pathway: ethanol degradation
A;Note: human alcohol dehydrogenase 1 is expressed predominantly in fetal and neonatal li
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidore
F;2-375/Product: alcohol dehydrogenase 1 #status predicted <MAT>
F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 44.2%; Score 46; DB 1; Length 375;
Best Local Similarity 54.5%; Pred. No. 22; Mismatches 12; Conservative 0; Indels 4; Gaps 1;
Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFSSKDNVGVGTGGKTC 18
Db 175 CGFSTGYGSANVAVKVPFGSTC 196

RESULT 5
DEHUAB
alcohol dehydrogenase (EC 1.1.1.1) 2 [validated] - human
N;Alternate names: alcohol dehydrogenase beta chain; class I alcohol dehydrogenase
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1985 #sequence_revision 02-Aug-1994 #text_change 15-Sep-2000
C;Accession: A23607; I39399; A26281; I39402; I39401; S05202; S10621; I39400; A00:
R;Heden, L.O.; Hoog, J.O.; Larsson, K.; Lake, M.; Lagerholm, E.; Holmgren, A.; Valles, B
FEBS Lett. 194, 327-332, 1986
A;Title: cDNA clones coding for the beta-subunit of human liver alcohol dehydrogenase hav
A;Reference number: A23607; MUID:86082371; PMID:3000832
A;Accession: A23607
A;Molecule type: mRNA
A;Residues: 1-375 <HED>

A;Cross-references: EMBL:X03350; NID:g28415; PIDN:CAA27056.1; PID:g28416
 R;Ikuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2703-2707, 1985
 A;Title: Molecular cloning of a full-length cDNA for human alcohol dehydrogenase.
 R;Hempel, J.; Buhler, R.; Kaiser, R.; Holmquist, B.; de Zalsenski, C.; von Wartburg, J.P.;
 Eur. J. Biochem. 145, 437-445, 1984
 A;Reference number: A38916; MUID:85190565; PMID:2986130
 A;Accession: A38916
 A;Molecule type: mRNA
 A;Residues: 1-375 <IKU>
 A;Cross-references: GB:M24317; NID:g178097
 R;Ikuta, T.; Fujiyoshi, T.; Kurachi, K.; Yoshida, A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5578, 1985
 A;Reference number: A38917
 A;Contents: annotation; erratum
 R;Yokoyama, S.; Yokoyama, R.; Rotwein, P.
 Jpn. J. Genet. 62, 241-256, 1987
 A;Title: Molecular characterization of cDNA clones encoding the human alcohol dehydrogenase gene family and n
 A;Reference number: I39399
 A;Accession: I39399
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-375 <YOK>
 A;Cross-references: GB:P00137; NID:g219427; PIDN:BAA00084.1; PID:g219428
 R;Duester, G.; Smith, M.; Bilanchone, V.; Hatfield, G.W.
 J. Biol. Chem. 261, 2027-2033, 1986
 A;Title: Molecular analysis of the human class I alcohol dehydrogenase gene family and n
 A;Reference number: A26281; MUID:86111889; PMID:2935533
 A;Accession: A26281
 A;Molecule type: DNA
 A;Residues: 1-229, 'K', 231-375 <DUE>
 A;Cross-references: GB:M24317; GB:K01883; NID:g178097; PIDN:AAA51884.1; PID:g178098
 A;Note: the authors translated the codon AAA for residue 230 as Phe
 R;Yasunami, M.; Kikuchi, I.; Sarapata, D.; Yoshida, A.
 Genomics 7, 152-158, 1990
 A;Title: The human class I alcohol dehydrogenase gene cluster: three genes are tandemly
 A;Reference number: I39398; MUID:90269803; PMID:2347582
 A;Accession: I39402
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-6 <YAS>
 A;Cross-references: GB:M37067; NID:g178114; PIDN:AAA51593.1; PID:g178115
 R;Stewart, M.J.; McBride, M.S.; Winter, L.A.; Duester, G.
 Gene 90, 271-279, 1990
 A;Title: Promoters for the human alcohol dehydrogenase genes ADH1, ADH2, and ADH3: inter
 A;Reference number: I39397; MUID:90382676; PMID:2169444
 A;Accession: I39401
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <STE>
 A;Cross-references: GB:M32657; NID:g178112; PIDN:AAA52277.1; PID:g178113
 R;Matsuo, Y.; Yokoyama, R.; Yokoyama, S.
 Eur. J. Biochem. 183, 317-320, 1989
 A;Title: The genes for human alcohol dehydrogenases beta(1) and beta(2) differ by only c
 A;Reference number: S05202; MUID:89338401; PMID:2547609
 A;Accession: S05202
 A;Molecule type: DNA
 A;Residues: 1-47, 'H', 49-375 <MATS>
 A;Cross-references: EMBL:X15447; NID:g28385
 A;Note: allelic beta-2 variant found predominately in oriental populations
 A;Note: the sequence in GenBank entry HSADH221, release 103 (PID:e228260), has an incorr
 R;Ehrig, T.; von Wartburg, J.P.; Wermuth, B.
 FEBS Lett. 234, 53-55, 1988
 A;Title: cDNA sequence of the beta(2)-subunit of human liver alcohol dehydrogenase.
 A;Reference number: S10621; MUID:88271624; PMID:2968918
 A;Accession: S10621
 A;Molecule type: mRNA
 A;Residues: 1-47, 'H', 49-343 <EHR>
 A;Note: only a list of differences from various previously published sequences is shown
 R;Xu, Y.L.; Carr, L.G.; Bosron, W.F.; Li, T.K.; Edenberg, H.J.
 Genomics 2, 209-214, 1988
 A;Title: Genotyping of human alcohol dehydrogenases at the ADH2 and ADH3 loci following
 A;Reference number: I39400; MUID:88284699; PMID:3397059
 A;Accession: I39400

A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-7, 'M', 9-56, 'K', 58-165, 'K', 167-234, 'V', 236-375 <RE3>
 A;Cross-references: GB:M21692; NID:g178099; PIDN:AAA51592.1; PID:g178100
 R;Hempel, J.; Buhler, R.; Kaiser, R.; Holmquist, B.; de Zalsenski, C.; von Wartburg, J.P.;
 Eur. J. Biochem. 145, 437-445, 1984
 A;Title: Human liver alcohol dehydrogenase. 1. The primary structure of the beta-1beta-1
 A;Reference number: A00335; MUID:85076637; PMID:6391920
 A;Accession: A00335
 A;Molecule type: protein
 A;Residues: 2-129, 131-375 <HEM>
 A;Note: allelic beta-1 variant found predominately in caucasian and negroid populations
 R;Buhler, R.; Hempel, J.; Kaiser, R.; von Wartburg, J.P.; Vallee, B.L.; Jornvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6320-6324, 1984
 A;Title: Human alcohol dehydrogenase: structural differences between the beta and gamma s
 ndants in livers of different mammals.
 A;Reference number: A05182; MUID:85038508; PMID:6387702
 A;Accession: A05182
 A;Molecule type: protein
 A;Residues: 12-34, 'V', 36-38, 41-85, 101-114, 131-160, 170-213, 273-313, 317-331, 341-367 <BUH>
 R;Burnell, J.C.; Carr, L.G.; Dulet, F.E.; Edenberg, H.J.; Li, T.K.; Bosron, W.F.
 Biochem. Biophys. Res. Commun. 146, 1227-1233, 1987
 A;Title: The human beta-3 alcohol dehydrogenase subunit differs from beta-1 by a Cys for
 A;Reference number: A26826
 A;Accession: A26826
 A;Molecule type: protein
 A;Residues: 368-369, 'C', 371-375 <BUR>
 A;Note: allelic beta-3 variant found as a minor form occurring to a greater extent in nei
 R;Hurley, T.D.; Bosron, W.F.; Hamilton, J.A.; Amzel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8149-8153, 1991
 A;Title: Structure of human beta-1 alcohol dehydrogenase: catalytic effects of none
 A;Reference number: A40987; MUID:91376103; PMID:1896463
 A;Contents: annotation; X-ray crystallography, 3.0 angstroms
 A;Note: structure of beta-1 variant dimer
 R;Hurley, T.D.; Bosron, W.F.; Hamilton, J.A.; Amzel, L.M.
 submitted to the Brookhaven Protein Data Bank, January 1993
 A;Reference number: A52127; PDB:3H0D
 A;Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 2-375
 A;Comment: Class I alcohol dehydrogenases are pyrazole-sensitive and have a high activity
 C;Genetics:
 A;Gene: GDB:ADH2
 A;Cross-references: GDB:119651; OMIM:103720
 A;Map position: 4q22-4q22
 A;Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
 A;Complex: homo- or heterodimer of three types of chains (alpha, beta, or gamma) coded by
 C;Function:
 A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
 A;Pathway: alcohol degradation
 A;Note: human alcohol dehydrogenase beta is expressed predominately in fetal lung and nec
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidore
 F;2-375/Product: alcohol dehydrogenase 2 #status experimental <NAT>
 F;32-366/Domain: long-chain alcohol dehydrogenase homology <IAOH>
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status
 F;47, 68, 175/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
 F;98, 101, 104, 112/Binding site: zinc, noncatalytic (Cys) #status experimental
 Query Match 44.2%; Score 46; DB 1; Length 375;
 Best Local Similarity 54.5%; Pred. No. 22;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CCFS----SKDNVGVKVTGGKTC 18
 Db 175 CGFSTGSGAVNVAKVTPGSTC 196
 RESULT 6
 T05936
 agglutinin isolectin 1 precursor - barley
 C;Species: Hordeum vulgare (barley)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
 C;Accession: T05936

R:Lerner, D.R.; Raikhel, N.V.
Plant Physiol. 91, 124-129, 1999
A:Title: Cloning and characterization of root-specific barley lectin.
A:Reference number: Z15461

A:Accession: T05936
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-212 <LER>
A:Cross-references: EMBL:J029280; NID:g167070; PIDN:AAA32969.1; PID:g167071

A:Superfamily: wheat agglutinin; hevein chitin-binding domain homology

C:Keywords: lectin

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-212/Product: agglutinin isolectin I #status predicted <MAT>

F:27-69/Domain: hevein chitin-binding domain homology <HCB>

Query Match 42.8%; Score 44.5; DB 2; Length 212;

Best Local Similarity 52.9%; Pred. No. 23;

Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 2 CFSSKDNVGVGTGGKTC 18

Db 66 CYTSK-RCGTQAGKTC 81

RESULT 7

T28675

alpha-51D immobilization antigen - Paramesitium tetraurelia

C:Species: Paramesitium tetraurelia

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T28675

R:Schwegmann, K.J.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20506

A:Accession: T28675

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2533 <SCH>

A:Cross-references: EMBL:X96400; PIDN:CAA65264.1

C:Genetics:

A:Gene: alpha-51D

A:Genetic code: SGC5

A:Introns: 280/3; 538/2; 1248/2

C:Superfamily: G surface protein

Query Match 42.8%; Score 44.5; DB 2; Length 2533;

Best Local Similarity 41.7%; Pred. No. 2e+02;

Matches 10; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

Qy 2 CFSSKDN-----VGKVTGGKTC 18

Db 2291 CFTGDTGECTFALPVGATTTGKTC 2314

RESULT 8

T28674

alpha-51D-immobilization antigen - Paramesitium tetraurelia

C:Species: Paramesitium tetraurelia

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T28674

R:Schmidt, H.J.

submitted to the EMBL Data Library, March 1995

A:Reference number: Z20505

A:Accession: T28674

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2533 <SCH>

A:Cross-references: EMBL:X85135; NID:g728634; PID:g728635; PIDN:CAA59447.1

C:Genetics:

A:Genetic code: SGC5

A:Note: alpha-51D

C:Superfamily: G surface protein

Query Match 42.8%; Score 44.5; DB 2; Length 2533;

Best Local Similarity 41.7%; Pred. No. 2e+02;
Matches 10; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

Qy 2 CFSSKDN-----VGKVTGGKTC 18

Db 2291 CFTGDTGECTFALPVGATTTGKTC 2314

RESULT 9

T31687

surface antigen - Paramesitium primaurelia

C:Species: Paramesitium primaurelia

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001

C:Accession: T31687

R:Bourgain-Guglielmini, F.; Caron, F.

Journal of Eukaryot. Microbiol. 43, 303-314, 1996

A:Title: Molecular characterization of the D surface protein gene subfamily in Paramesitium

A:Reference number: Z21061; MUID:96313351; PMID:8768434

A:Accession: T31687

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2543 <BOU>

A:Cross-references: EMBL:X96616; NID:g1235576; PIDN:CAA65436.1

C:Genetics:

A:Genetic code: SGC5

C:Superfamily: G surface protein

Query Match 42.8%; Score 44.5; DB 2; Length 2543;

Best Local Similarity 41.7%; Pred. No. 2e+02;

Matches 10; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

Qy 2 CFSSKDN-----VGKVTGGKTC 18

Db 2301 CFTGDTGECTFALPVGATTTGKTC 2324

RESULT 10

JQ1472

trypsin (EC 3.4.21.4) V precursor, b-form - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999

C:Accession: JQ1472

R:Kang, J.; Wiegand, U.; Mueller-Hill, B.

Gene 110, 181-187, 1992

A:Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.

A:Reference number: JQ1471; MUID:92165057; PMID:1537555

A:Accession: JQ1472

A:Molecule type: mRNA

A:Residues: 1-246 <KAN>

A:Cross-references: EMBL:X59013; NID:g57414; PIDN:CAA41752.1; PID:g57415

A:Experimental source: pancreas

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; protein digestion; serine proteinase; zymogen

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-24/Domain: activation peptide #status predicted <ACT>

F:25-246/Product: trypsin V, b-form #status predicted <MAT>

F:25-239/Domain: trypsin homology <TRY>

F:31-160,49-65,133-233,140-206,171-185/disulfide bonds: #status predicted

F:64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 42.3%; Score 44; DB 2; Length 246;

Best Local Similarity 43.8%; Pred. No. 31;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVGVGTGGKTC 18

Db 16 FPTEDNDNDRIVGGYTC 31

RESULT 11

JQ1471

trypsin (EC 3.4.21.4) V precursor, a-form - rat

C:Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C;Accession: JQ1471; S23784
R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Title: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: JQ1471; MUID:92165057; PMID:1537555

A;Accession: JQ1471
A;Molecule type: mRNA
A;Residues: 1-246 <KAN>
A;Cross-references: EMBL:X59012; NID:g57412; PIDN:CAA41751.1; PID:g57413
A;Experimental source: pancreas
A;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-24/Domain: activation peptide #status predicted <ACT>
F;25-246/Product: trypsin V, a-form #status predicted <MAT>
F;25-239/Domain: trypsin homology <TRY>
F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted
F;64,108,200/Active site: His, Asp, Ser #status predicted

Query Match 42.3%; Score 44; DB 2; Length 246;
Best Local Similarity 43.8%; Pred. No. 31;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVKGVTGGKTC 18
| : : | : : | : : |
Db 16 FPTEDNDRIVGVTGTC 31

RESULT 12

A47328
N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: A47328
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
A;Reference number: A47328; MUID:93133824; PMID:8421688

A;Accession: A47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1403 <AND>
A;Cross-references: GB:L04288; NID:g181251; PIDN:AAA35734.1; PID:g181252
A;Experimental source: NK killer cells from adult blood
A;Note: sequence extracted from NCBI backbone (NCBIN:122798, NCBI:122800)
C;Genetics:
A;Gene: GDB:NKTR
A;Cross-references: GDB:I37171; OMIM:161565
A;Map position: 3p23-3p21
C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C;Keywords: alternative splicing; lymphocyte
F;60-230/Domain: cyclophilin homology <CYP>

Query Match 42.3%; Score 44; DB 1; Length 1403;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
| : : | : : | : : |
Db 95 CLCSGKGLGKTGCKLKC 112

RESULT 13

B47328
N;Alternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tumor
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 05-Nov-1999
C;Accession: B47328; I77662
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993

A;Title: A cyclophilin-related protein involved in the function of natural killer cells.
A;Reference number: A47328; MUID:93133824; PMID:8421688
A;Accession: B47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1507 <AND>
A;Cross-references: GB:L04289; NID:g192866
A;Note: authors translated the codon AGT for residue 972 as Arg
R;Rinfret, A.; Anderson, S.K.
Mol. Immunol. 30, 1307-1313, 1993
A;Title: IL-2 regulates the expression of the NK-TR gene via an alternate RNA splicing mechanism.
A;Reference number: I57820; MUID:94019422; PMID:8413330
A;Accession: I77662
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 235-237;263-294 <RIN>
A;Cross-references: GB:S65998; NID:g425701; PIDN:AAB28500.1; PID:g425702
C;Genetics:
A;Gene: NK-TR
C;Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C;Keywords: alternative splicing; lymphocyte
F;60-230/Domain: cyclophilin homology <CYP>

Query Match 42.3%; Score 44; DB 2; Length 1507;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
| : : | : : | : : |
Db 95 CLCSGKGLGKTGCKLKC 112

RESULT 14

A28401
aggglutinin isolectin 3 precursor - wheat (fragment)
N;Alternate names: agglutinin isolectin B
C;Species: Triticum aestivum (common wheat)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 24-Nov-1999
C;Accession: A28401; S10045
R;Raikhel, N.V.; Wilkins, T.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 6745-6749, 1987
A;Title: Isolation and characterization of a cDNA clone encoding wheat germ agglutinin.
A;Reference number: A28401
A;Accession: A28401
A;Molecule type: mRNA
A;Residues: 1-186 <RAI>
A;Cross-references: GB:J02961; NID:g170667; PIDN:AAA34257.1; PID:g170668
R;Wright, C.S.; Raikhel, N.
J. Mol. Evol. 28, 327-336, 1989
A;Title: Sequence variability in three wheat germ agglutinin isolectins: products of mult

A;Accession: S10045
A;Molecule type: protein
A;Residues: 1-171 <WRI>
C;Comment: The three isolectins associate randomly into dimers in vivo.
C;Superfamily: wheat agglutinin; hevein chitin-binding domain homology
C;Keywords: blocked amino end; dimer; duplication; glycoprotein; lectin
F;1-171/Product: agglutinin isolectin 3 #status experimental <MAT>
F;1-43/Domain: hevein chitin-binding domain homology <HCB1>
F;44-86/Domain: hevein chitin-binding domain homology <HCB2>
F;87-129/Domain: hevein chitin-binding domain homology <HCB3>
F;130-172/Domain: hevein chitin-binding domain homology <HCB4>
F;172-186/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status
F;3-18,12-24,17-31,35-40,46-61,55-67,60-74,78-83,89-104,98-110,103-117,121-126,132-147,14

Query Match 41.8%; Score 43.5; DB 2; Length 186;
Best Local Similarity 52.9%; Pred. No. 29;
Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 2 CCFSSKDNVKGVTGGKTC 18
| : : | : : | : : |

Db 40 CWTSC-RGQAGGKTC 55

RESULT 15

A44307
 calcineurin regulatory chain 1 - fruit fly (Drosophila melanogaster)
 N:Alternate names: calcineurin beta subunit; calcineurin chain B-1; phosphoprotein phosph
 C:Species: Drosophila melanogaster
 C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change.13-Aug-1999
 C/Accession: A44307
 R:Guerini, D.; Montell, C.; Klee, C.B.
 J. Biol. Chem. 267, 22542-22549, 1992
 A>Title: Molecular cloning and characterization of the genes encoding the two subunits o
 A:Reference number: A44307; MUID:93054551; PMID:1331060
 A:Accession: A44307
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-170 <GUE>
 A:Cross-references: GB:M97215; NID:g157048; PIDN:AAA28411.1; PID:g157049
 A:Note: sequence extracted from NCBI backbone (NCBIP:117113)
 C:Genetics:
 A:Gene: FlyBase:CanB
 A:Cross-references: FlyBase:FBgn0010014
 C:Complex: heterodimer with calcineurin catalytic chain
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop
 F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
 F:18-49/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>
 F:87-119/Domain: calmodulin repeat homology <EF3>
 F:128-160/Domain: calmodulin repeat homology <EF4>
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 41.3%; Score 43; DB 2; Length 170;

Best Local Similarity 41.2%; Pred.No. 32;

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 2 CFSSKDNVGVTKGKTC 18

||: || ||::: |

Db 138 CFADKDEGDKISDFDFC 154

Search completed: October 15, 2003, 17:06:26

Job time : 14.6886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:22:43 ; Search time 7.32934 Seconds
(without alignments)
115.492 Million cell updates/sec

Title: US-09-555-115A-17
Perfect score: 104
Sequence: 1 CCFSSKDNVKGVTGGKTC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	89.4	266	ETC1_STAUA	P01553 staphylococ
2	93	89.4	266	ETC2_STAUA	P34071 staphylococ
3	93	89.4	266	ETC3_STAAM	P23313 staphylococ
4	46	44.2	374	ADHA_HUMAN	P07327 homo sapien
5	46	44.2	374	ADHB_HUMAN	P00325 homo sapien
6	44.5	42.8	212	AGI_HORVU	P15312 hordeum vul
7	44	42.3	246	TRIA_RAT	P32821 rattus norv
8	44	42.3	246	TRYB_RAT	P32822 rattus norv
9	44	42.3	1453	NKCR_MOUSE	P30415 mus musculu
10	44	42.3	1462	NKCR_HUMAN	P30414 homo sapien
11	43.5	41.8	186	AG13_WHEAT	P10969 triticum ae
12	43	41.3	170	CALB_DROME	P48451 drosophila
13	42	40.4	375	ADH1_PANPE	P22797 rana perezi
14	42	40.4	399	HM39_CABEL	Q22812 caenorhabdi
15	41	39.4	139	PA21_TRIOK	P00625 trimeresuru
16	41	39.4	263	ITMA_MOUSE	Q61500 mus musculu
17	41	39.4	368	ADH6_HUMAN	P28130 homo sapien
18	41	39.4	374	ADH_PAPHA	P14139 papio hamad
19	41	39.4	558	ILVD_CAMJE	Q9PJ98 campylobact
20	41	39.4	705	CDCS_YEAST	P32562 saccharomyc
21	41	39.4	905	YD83_HUMAN	Q9P294 homo sapien
22	41	39.4	4377	ANK3_HUMAN	Q12955 homo sapien
23	40.5	38.9	152	YCHJ_ECO57	Q8XDB3 escherichia
24	40.5	38.9	152	YCHJ_ECOLI	P37052 escherichia
25	40.5	38.9	152	YCHJ_SHIFL	P38481 shigella fl
26	40	38.5	242	RS4E_METTH	O26123 methanobact
27	40	38.5	265	RL7A_CHICK	P32429 gallus gall
28	40	38.5	373	ADHS_HORSE	P00328 equus cabal
29	40	38.5	374	ADH1_RABIT	Q03505 oryctolagus
30	40	38.5	374	ADHA_MOUSE	P00329 mus musculu
31	40	38.5	374	ADHA_PERMA	P41680 peromyscus
32	40	38.5	374	ADHE_HORSE	P00327 equus cabal
33	40	38.5	374	ADHG_HUMAN	P00326 homo sapien

RESULT 1
ETC1_STAUA
ID ETC1_STAUA STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SECL).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic toxins";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
J. Biol. Chem. 258:6300-6306(1983).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.

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EMBL: X05815; CAA29260.1; --
PIR: S06356; ENSAC1.
HSSP: P34071; ISE2.
InterPro: IPR006177; Bctr1 tox.
InterPro: IPR006123; Staph/Strep toxin.
InterPro: IPR006126; Staph/Strep tox.
InterPro: IPR006173; Staph tox OB.
Pfam: PF01123; Staph_Strep_tox_C; 1.
Pfam: PF02876; Staph_Strep_tox_C; 1.
PRINTS: PR00279; BACTRLTOXIN.
PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).

P28469 macaca mula
P06757 rattus norv
Q22811 caenorhabdi
P54771 papaver som
Q02482 caenorhabdi
P50528 schizosacch
Q06419 bacterioph
O54990 mus musculu
P35441 mus musculu
P71940 mycobacteri
Q04833 caenorhabdi
P56678 leivirus qui

ALIGNMENTS

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SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59AB986853B CRC64;
Query Match 89.4%; Score 93; DB 1; Length 266;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 2
ETC2 STAAU
ID ETC2 STAAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-2 precursor (SEC2).
GN ETC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2.";
RL Infect. Immun. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; PubMed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Br hm R.D., Tranter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT Staphylococcus aureus reveals a zinc-binding site.";
RL Structure 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
RN [5]
RP J. Mol. Biol. 269:270-280(1997).
CC -!- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
DR PIR; A60114; A60114.
DR PDB; 1STE; 23-DEC-96.
DR PDB; 1SE2; 08-MAR-96.
DR PDB; 1CQV; 19-SEP-01.
DR PDB; 1I4P; 19-SEP-01.
DR PDB; 1I4Q; 19-SEP-01.
DR PDB; 1I4R; 19-SEP-01.
DR PDB; 1I4X; 19-SEP-01.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Stap/Strep_tox.
DR InterPro; IPR006173; Stap tox OB.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.

Pfam: PF01123; Stap_Strp_toxin; 1.
PRINTS: PR00279; BACTELTOXIN
PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
3D-structure.
FT SIGNAL 1 27 ENTEROTOXIN TYPE C-2.
FT CHAIN 28 266
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
FT HELIX 35 37
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 55
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 79
FT TURN 83 86
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 109 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 128 129
FT STRAND 136 139
FT STRAND 142 144
FT TURN 146 147
FT STRAND 149 149
FT HELIX 151 153
FT STRAND 156 164
FT TURN 165 166
FT STRAND 167 176
FT STRAND 178 178
FT STRAND 180 182
FT HELIX 183 198
FT STRAND 208
FT TURN 218 219
FT STRAND 222 226
FT STRAND 232 232
FT HELIX 237 241
FT STRAND 242 246
FT TURN 249 251
FT TURN 252 254
FT STRAND 256 263
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 89.4%; Score 93; DB 1; Length 266;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 3
ETC3 STAAU
ID ETC3 STAAU STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN ETC3 OR SAV2009 OR SA1817.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.

```


[15] X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 MEDLINE=96291846; PubMed=8663387;
 Davis G.J., Boston W.F., Stone C.L., Owusu-Dekyi K., Hurley T.D.;
 "X-ray structure of human beta3beta3 alcohol dehydrogenase. The
 contribution of ionic interactions to coenzyme binding.";
 R.L. J. Biol. Chem. 271:17057-17061(1996).
 CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -1- COPACTOR: Binds 2 zinc ions per subunit.
 CC -1- SUBUNIT: Dimer of identical or nonidentical chains of three types;
 alpha, beta and gamma.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE BETA-1 VARIANT
 MAINLY FOUND IN CAUCASIANS, THE BETA-2 VARIANT IS FOUND IN
 ORIENTALS.
 CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN;
 THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
 PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
 CLASS-V: ADH6.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 family.
 CC
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 CC
 DR EMBL; D00137; BAA00084.1; -.
 DR EMBL; X03350; CAA27056.1; -.
 DR EMBL; M24316; AAB59496.1; -.
 DR EMBL; M24308; AAB59496.1; JOINED.
 DR EMBL; M24309; AAB59496.1; JOINED.
 DR EMBL; M24310; AAB59496.1; JOINED.
 DR EMBL; M24311; AAB59496.1; JOINED.
 DR EMBL; M24312; AAB59496.1; JOINED.
 DR EMBL; M24313; AAB59496.1; JOINED.
 DR EMBL; M24314; AAB59496.1; JOINED.
 DR EMBL; M24317; AAB51884.1; -.
 DR EMBL; X15447; CAA33487.1; -.
 DR EMBL; X15448; CAA33487.1; JOINED.
 DR EMBL; X15449; CAA33487.1; JOINED.
 DR EMBL; X15450; CAA33487.1; JOINED.
 DR EMBL; X15451; CAA33487.1; JOINED.
 DR EMBL; X15452; CAA33487.1; JOINED.
 DR EMBL; X15453; CAA33487.1; JOINED.
 DR EMBL; X15454; CAA33487.1; JOINED.
 DR EMBL; X15455; CAA33487.1; JOINED.
 DR EMBL; L38290; AAB48003.1; -.
 DR EMBL; L38283; AAB48003.1; JOINED.
 DR EMBL; L38284; AAB48003.1; JOINED.
 DR EMBL; L38285; AAB48003.1; JOINED.
 DR EMBL; L38286; AAB48003.1; JOINED.
 DR EMBL; L38287; AAB48003.1; JOINED.
 DR EMBL; L38288; AAB48003.1; JOINED.
 DR EMBL; L38289; AAB48003.1; JOINED.
 DR EMBL; AF153821; AAD37446.1; -.
 DR EMBL; M21692; AAB51592.1; -.
 DR EMBL; AF040967; AAB96912.1; -.
 DR PIR; A23607; DEHUB.
 DR PDB; 1HDX; 31-JAN-94.
 DR PDB; 1HDY; 31-JAN-94.
 DR PDB; 1HDZ; 31-JAN-94.
 DR PDB; 3HUD; 31-JAN-94.
 DR PDB; 1DEH; 08-MAR-96.
 DR PDB; 1HTB; 07-DEC-95.
 DR PDB; 1HSZ; 27-APR-01.
 DR Genew; HGNC:250; ADH1B.
 DR GK; P00325; -.
 DR MIM; 103720; -.

DR GO; GO:0004024; F:alcohol dehydrogenase, zinc-dependent activity; TAS.
 DR GO; GO:0005489; F:electron transporter activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR GO; GO:0006069; P:ethanol oxidation; TAS.
 DR InterPro; IPR002328; ADH_zn_family.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 DR Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 KW Acetylambion; Polymorphism; 3D-structure.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT METAL 46 46 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 97 97 ZINC 2.
 FT METAL 100 100 ZINC 2.
 Query Match 44.2%; Score 46; DB 1; Length 374;
 Best Local Similarity 54.5%; Pred. No. 7.5;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;
 QY 1 CCPS----SKDNVGVKVTGKTC 18
 Db 174 CGFTGYGSANVAVKVTGKTC 195
 RESULT 6
 AGI_HORVU STANDARD; PRT; 212 AA.
 ID AGI_HORVU
 AC P15312;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Root-specific lectin precursor.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lerner D.R., Raikhel N.V.;
 RT "Cloning and characterization of root-specific barley lectin.";
 RL Plant Physiol. 91:124-129(1989).
 CC -1- FUNCTION: CARBOHYDRATE BINDING.
 CC -1- SIMILARITY: Contains 4 chitin-binding domains.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M29280; AAA32969.1; -.
 DR PIR; T05936; T05936.
 DR HSPSP; P10969; 1WGT.
 DR InterPro; IPR001002; Chitin binding_1.
 DR Pfam; PF00187; Chitin_bind_1; 4.
 DR PRINTS; PR00451; CHITINBINDING.
 DR SMART; SM00270; ChtBD1; 4.
 DR PROSITE; PS00026; CHITIN BINDING; 4.
 KW Lectin; Repeat; Chitin-binding; Glycoprotein; Signal;
 KW Pyrolidone carboxylic acid.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 212 ROOT-SPECIFIC LECTIN.
 FT DOMAIN 27 69 CHITIN-BINDING 1.
 FT DOMAIN 70 112 CHITIN-BINDING 2.
 FT DOMAIN 113 155 CHITIN-BINDING 3.
 FT DOMAIN 156 197 CHITIN-BINDING 4.
 FT MOD_RES 27 27 PYROLIDONE CARBOXYLIC ACID
 (BY SIMILARITY).

```
FT DISULFID 29 44 BY SIMILARITY.
FT DISULFID 38 50 BY SIMILARITY.
FT DISULFID 43 57 BY SIMILARITY.
FT DISULFID 61 66 BY SIMILARITY.
FT DISULFID 72 87 BY SIMILARITY.
FT DISULFID 81 93 BY SIMILARITY.
FT DISULFID 86 100 BY SIMILARITY.
FT DISULFID 104 109 BY SIMILARITY.
FT DISULFID 115 130 BY SIMILARITY.
FT DISULFID 124 136 BY SIMILARITY.
FT DISULFID 129 143 BY SIMILARITY.
FT DISULFID 147 152 BY SIMILARITY.
FT DISULFID 158 173 BY SIMILARITY.
FT DISULFID 167 179 BY SIMILARITY.
FT DISULFID 172 186 BY SIMILARITY.
FT DISULFID 190 195 BY SIMILARITY.
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 212 AA; 21209 MW; 8D948245D6B625A5 CRC64;

Query Match 42.8%; Score 44.5; DB 1; Length 212;
Best Local Similarity 52.9%; Pred. No. 7.6;
Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 2 CFSSKDNVGVTKGKTC 18
|:|:| | | | |
Db 66 CYTSK-RCGTQAGKTC 81

RESULT 7
TRYB_RAT
ID TRYB_RAT STANDARD; PRT; 246 AA.
AC P32821;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin V-A precursor (EC 3.4.21.4).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=92165057; PubMed=1537555;
RA Kang J., Wiegand U., Mueller-Hill B.;
RT "Identification of cDNAs encoding two novel rat pancreatic-serine
proteases."
RL Gene 110:181-187(1992).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X59012; CAA41751.1; -.
CC PIR; JQ1471; JQ1471.
CC HSSP; P00763; IDPO.
CC MEROPS; S01.092; -.
CC InterPro; IPR001314; Chymotrypsin.
CC IntraPro; IPR001254; Ser_protease_Try.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
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```
KW Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 24 ACTIVATION PEPTIDE.
FT CHAIN 25 246 TRYPsin V-A.
FT ACT_SITE 64 64 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 31 160 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 133 233 BY SIMILARITY.
FT DISULFID 140 206 BY SIMILARITY.
FT DISULFID 171 185 BY SIMILARITY.
FT DISULFID 196 220 BY SIMILARITY.
FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 246 AA; 26900 MW; 1EB59D88AB1715 CRC64;

Query Match 42.3%; Score 44; DB 1; Length 246;
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVGVTKGKTC 18
|:|:| | | | |
Db 16 FPTEDNDRIVGGYTC 31

RESULT 8
TRYB_RAT
ID TRYB_RAT STANDARD; PRT; 246 AA.
AC P32822;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin V-B precursor (EC 3.4.21.4).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=92165057; PubMed=1537555;
RA Kang J., Wiegand U., Mueller-Hill B.;
RT "Identification of cDNAs encoding two novel rat pancreatic serine
proteases."
RL Gene 110:181-187(1992).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X59013; CAA41752.1; -.
CC PIR; JQ1472; JQ1472.
CC HSSP; P00763; IDPO.
CC MEROPS; S01.093; -.
CC InterPro; IPR001254; Ser_protease_Try.
CC Pfam; PF00089; trypsin; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 24 ACTIVATION PEPTIDE.
FT CHAIN 25 246 TRYPsin V-B.
FT ACT_SITE 64 64 CHARGE RELAY SYSTEM (BY SIMILARITY).
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FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 31 160 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 133 233 BY SIMILARITY.
FT DISULFID 140 206 BY SIMILARITY.
FT DISULFID 171 185 BY SIMILARITY.
FT DISULFID 196 220 BY SIMILARITY.
FT SITE 194 194 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 246 AA; 26819 MW; 1EB899CA1BAB0025 CRC64;

Query Match 42.3%; Score 44; DB 1; Length 246;
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FSSKDNVKGVTGGKTC 18
Db 16 PFTEDNDRIVGGYTC 31

RESULT 9
NKCR_MOUSE STANDARD; PRT; 1453 AA.
AC P30415;
DT 01-APR-1993 (Rel. 25, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NK-tumor recognition protein (Natural-killer cells cyclophilin-
DE related protein) (NK-TR protein).
GN NKTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93133824; PubMed=8421688;
RA Anderson S.K.; Gallinger S., Roder J., Frey J., Young H.A.,
RA Ortaldo J.R.;
RT "A cyclophilin-related protein involved in the function of natural
RT killer cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:542-546 (1993).
RN [2]
RP REVISIONS TO C-TERMINUS.
RC STRAIN=BALB/c; TISSUE=Blood;
RA Anderson S.K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
CC -!- INVOLVED IN THE FUNCTION OF NK CELLS.
CC -!- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.
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CC -----
DR EMBL; L04289; AAA37500.2; ALT_INIT.
DR HSSP; Q27450; 1A33.
DR MGD; MGI:97346; Nktr.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Repeat; Transmembrane.
FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.
FT DOMAIN 222 241 ARG/LYS-RICH (BASIC).
FT DOMAIN 422 459 ARG/LYS-RICH (BASIC).
FT DOMAIN 964 1003 ARG/LYS-RICH (BASIC).
FT DOMAIN 198 273 ARG/SER-RICH.
FT DOMAIN 468 565 ARG/SER-RICH.
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FT DOMAIN 658 812 ARG/SER-RICH.
FT DOMAIN 1303 1453 ARG-SER TANDDEM REPEAT-RICH.
SQ SEQUENCE 1453 AA; 163439 MW; DF1173FF814B283E CRC64;

Query Match 42.3%; Score 44; DB 1; Length 1453;
Best Local Similarity 44.4%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
Db 41 CLCSGEKGLGKTTGKKLC 58

RESULT 10
NKCR_HUMAN STANDARD; PRT; 1462 AA.
AC P30414;
DT 01-APR-1993 (Rel. 25, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NK-tumor recognition protein (Natural-killer cells cyclophilin-
DE related protein) (NK-TR protein).
GN NKTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93133824; PubMed=8421688;
RA Anderson S.K.; Gallinger S., Roder J., Frey J., Young H.A.,
RA Ortaldo J.R.;
RT "A cyclophilin-related protein involved in the function of natural
RT killer cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:542-546 (1993).
RN [2]
RP REVISIONS.
RA Anderson S.K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF A PUTATIVE TUMOR-RECOGNITION COMPLEX.
CC -!- INVOLVED IN THE FUNCTION OF NK CELLS.
CC -!- SUBCELLULAR LOCATION: Membrane-anchored. Attached to the membrane
CC via its N-terminus.
CC -!- SIMILARITY: Contains 1 cyclophilin-like PPIase domain.
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CC -----
DR EMBL; L04288; AAA35734.2; -.
DR EMBL; AF184110; AAD56402.1; -.
DR HSSP; Q27450; 1A33.
DR Genew; HGNC:7833; NKTR.
DR MTM; 163565; -.
DR GO; GO:0004600; F:cyclophilin; TAS.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Repeat; Membrane.
FT DOMAIN 1 176 PPIASE, CYCLOPHILIN-TYPE.
FT DOMAIN 219 240 ARG/LYS-RICH (BASIC).
FT DOMAIN 421 457 ARG/LYS-RICH (BASIC).
FT DOMAIN 970 1010 ARG/LYS-RICH (BASIC).
FT DOMAIN 194 244 ARG/SER-RICH.
FT DOMAIN 466 574 ARG/SER-RICH.
FT DOMAIN 664 814 ARG/SER-RICH.
```

```
FT DOMAIN 1311 1348 ARG-SER TANDEM REPEAT-RICH.
SQ SEQUENCE 1462 AA; 165676 MW; D98A1147763EF527 CRC64;

Query Match 42.3%; Score 44; DB 1; Length 1462;
Best Local Similarity 44.4%; Pred. No. 56;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CFPSSKDNVKGVTGGKTC 18
Db 41 CLCSGEKGLGKTGKLC 58

RESULT 11
AG13_WHEAT
ID AG13_WHEAT STANDARD; PRT; 186 AA.
AC P10969;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Agglutinin isolectin 3 precursor (WGA3) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Raikhel N.V., Wilkins T.A.;
RT "Isolation and characterization of a cDNA clone encoding wheat germ
RT agglutinin.";
RL proc. Natl. Acad. Sci. U.S.A. 84:6745-6749(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA Harata K., Nagahora H., Jigami Y.;
RT "X-ray structure of wheat germ agglutinin isolectin 3.";
RL Acta Crystallogr. D 51:1013-1019(1995).
CC -!- FUNCTION: N-ACETYL-D-GLUCOSAMINE / N-ACETYL-D-NEURAMINIC ACID
CC BINDING LECTIN.
CC -!- SUBUNIT: HOMODIMER, U-SHAPED.
CC -!- MISCELLANEOUS: THE 4 SITES PROPOSED FOR BINDING TO CARBOHYDRATES
CC (N-ACETYL-D-GLUCOSAMINE) OF RECEPTOR MOLECULES ARE ON THE SURFACE
CC OF THE AGGLUTININ MOLECULE.
CC -!- SIMILARITY: THERE ARE THREE VARIANTS OF WGA: VARIABILITY AMONG
CC THEM IS OBSERVED AT A TOTAL OF 10 POSITIONS.
CC -!- SIMILARITY: Contains 4 chitin-binding domains.
CC -----
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CC -----
DR EMBL; J02961; AAA34257.1; -.
DR PIR; A28401; A28401.
DR PDB; 1WGT; 10-JUL-95.
DR PDB; 1K7U; 04-DEC-02.
DR PDB; 1K7V; 04-DEC-02.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00187; Chitin bind_1; 4.
DR ProDom; PD000609; Chitin binding_1; 4.
DR SMART; SMO0270; ChtBD1; 4.
DR PROSITE; PS00026; CHITIN BINDING; 4.
KW Lectin; Repeat; Chitin-binding; Glycoprotein; 3D-structure;
KW Pyrrolidone carboxylic acid.
FT CHAIN 1 171 AGGLUTININ ISOLECTIN 3.
FT PROPEP 172 186
FT DOMAIN 1 43 CHITIN-BINDING 1.
FT DOMAIN 44 86 CHITIN-BINDING 2.
FT DOMAIN 87 129 CHITIN-BINDING 3.

FT DOMAIN 130 171
FT MOD_RES 1 1
FT DISULFID 3 18
FT DISULFID 12 24
FT DISULFID 17 31
FT DISULFID 35 40
FT DISULFID 46 61
FT DISULFID 55 67
FT DISULFID 60 74
FT DISULFID 78 83
FT DISULFID 89 104
FT DISULFID 98 110
FT DISULFID 103 117
FT DISULFID 121 126
FT DISULFID 132 147
FT DISULFID 141 153
FT DISULFID 146 160
FT DISULFID 164 169
FT CARBOHYD 180 180
FT STRAND 4 4
FT HELIX 5 7
FT TURN 8 9
FT STRAND 10 11
FT HELIX 13 15
FT STRAND 17 18
FT TURN 20 21
FT STRAND 24 26
FT HELIX 28 31
FT TURN 33 34
FT STRAND 37 37
FT STRAND 45 45
FT STRAND 47 47
FT HELIX 48 50
FT TURN 51 52
FT STRAND 53 53
FT HELIX 56 58
FT STRAND 60 61
FT TURN 63 64
FT STRAND 66 69
FT HELIX 71 74
FT TURN 76 77
FT STRAND 80 80
FT STRAND 88 88
FT STRAND 90 90
FT TURN 91 95
FT STRAND 96 96
FT HELIX 99 101
FT STRAND 103 104
FT TURN 106 107
FT STRAND 109 112
FT HELIX 114 117
FT TURN 119 120
FT STRAND 123 123
FT TURN 127 128
FT STRAND 133 133
FT TURN 134 138
FT STRAND 139 139
FT TURN 143 144
FT STRAND 146 147
FT TURN 149 150
FT STRAND 153 155
FT HELIX 157 160
FT TURN 162 163
FT STRAND 166 166
SQ SSEQUENCE 186 AA; 18756 MW; 68461A20339378FD CRC64;

Query Match 41.8%; Score 43.5; DB 1; Length 186;
Best Local Similarity 52.9%; Pred. No. 9.6;
Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 2 CFPSSKDNVKGVTGGKTC 18
Db 40 CWTSSK-RCGSQAGGKTC 55
```

CHITIN-BINDING 4.
PYRROLIDONE CARBOXYLIC ACID.

N-LINKED (GLCNAC. . .).

RESULT 12

CALB	DROME	STANDARD;	PRT;	170 AA.
ID	P8451; Q9W4D0;			
AC	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DT	Calcineurin B subunit, isoform 1 (protein phosphatase 2B regulatory subunit)			
DE	CANB OR CANB1 OR CNB1 OR CNB OR CG4209.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93054551; PubMed=1331060;			
RT	Guerrini D., Montell C., Klee C.B.;			
RT	"Molecular cloning and characterization of the genes encoding the two			
RT	subunits of Drosophila melanogaster calcineurin.";			
RT	J. Biol. Chem. 267:22542-22549 (1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=Berkeley;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,			
RA	Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brodstein P., Brottier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser M.,			
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,			
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	"The genome sequence of Drosophila melanogaster.";			
RL	Science 287:2185-2195(2000).			
CC	-1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING			
CC	PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS. IT IS A CALCIUM			
CC	DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY			
CC	SIMILARITY).			
CC	-1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B). THE A COMPONENT IS			
CC	THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM			
CC	SENSITIVITY (BY SIMILARITY).			

DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Signal.
FT SIGNAL 1 16
FT CHAIN 17 139 PHOSPHOLIPASE A2 PLA2-01.
FT ACT_SITE 63 63 BY SIMILARITY.
FT ACT_SITE 105 105 BY SIMILARITY.
FT DISULFID 42 132 BY SIMILARITY.
FT DISULFID 44 60 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 65 139 BY SIMILARITY.
FT DISULFID 66 104 BY SIMILARITY.
FT DISULFID 73 97 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 45 45 (BY SIMILARITY).
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 (BY SIMILARITY).
FT METAL 64 64 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 64 64 (BY SIMILARITY).
FT CONFLICT 39 41 CALCIUM (BY SIMILARITY).
FT CONFLICT 83 83 MISSING (IN REF. 1; BAA08385).
FT CONFLICT 86 86 S -> T (IN REF. 2).
FT CONFLICT 90 90 N -> E (IN REF. 2).
FT CONFLICT 94 95 T -> S (IN REF. 2).
FT CONFLICT 117 117 EN -> ND (IN REF. 2).
FT CONFLICT 120 120 D -> N (IN REF. 2).
FT CONFLICT 135 136 N -> D (IN REF. 2).
SQ SEQUENCE 139 AA; 15584 MW; E0PBB7B688925137 CRC64;
ES -> SE (IN REF. 2).

Query Match 39.4%; Score 41; DB 1; Length 139;
Best Local Similarity 52.9%; Pred. NO. 18;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Oy 1 CCFSSKDNVGVTKGKT 17
Db 59 CCFVHDCYGVTKCNT 75

Search completed: October 15, 2003, 16:58:18
Job time : 8.42934 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 16:46:18 ; Search time 36.8623 Seconds
(without alignments)
126.008 Million cell updates/sec

Title: US-09-555-115A-17

Perfect score: 104

Sequence: 1 CCFSSKDNVGVTKGKTC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	239	2 Q06534	Q06534 staphylococ
2	93	89.4	234	2 Q05X4	Q05X4 staphylococ
3	93	89.4	239	2 Q05157	Q05157 staphylococ
4	93	89.4	239	2 Q03678	Q03678 staphylococ
5	93	89.4	239	2 Q06532	Q06532 staphylococ
6	93	89.4	239	2 Q06531	Q06531 staphylococ
7	93	89.4	239	2 Q06533	Q06533 staphylococ
8	93	89.4	266	16 Q05XJ6	Q05XJ6 staphylococ
9	93	89.4	271	2 Q05XJ6	Q05XJ6 staphylococ
10	87	83.7	239	2 Q06535	Q06535 staphylococ
11	51	49.0	107	4 Q05L82	Q05L82 homo sapien
12	46	44.2	269	6 Q05XN3	Q05XN3 gorilla gor
13	46	44.2	511	16 Q05XJ6	Q05XJ6 fusobacteri
14	45	43.3	505	2 Q05203	Q05203 xanthobacte
15	45	43.3	818	11 Q05201	Q05201 mus musculu
16	44.5	42.8	2533	5 P90589	P90589 paramecium

17	44.5	42.8	2533	5	Q27183	Q27183 paramecium
18	44.5	42.8	2543	5	P90649	P90649 paramecium
19	44	42.3	299	10	Q8LAK6	Q8LAK6 arabidopsis
20	44	42.3	966	11	Q8CBP6	Q8CBP6 mus musculu
21	43	41.3	274	10	Q8STR7	Q8STR7 arabidopsis
22	43	41.3	315	10	Q93VK9	Q93VK9 arabidopsis
23	43	41.3	368	5	Q9XXJ6	Q9XXJ6 caenorhabdi
24	43	41.3	401	10	Q9ARY4	Q9ARY4 oryza sativ
25	43	41.3	953	5	Q815Q5	Q815Q5 plasmodium
26	43	41.3	1022	5	Q9W3E1	Q9W3E1 drosophila
27	42	40.4	120	13	Q9UAD1	Q9UAD1 eptaretus
28	42	40.4	137	5	Q24960	Q24960 giardia lam
29	42	40.4	156	4	Q9HEN7	Q9HEN7 homo sapien
30	42	40.4	161	17	Q8TLN3	Q8TLN3 methanosarc
31	42	40.4	184	2	Q8KVH1	Q8KVH1 uncultured
32	42	40.4	278	2	Q51311	Q51311 nostoc punc
33	42	40.4	283	10	Q48807	Q48807 arabidopsis
34	42	40.4	377	11	Q9QYI9	Q9QYI9 mus musculu
35	42	40.4	430	16	Q9AJU5	Q9AJU5 caulobacter
36	42	40.4	450	6	Q9BGM5	Q9BGM5 ovis aries
37	42	40.4	751	10	Q8RY17	Q8RY17 arabidopsis
38	42	40.4	1487	10	Q9MA08	Q9MA08 arabidopsis
39	41.5	39.9	319	16	Q8UDA2	Q8UDA2 agrobacteri
40	41	39.4	65	16	Q8E531	Q8E531 streptococc
41	41	39.4	65	16	Q8DZG5	Q8DZG5 streptococc
42	41	39.4	97	10	Q9TQ32	Q9TQ32 arabidopsis
43	41	39.4	168	2	Q9RQ17	Q9RQ17 listeria mo
44	41	39.4	230	4	Q96NQ5	Q96NQ5 homo sapien
45	41	39.4	233	11	Q9CRW4	Q9CRW4 mus musculu

ALIGNMENTS

RESULT 1

Q06534 ID Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DC 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect.Immun. 61:4254-4262(1993).
DR EMBL; L13379; AAA26623.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strept tox.
DR Pfam; PF01123; Staph_Strep_toxin; OB.
DR Pfam; PF02876; Staph_Strep_toxin; C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 100.0%; Score 104; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVTKGKTC 18

|||||

93 CCFSSKDNVGVTKGKTC 110

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RESULT 2
Q9R5X4 ID Q9R5X4 PRELIMINARY; PRT; 234 AA.
AC Q9R5X4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A.; Lyon J.D.; Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7BA5FB9810052 CRC64;

Query Match 89.4%; Score 93; DB 2; Length 234;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
DB 88 CYFSSKDNVGVGTGGKTC 105

RESULT 3
Q05157 ID Q05157 PRELIMINARY; PRT; 239 AA.
AC Q05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=95-011195;
RA Edwards V.M.; Deringer J.R.; Callantine S.D.; Deobald C.F.;
RA Berger P.H.; Kapur V.; Stauffacher C.V.; Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
Staphylococcus intermedius pyoderma isolates.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 239
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 89.4%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
DB 93 CYFSSKDNVGVGTGGKTC 110

RESULT 4
Q53678 ID Q53678 PRELIMINARY; PRT; 239 AA.
AC Q53678;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C.; Lyon J.D.; Roberson J.R.; Luper M.; Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 239
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 89.4%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCFSSKDNVGVGTGGKTC 18
| | | | | | | | | | | | | | | | | |
DB 93 CYFSSKDNVGVGTGGKTC 110

RESULT 5
Q06532 ID Q06532 PRELIMINARY; PRT; 239 AA.
AC Q06532;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=740N;
RA MEDLINE=94011313; PubMed=8406814;
RA Marr J.C.; Lyon J.D.; Roberson J.R.; Luper M.; Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bctrl tox.
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DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 89.4%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
Db 93 CYFSSKDNVKGVTGGKTC 110

RESULT 6
Q06531
ID Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RC STRAIN=4446;
RA MEDLINE=94011313; PubMed=8406814;
RT "Characterization of novel type C staphylococcal enterotoxins: biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSP; P34071; ISTE.
DR InterPro; IPR006177; Bctrl toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 89.4%; Score 93; DB 2; Length 239;
Best Local Similarity 94.4%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
Db 93 CYFSSKDNVKGVTGGKTC 110

RESULT 8
Q8XJ6
ID Q8XJ6 PRELIMINARY; PRT; 266 AA.
AC Q8XJ6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RC MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR InterPro; IPR006177; Bctrl toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 89.4%; Score 93; DB 16; Length 266;
Best Local Similarity 94.4%; Pred. No. 2.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVKGVTGGKTC 18
Db 120 CYFSSKDNVKGVTGGKTC 137

RESULT 7
Q06533
ID Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;

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RESULT 9
Q9FOL6 PRELIMINARY; PRT; 271 AA.
AC Q9FOL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Staphylococcus aureus enterotoxin C-bovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901;
RA Fitzgerald J.R., Mondy S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70(2001).
DR EMBL; AF217235; AAG29599.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strp_toxin; 1.
DR Pfam; PF02876; Staph_strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 89.4%; Score 93; DB 2; Length 271;
Best Local Similarity 94.4%; Pred. No. 2.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVGVKVTGGKTC 18
| | | | | | | | | | | | | | | |
Db 125 CYFSSKDNVGVKVTGGKTC 142

RESULT 10
Q06535 PRELIMINARY; PRT; 239 AA.
AC Q06535;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 909;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; U13377; AAA26621.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strp_toxin; 1.
DR Pfam; PF02876; Staph_strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

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FT NON_TER 1
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

Query Match 83.7%; Score 87; DB 2; Length 239;
Best Local Similarity 88.9%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFFSSKDNVGVKVTGGKTC 18
| | | | | | | | | | | | | | | |
Db 93 CYFSSKDNVGVKVTGGKTC 110

RESULT 11
Q9UL82 PRELIMINARY; PRT; 107 AA.
AC Q9UL82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035032; AAD56268.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11445 MW; 52F0CC1AB26821DC CRC64;

Query Match 49.0%; Score 51; DB 4; Length 107;
Best Local Similarity 56.2%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CFFSSKDNVGVKVTGGKT 17
| | | | | | | | | | | | | |
Db 87 CYSASDNNGRVFGGT 102

RESULT 12
Q8WNN3 PRELIMINARY; PRT; 269 AA.
AC Q8WNN3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alcohol dehydrogenase 1 (Fragment).
GN ADH1
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Stauffer R.L., Walker A., Ryder O., Lyons-Weiler M., Hedges S.B.;
RT "Human and ape molecular clocks and constraints on paleontological
RT hypotheses.";
RL J. Hered. 92:0-0(2001).

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CC -|- COFACTOR: ZINC (BY SIMILARITY).
 DR EMBL; AF354624; AAL56229.1; -;
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; adh_zinc; 1.
 DR PROSITE; PS00059; adh_zinc; 1.
 KW Metal-binding; Oxidoreductase; Zinc.
 FT NON TER 1
 FT NON TER 269
 SQ SEQUENCE 269 AA; 28674 MW; 1F2D3C01A5F4F094 CRC64;

Query Match 44.2%; Score 46; DB 6; Length 269;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 12; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

Qy 1 CCFSSKDNVGVGGKTC 18
 ||| | | | | | | | | |
 Db 169 CGFSTGYGSANVAKVPGSTC 190

RESULT 13

Q8RI66 PRELIMINARY; PRT; 511 AA.

AC Q8RI66;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cysteine permease.
 GN FN1747.

OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.

NCBI_TaxID=76856;

[1]

SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

REMEDLINE=21886394; PubMed=11899109;

RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

RA Larsen N., D'Souza M., Walunas T., Busch G., Haselkorn R.,

RA Fontstein M., Kyripides N., Overbeek R.;

RT "Genome sequence and analysis of the oral bacterium Fusobacterium

RT nucleatum strain ATCC 25586."

RL J. Bacteriol. 184:2005-2018(2002).

DR EMBL; AE010479; AAL93862.1; -;

DR InterPro; IPR002293; AA/rel_permease1.

DR InterPro; IPR001463; Na/Ala_symport.

DR Pfam; PF01235; Na_Ala_symp; 1.

DR TIGRFAMs; TIGR00835; agcs; 1.

DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.

KW Complete proteome.

SQ SEQUENCE 511 AA; 56196 MW; 03D8A2859135EF3D CRC64;

Query Match 44.2%; Score 46; DB 16; Length 511;
 Best Local Similarity 47.1%; Pred. No. 38;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVGGKTC 17
 | : ||| | : |||
 Db 128 CYRSKDETGRYFGGST 144

RESULT 14

O50203 PRELIMINARY; PRT; 505 AA.

AC O50203;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Chloroacetaldehyde dehydrogenase.
 GN ALDA.
 OS Xanthobacter autotrophicus.

OG Plasmid linear plasmid pXAU1.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Xanthobacter.
 OX NCBI_TaxID=280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GJ10;
 RX MEDLINE=98172729; PubMed=9511738;
 RA Bergeron H., Labbe D., Turmel C., Lau P.C.;

RT "Cloning, sequence and expression of a linear plasmid-based and a
 RT chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
 RT in Xanthobacter autotrophicus GJ10.";
 RL Gene 207:9-18(1998).
 CC -|- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
 DR EMBL; AF029733; AAC13641.1; -;
 DR HSP; P05091; ICW3.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Oxidoreductase; Plasmid.
 SQ SEQUENCE 505 AA; 54945 MW; AD6A9EDB0297BB04 CRC64;

Query Match 43.3%; Score 45; DB 2; Length 505;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 DNVGKVTGGKTC 18
 ||| | | | | | | | | |
 Db 36 DNTSPVTGGKIC 47

RESULT 15

Q91201 PRELIMINARY; PRT; 818 AA.

AC Q91201;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical 90.9 kDa protein (Fragment).

GN I110015K06RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010333; AAH10333.1; -;

DR MGD; MGI:1915760; I110015K06RIK.

KW Hypothetical protein.

FT NON TER 1

SQ SEQUENCE 818 AA; 90949 MW; A5128C8692BB7663 CRC64;

Query Match 43.3%; Score 45; DB 11; Length 818;
 Best Local Similarity 53.8%; Pred. No. 92;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCFSSKDNVGVGGKTC 13
 ||| | : : |||
 Db 396 CCRSNDSEIGKVT 408

Search completed: October 15, 2003, 17:04:16
 Job time : 38.8623 secs

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